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            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
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                                                                                                                             US-10-088-639A-2_COPY_158_162
25
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Listing first 150 summaries
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AAM57202
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ALIGNMENTS

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Human, ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemctactic; chemckinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                         Human ORF2586 protein, SEQ ID NO:5172.
                 ABP33613 standard; protein; 69 AA
                                                                                                08-JUL-2002 (first entry)
                                                          ABP33613;
ABP33613
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Compared ORF (open reading free) 1-4334, and sequences ABM75054ABM79587 represent cDNAs encoding them. The invention also encompasses
DAN79587 represent cDNAs encoding them. The invention also encompasses
DAN79587 represent cDNAs encoding them. The invention also encompasses
DAN79587 represent cDNAs encoding them. The invention also encompasses
CC feetred to as ORFX proteins, polymucleotides at least 85% identical to
DAN79587 nucleic acid sequences, vectors and host cells comprising ORFX
DAN79587 nucleic acid sequences, vectors and host cells comprising ORFX
DAN79587 nucleic acid sequences, vectors and host cells comprising ORFX
DAN79587 nucleic acid sequences, vectors and host cells comprising ORFX
DAN79587 compression or company of ORFX proteins, antibods of screening individuals for a predisposition or compression or compression activities, such as cytokine, cell proliferation, company of screening individuals for a predisposition to an CC ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activity, hamome medulation, nammatopolesis regulation, coll differentiation, immune medulation, intended the certivity, coll disposition activity, coll and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or bodily characteristics, fertility and behaviour. ORFX proteins, colliferative disorders such as poriasis and benign tumours, colliferative disorders such as poriasis and benign tumours, colliferative disorders such as poriasis and Alabeimer's disease, and infectious diseases caused by viral, bacterial, characterial, and other proliferative minions of the produce transgenic animals of promoters of primers and probes, in the detection of ORFX genomic sequences or transcripts in the identification and cloning of homologous currence of primers and probes, in the detection of produce transgenic animals any additionally be used to produce transgenic animals and animals and inference of primers and infection and inference cardiovascular disease; immune system disorder; organ transplantation; itsue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; enteroprotective; antidentoscalerotic; anticoaquiant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ Sequences ABP31028-ABP35561 represent 4534 novel human proteins Claim 10; Page 1545; 2508pp; English. 24-MAY-2001; 2001WO-US017076. 24-MAY-2000; 2000US-0206690P. Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. WPI; 2002-106200/14. N-PSDB; ABN77639. transplantation. #0200190366-A2. Homo gapiens. 29-NOV-2001.

Sequence 69 AA;

Gaps ö 100.0%; Score 25; DB 5; Length 69; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 5; Conservative

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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 76 AA;
                                                   WO200157273-A2
                                   Homo sapiens.
                                                                                                              26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                          brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system epilepses such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarxay; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 29307.
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                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human
                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
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                                                         AAM57202 standard; protein; 76 AA.
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                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                           30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0063236.
21-SEP-2000; 2000US-02364697P.
27-SEP-2000; 2000US-0236359P.
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SSVMH
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                                                                                                                                                        Homo sapiens.
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, compitaing one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Asc1340. Asc59590 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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Claim 20; Page 238; 1963pp; English.
                                             05-FEB-2001; 2001WO-US003800.
                                                   03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                   Tang YT, Liu C, Drmanac RT;
                                                                          2001-457740/49.
                                                             (HYSE-) HYSEQ INC.
                                                                             N-PSDB; ABA08992
                                                                                                                                                                                                                                   Sequence 96 AA;
                                WO200157188-A2.
                         Homo sapiens.
                                      09-AUG-2001
                                                                                           and cancer
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proteosome analysis; cell profiferative disorder; arteriosclerosis; cancer; neurological disorder; Huntington's disease; Parkinson's disease; cardiovascular disorder; atherosclerosis; congestive heart failure; gastrointestinal disorder; gastrilis; nausea; autoimmune; anaemia; inflammatory disorder; acquired immunodeficiency syndrome; AlDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a human G-protein coupled receptor, GCREC-5 protein. The GCRECs are used for treating or preventing disorders associated with decreased expression of functional GCREC, and for identifying specific agonists and antagonists, also binding agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human G-protein coupled receptors, useful for treatment and diag
of e.g. cell proliferation, also screening for specific modulators,
related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R, Khan F)
Hafalia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Visual pigments retinal binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81. .97
/label= G-protein_coupled_receptor_domain
                                              Indels
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Lal P, Au-Young J, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; G-protein coupled receptor; GCREC; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28. .112
'note= "Mature human GCREC-5 protein"
                     Pred. No. 1.6e+02;
Mismatches 0;
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/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein coupled receptor, GCREC-5.
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                     AAE12026 standard; protein; 112 AA.
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2000US-0199084P.
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                                                 5; Conservative
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                     Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                    39 SSVMH 43
                                                                                                  1 SSVMH 5
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Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                         AAE12026;
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                                                                                                                                                                                                                                 RESULT 5
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                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                 Thrention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or nucleotides or antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may chave various activities; including cytokine, cell proliferation or cell differentiation activities; including cytokine, cell proliferation or cell municomodulatory activity; activin- or inhibin-related activities; chromolyric activities; haemostatic, thrombotic or thrombolyric activities; reaceptor or ligand activities; or metastasis.

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolyric activities; reaceptor or ligand activities; or metastasis.

CC thrombolyric activities; receptor or ligand activities; or metastasis.

CC the invention are useful for preventing or metastasis.

CC conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders (e.g., myeloid or lymphoid cell cancers), chronic inflammatory conditions (e.g., acthoric inflammatory conditions (e.g., myeloid or lymphoid cell carcatic erconding them) may be used to promote wound tracial infections in addition to immune disorders (e.g., of burns, incisions and ulcers), while those with toward for unclaid activity may be used in cell cultures to summart or real growth. For example, such polypeptides may be used to neuroeppthelial and the manipulate stem cells in culture to give prese to neuroeppthelial and event or real preserved to neuroeppthelial and promote cell growth. For example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                   atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antisarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiuloer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening techniques. The present sequence represents a novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 4; Length 96;
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and diagnosis

Query Match

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for processome analysis. Disorders that can be treated include cell proliferative disorders, e.g., arteriosclerosis and cancer, neurological disorders, e.g., Huntington's disease and Parkinson's disease, cardiovascular disorders, e.g., atherosclerosis and congestive heart failure, gastrointestinal disorders, e.g., acquired immunodeficiency syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and obesity and viral infections. Nucleic acids that encode GCREC are used for identifying agents that alter its expression, for assessing toxicity of test compounds, and as sources of primers and probes for diagnostic.
                                                                                                                                                                                                                                                                                                                          sequences. They can also be used in gene therapy, for chromosomal mapping, and for recombinant production of GCREC. The antibodies are useful for diagnosis and monitoring of diseases associated with GCREC expression, for detecting and purifying GCREC, and as therapeutic agents
modulators. They can also be used for generating specific antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                       and for drug screening
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Seguence 112 AA;

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Gaps
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100.0%; Score 25; DB 4; Length 112; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indel8
                             5; Conservative
                lest Local Similarity
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  Query Match
                             Matches
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SSVMH 59 8

AAG72494 standard; protein; 117 AA. AAG72494;

30-JUL-2001 (first entry)

Human OR-like polypeptide query sequence, SEQ ID NO: 2175.

Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.

Homo sapiens.

WO200127158-A2

06-OCT-2000; 2000WO-US027582. 19-APR-2001

08-OCT-1999; 99US-0158615P. 24-FEB-2000; 2000US-0184809P.

(DIGI-) DIGISCENTS. (YEDA) YEDA RES & DEV CO LTD.

New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists. WPI; 2001-290713/30.

Fuchs T,

Glusman G,

Lancet D,

Smith D,

Bellenson J,

Example 6; Page 1464-1465; 1857pp; English.

The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents of odour receptors the construction of a scent representation (also called scent fine enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different

The present sequence is a polypeptide encoded by one of 344 newly mined human genee. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these

Sequence 117 AA;

individuals

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primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
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                                                                                                                                                                  100.0%; Score 25; DB 4; Length 117; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Human olfactory receptor polypeptide, SEQ ID NO: 1476.
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                                                                                                                                                                                                                                                                                                                          AAG71795 standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                         Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2001
                                                                                                               individuals
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                                                                                                                                                                                                                                                                                               RESULT 7
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed corpus (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupylepptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forgenetic disorders or other traits to assess bloidversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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0
                  Score 25; DB 4; Length 117;
Pred. No. 2e+02;
); Mismatches 0; Indels
                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #10756.
                                                                                                                                                                                                                   ABG10765 standard; protein; 133 AA.
                    100.0%;
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Query Match
Best Local Similarity 100...
5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                            63 SSVMH 67
                                                                                           SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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100.0%; Score 25; DB 4; Length 133;

Query Match

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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid operably linked to chosen from 364 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) bacteraemia, endocarditis, wounds and abdominal pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faccine infections. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    Gaps
                                                                                                                                                                                                                                                                                                                    Vaccine, urinary tract infection; bacteraemia; endocarditis; wound;
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                  Indels
 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 7091; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                 E. faecium protein sequence SEQ ID 7091.
                                                                                                                                                                               ADC97464 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00107532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0051571P.
98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                        abdominal-pelvic infection
                                                                                                                                                                                                                                                  (first entry)
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                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecium.
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N-PSDB; ADC93810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doucette-Stamm LA,
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Best Local Similarity
Matches 5; Conserv
Best Local Similarity
Matches 5; Conserv
                                                                                       12 SSVMH 16
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                                                      1 SSVMH 5
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14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                             US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1998;
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                                                                                                                                                                                                                 ADC97464;
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                                                                                                                                            RESULT 9
ADC97464
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    167
    /note= "residues Xaa are encoded by internal stop codons"

                                                                                                                            G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine; cervical; stomach; rectal; cytostatic; vaccine; cell function regulator; human; prostate homologue of olfactory receptor-1.
                                                                                                                                                                                                                                                                                                                                                                                         Novel gene designated PHOR-1, a G-protein-coupled receptor up-regulated in prostate cancer, useful as diagnostic marker and therapeutic target for cancers of prostate, kidney, uterus.
                                                                                                                                                                                                                                                                                                                                 Jakobovits A, Faris M, Hubert RS;
                                                                                                          Amino acid sequence of AI138218, a PHOR-1 family member.
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 22; 139pp; English.
                                               AAB85005 standard; protein; 167 AA.
                                                                                                                                                                                                                                                                      05-OCT-2000; 2000WO-US027543.
                                                                                                                                                                                                                                                                                         99US-0157902P
                                                                                      06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                Afar DEH, J
Saffran DC;
                                                                                                                                                                                                                                                                                                            (UROG-) UROGENESYS INC.
                                                                                                                                                                                                                                                                                                                                                             2001-367230/38.
                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF83882
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 167 AA;
 SSVMH
                                                                                                                                                                                                                               WO200125434-A1
                                                                                                                                                                                                                                                                                                                               Raitano AB, 1
Mitchell SC,
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                         05-OCT-1999;
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                                                                   AAB85005;
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The invention relates to a novel G-protein-coupled receptor up-regulated in prostate cancer, termed PHOR-1. The encoding cDNA is contained in plasmid designated plothsAll deposited with ATCC as Accession No.PTA-312. PHOR-1 polypeptides and polymucleotides are useful for diagnosing the presence of cancer, especially prostate, kidney, uterine, cervical, stomach or rectal cancer by determining and comparing the level of the protein or mRNA expression in test and mormal tissue samples. Pharmaceutical compositions comprising PHOR-1 is useful for treating cancer. PHOR-1 proteins are useful for identifying ligands and other segents and cellular constituents that binds to PHOR-1 gene product and for generating antibodies which are useful in diagnostic, prognostic and imaging methodologies and for the treatment of prostate cancer. Cell lines expressing PHOR-1 are useful for identifying protein-protein. interactions mediated by PHOR-1. The present sequence represents the amino acid sequence of AI138218, a PHOR-1 family member

Gaps ö 100.0%; Score 25; DB 4; Length 167; Similarity 100.0%; Pred. No. 2.8e+02; 5; Conservative 0; Mismatches 0; Indels Local Similarity Query Match Best Loca Matches

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ABR43245 standard; protein; 248 AA ABR43245

(first entry) 07-JUL-2003

Human PMMM-6 protein SEQ ID NO:6.

Human; protein modification and maintenance molecule; PMMM; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.

WO2003025131-A2.

27-MAR-2003

13-SEP-2002; 2002WO-US029221.

2001US-0322196P. 2001US-0324134P. 2001US-0327233P. 2001US-0346198P. 05-OCT-2001;

26-OCT-2001;

02-NOV-2001; 2001US-0343980P. 09-NOV-2001; 2001US-0348887P. 16-NOV-2001; 2001US-0332423P. 2001US-0334145P 28-NOV-2001;

28-NOV-2001;

2001US-0334229P. 2001US-0337451P. 2002US-0351928P. 2002US-0366837P 21-MAR-2002; 06-DEC-2001; 25-JAN-2002;

(INCY-) INCYTE GENOMICS INC.

Chawla NK, Warren BA, Tang YT, Elliott VS; Li JX, Griffin JA, Gietzen KJ, Yang J, Lu DAM; Duggan BW, Richardson TW, Lee SY, Ramkumar J, Becha SD; Swarnakar A, Tran UK, Kable AE, Hafalia AJA, Khare R; Chawla NK, Li JX, Marquis JP, Li Emerling BM, Duc Lehr-Mason PM, Sprague WW,

WPI; 2003-354597/33. N-PSDB; ACC59964.

New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or infections.

Claim 1; Page 213-214; 270pp; English.

ACC59959 to ACC59989 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated remaintenance molecule proteins given in ABR43240 to ABR43270, designated PMM-11 (1). (1) have cytostatic, antiatioscritical matriconvulsant, nootropic, neuroprotective, carboroprotective, anti-HIV, antiallergic, antinflammatory and thyromimetic activities, and can be useful in gene therapy. The PWMM polypeptides and polymucleotides are useful in diagnosing, treating apprehension or overexpression of PMMM, such as sociated with the decreased expression or overexpression of PMMM, such as call proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) cisorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMMM. The PMMMs or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein

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The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alpha6beta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premallignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                              158 SSVMH 162
                                                                                                                                                                                                                                        1 SSVMH 5
                                                                                                                                                                      Sequence 249 AA;
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12-DEC-2000;
17-JAN-2001;
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22-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2000;
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15-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2002
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Colman SD,
                                                                                                                                                                                             Query Match
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Matches
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ABG66935
  X88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                    "Complementarity determining region (CDR) 1 of the
                                                                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complementarity determining region (CDR) 3 of the
                                                                                                                                                                                                                                                                                                                                                                                                     "Complementarity determining region (CDR) 2 of
chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complementarity determining region (CDR) 1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 of
                                                                   Gaps
interactions, drug-target interactions, and gene expression profiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tordsson MJ, Kearney PP;
                                                                                                                                                                                                                                                            Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                                                                                                                        An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .77. .193
note= "Complementarity determining region (CDR)
                                                                   ö
                                            Length 248;
                                                                  Indels
                                            100.0%; Score 25; DB 6; L
100.0%; Pred. No. 4.3e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                      AAB68087 standard; protein; 249 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              110. .127
/note= "linker"
158. .162
/note= "Compleme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ight chain"
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                                                                   Conservative
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/note= "
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88. .9
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N-PSDB; AAF84797.
                                                       Local Similarity
nes 5; Conser
                                                                                                              234 SSVMH 238
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                       Sequence 248 AA
                                                                                          1 SSVMH
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                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                             AAB68087;
                                              Query Match
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                                                                                                                                                                                                                                                                                                                                               Key
Region
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                                                                  Matches
                                                                                                                                                 RESULT 12
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                                                                                                                                                                                        Gaps
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Ballinger RA, Padigaru M, Wolenc AR, Shenoy SG;
                                                                                                                         Length 249;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel G-protein coupled receptor related protein #12.
                                                                                                                         100.0%; Score 25; DB 4; I
100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG66935 standard; protein; 253 AA.
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2001US-0263340P.
2001US-0264118P.
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2001US-0269031P.
2001US-0308203P.
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tumour deposits in humans
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RESULT 15
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12) polypeptide, especially an olfactory receptor. GPCRX polypeptides are
12) useful for identifying an agent that binds to the polypeptide and for
13 identifying a candidate substance or ligand molecules interacting with an
14 confectory receptor polypeptide. The polypeptide, (I) and (II) are also
15 consciolated and diseases and disorders related to cell signal
16 processing and metabolic pathway modulation e.g. cardiomyopathy,
17 catheroscierosis and diabetes, and developmental diseases, immune
17 corriconeurogenic disease, signal transduction pathway disorders,
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, acute
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, acute
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, ulcers,
19 corriconeurogenic disorders, genetic disorders,
10 cheart failure, urinary retention, osteoporosis, Crohn's disease, ulcers,
20 clertility, Panorealtiis, Hyperthyroidism and Endometriosis GPCRX
21 certility, Panorealtiis, Hyperthyroidism and Endometriosis GPCRX
22 certility, panorealtiis, Hyperthyroidism and Endometriosis GPCRX
23 considers are also useful for identifying a cell or tissue type in a
23 biology. Cells comprising (I) are useful for producing non-human
23 cranspanic animals for studying the function and/or activity of GPCRX
24 protein and for identifying and/or evaluating modulators of GPCRX
25 protein and for identifying and/or evaluating modulators of GPCRX
27 receptor described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Gerlach V, Gangolli EA, Macdougall JR, Smithson G; stone DJ, Gunther E, Ellerman K, Grosse WM, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. gossypii cell wall/cytoskeleton oligo 103 protein fragment SEQ ID 18.
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                                                                                                                                                                 Novel G protein coupled receptor especially olfactory receptor polypeptides and nucleic acids for diagnosing and treating atherosclerosis, cardiomyopathy and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wall construction, cytoskeleton construction; vitamin B2; supplement; Oligo 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 5; Length 253; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB47696 standard; protein; 259 AA
                                                                                                                                                                                                                                                                   Claim 1, Page 48; 309pp; English.
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22-AUG-2001; 2001DE-01041058.
22-AUG-2001; 2001DE-01041060.
22-AUG-2001; 2001DE-01041061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003 (first entry)
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                         Stone DJ, (
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eremothecium gossypii
                                                                                               2002-500205/53.
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                                                                                             WPI; 2002-5002U5/
N-PSDB; ABK95453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003018626-A2
  Edinger SR,
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                                                  Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199
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110 ADB4

AC ADB4

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This invention describes novel polynucleotides isolated from Ashbya gossypii (also known as Eremothecium gossypii), that encode a protein associated with construction of the cell wall and/or cytoskeleton. Modulating the construction of the cell wall cytoskeleton, especially such that the cells are stabilised, improves microbial production of Vitamin B2, a human and animal food supplement. This sequence represents a fragment of Oligo 103 which encodes an A. gossypii cell wall/cytoskeleton associated protein.Oligo 103 encodes a homologue of a Saccharomyces cerevisiae actin overexpression associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide from Ashbya gossypii, useful for increasing microbial production of Vitamin B2, encodes protein involved in construction of cell wall and cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metalloprotease; 65649; astacin; proteolytic; gene therapy; apoptosis; metastasis; wound healing; endometrial cycling; tumour cell invasion; bone eremodelling; neurological; cardiovascular; endothelial; cytostatic; immune; bone metabolism; neuroprotective; nootropic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 7; I
100.0%; Pred. No. 4.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 65649 metalloprotease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 90-91; 124pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA023391 standard; protein; 282 AA.
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2001DE-01041064.
2001DE-01041065.
2001DE-01041066.
2002DE-01009827.
2002DE-01016028.
                                                                                                                                                                                            2002DE-01021918.
2002DE-01021919.
2002DE-01021921.
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                                                                                                                                                                     2002DE-01021906
                                                                                                                                                                                                                                                                                     2002DE-01025411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.

Best Local Similarity 100.

Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-332820/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADB47695
                                                                                                                                                                                                                                                                                                                                       BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003022212-A1
                                                                                  06-MAR-2002;
11-APR-2002;
11-APR-2002;
                                                                                                                                                                                                  16-MAY-2002;
                                                                                                                                                                                                                          16-MAY-2002;
16-MAY-2002;
                                                                                                                                                                                                                                                                                     07-JUN-2002;
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                          22-AUG-2001;
                                                                                                                                                                     16-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA023391;
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WO200216566-A2
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                                      16-MAY-2002;
                         11-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB07687;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel human nucleic acid molecules that encode a metalloprotease family member designated the 65649 protein. The 65649 cativate growth factors, degrade polypepides and process extracellular proteins. Typically requiring zinc for catalysis, this enzyme can be used for drug screening, chromosome mapping, tissue typing and in forensis. Collogy. Furthermore, gene therapy using the 65649 molecules may be used to modulate tumour cell invasion, metastasis, tissue or organ integrity, wound healing, endometrial revoling, hair follicle cycling, bone remodelling, ovulation, embryonic development, and apoptosis. These may further be used to control or prevent e.g. cellular proliferative and/or differentiative disorders, as well as neurological, cardiovascular, endochelial and immune disorders, and bone metabolism disorders. Compositions of 65649 can therefore be described as cytostatic, reuroprotective, nootropic and immunosuppressive. The nucleic acids, proteins, and antibodies of the invention are useful in screening assays, proteins, and antibodies of the invention are useful in screening assays, proteins we medicine, and in therapeutic and prophylactic treatment. This polypeptide sequence is the human 65649 metalloprotease of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                     New human metalloprotease, 65649, polypeptides and polynucleotides, useful for modulating e.g. tumor cell invasion or metastasis, tissue or organ integrity, wound healing, endometrial cycling, hair follicle cycling, or ovulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. gossypii cell wall/cytoskeleton oligo 103 protein SEQ ID 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wall construction; cytoskeleton construction; vitamin B2; supplement; Oligo 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 25; DB 7; Length 282; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB47698 standard; protein; 286 AA.
                                                                                                                                                    Claim 17; Page 37; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2001; 2001DE-01041060.
22-AUG-2001; 2001DE-01041061.
22-AUG-2001; 2001DE-01041063.
22-AUG-2001; 2001DE-01041064.
22-AUG-2001; 2001DE-01041065.
22-AUG-2001; 2001DE-01041065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-2002; 2002WO-EP009355
(MILL-) MILLENNIUM PHARM INC.
                                                 WPI; 2003-584995/55.
N-PSDB; AAL56808, AAL56809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eremothecium gossypii.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 282 AA;
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                         Curtis RAJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell
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This invention describes novel polynuclectides isolated from Ashbya gossypii (also known as Eremothecium gossypii), that encode a protein associated with construction of the cell wall and/or cytoskeleton. Modulating the construction of the cell wall/cytoskeleton, especially such that the cells are stabilised, improves microbial production of Vitamin B2, a human and animal food supplement. This sequence represents an A. gossypii cell wall/cytoskeleton associated protein encoded by Oligo overexpression associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide from Ashbya gossypii, useful for increasing microbial production of Vitamin B2, encodes protein involved in construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, protease peptide, structural protein, extracellular reticulum, transgenic, gene therapy, enzyme.
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                                                                                                                                                                                                                                                                              Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 7; 100.0%; Pred. No. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 94-95; 124pp; German.
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                                                                            16-MAY-2002; 2002DE-01021918.
16-MAY-2002; 2002DE-01021919.
16-MAY-2002; 2002DE-01021921.
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2002DE-01016028
                          2002DE-01016034
                                                       2002DE-01021906
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                                                                                                                                                               07-JUN-2002; 2002DE-01025411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell wall and cytoskeleton.
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N-PSDB; ABA95224, ABA95225.
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protease peptide
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                                                                                                                                                                                                                                                                                                                                      WPI; 2003-332820/31
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"Casein kinase II (CK2) phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-2002; 2002WO-US015025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-2001; 2001US-0291940P.
13-MAY-2002; 2002US-00143575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-148472/14.
N-PSDB; AAD53974, AAD53975.
                                                                                                                                                                               268. .271
                        228. .231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zong JM, Yan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                              WO200295049-A2
                        Modified-site
                                                                                                   Modified-site
                                                                                                                                        Modified-site
                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
    장. 쉽
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                           The invention relates to an isolated human protease peptide. The peptide cleaves structural proteins in the extracellular reticulum. The encoding nucleic acids are useful as primers and probes e.g. in detection assays and in the polymerase chain reaction, genotyping, antisense therapy, and gene therapy. They are also used in recombinant vectors, expressing the protease peptide, and constructing recombinant cells and animals. Vectors comprising the nucleic acids are used to transform a host cell which can modulators are useful for treating a disease or condition mediated by a human protease protein. The protease peptide, antibodies and human protease protein. The present sequence represents the human protease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20. 30
/note= "Prokaryotic membrane lipoprotein lipid attachment
An isolated human protease peptide, for identifying modulators of its function to treat diseases and conditions mediated by protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; therapeutic; drug screening; immune response; pharmacogenomic analysis; tissue typing; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11. .93
'note= "Protein kinase C (PKC) phosphorylation site"
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:e= "Casein kinase II (CK2) phosphorylation site"
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note= "Casein kinase II (CK2) phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorylation site"
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195. .198
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                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 5; Length 300; Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109. .111
/note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152. .157 _ _
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-myristoylation site"
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te= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Casein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE35322 standard; protein; 300 AA
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/label= Helix 1
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                                                         Claim 1; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVMH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                     Sequence 300 AA;
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XXX AAE3

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XXX HOMM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ಹ
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note= "Casein kinase II (CK2) phosphorylation site"
                                                                  site"
                                                                                                                                                                                                                                                         /note= "Casein kinase II (CK2) phosphorylation site"
280. .285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human secreted protein useful for diagnosing or treat disease associated with an absence of, inappropriate or unwanted expression of the secreted protein, in drug screening assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
                                                                  phosphorylation
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                        744. .246
/note= "Protein kinase C (PKC) pl
262. .267
266. .269
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                         'note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                           295. .298 "wristoylation/note= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE11905 standard; protein; 306 AA.
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AAE11905
ID AAE11
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(first entry)

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The present sequence is human G-protein coupled receptor-11 (GPCR-11) protein. GPCR protein and DNA may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate CPCRX expression, obesity, diabetes mellitus, anorexia, cadhexia, cardiomyopathy, pain, atherosclerosis, neurodegenerative disorders (Alzheimer's disease, Parkinson's disease, Huntington's disease); bulimia, immune disorder, haematopoietic disorders, disorders related to cell signal processing and metabolic pathway modulation, retinal disorder (photoreception), bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm adenocarcinoma); angina pectoris, hypotension, hypotrension, asthma, Crohn's disease, multiple sclerosis, ulcers, neurological disorders (dementia, mental retardation, schizophrenia, anxiety); acute heart failure, osteoporosis, myocardial infarction and urinary retention
                                                                                                                                          atherosclerosis; diabetes; cardiant; cytostatic; cancer; obesity; pain; diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; retinal disorder; HIV; human immunodeficiency virus; adenocarcinoma; bulimia; asthma; ulcer; angine sectoris; hypertension; hypertension; Crohn's disease; anxiety; multiple sclerosis; schizophrenia; dementia; mental retardation; egene therapy; osteoporosis; urinary retention.
                                                                                                                              Human; G-protein coupled receptor 11; GPCR11; cardiomyopathy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-Protein coupled receptor polypeptides and NAs useful for preventing, diagnosing and treating cardiomyopathy, atherosclerosis,
                                                                                          Human G-protein coupled receptor 11 (GPCR11) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2000; 2000US-0199960P.
14-AUG-2000; 2000US-0275256P.
18-DEC-2000; 2000US-0256399P.
18-DEC-2000; 2000US-025624P.
22-DEC-2000; 2000US-0258159P.
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28-DEC-2000; 2000US-0258828P.
04-JAN-2001; 2001US-0259659P.
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Alsobrook JP, Burgess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancers and diabetes
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                     18-DEC-2001
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                 AAE11905,
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                                                                                                                                                                                                                                                                                                                                                                       Peptide
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44. .306 /label= Mature_GPCR11_protein 1. .43 /label= Signal_peptide Location/Qualifiers

tek KA, Grosse WM, Szekeres ES; Casman SJ, Lepley DM, Gangolli EA;

lishra V, Spytek KA,
Burgess CE, Casman
Smithson G;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                      Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
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   Length 306;
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                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lancet D, Glusman G, Fuchs T,
                                                                                                                                                                                                                                                                                       Human olfactory receptor polypeptide, SEQ ID NO: 1521.
; Score 25; DB 4; I
; Pred. No. 5.4e+02;
0; Mismatches 0;
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                                                                                                                                                                                       AAG71840 standard; protein; 313 AA.
   100.0%;
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(YEDA ) YEDA RES & DEV CO LTD
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                                                                                                                                                                                                                                                     (first entry)
   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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                                                                                                   249 SSVMH 253
                                                                    1 SSVMH 5
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                                                                                                                                                    RESULT 20
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RESULT 21 AAE11906

Sequence 306 AA;

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Human; G-protein coupled receptor 12; GPCR12; cardiomyopathy; vaccine; atherosclerosis; diabetes; cardiant; cytostatic; cancer; obseity; pain; diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; retinal disorder; HIV; human immunodeficiency virus; denocarcinoma; bulinia; asthma; ulcer; angina pectoris; hypotension; hypertension; Crohn's disease; anxiety; multiple sclerosis; schizophrenia; dementia; mental retardation;
                                                     Human G-protein coupled receptor 12 (GPCR12) protein.
                                                                                                                                                    gene therapy; osteoporosis; urinary retention.
                                                                                                                                                                                                                                                                              56. .314
/label= Mature_GPCR12_protein
                                                                                                                                                                                                                                      29. .52
/label= Membrane_helix_1
53. .58
/label= Inside_region_1
                                                                                                                                                                                                                     . .28
label= Outside_region_1
                                                                                                                                                                                                                                                                                                         label= Membrane_helix_2
                                                                                                                                                                                                                                                                                                                           Outside_region_2
                                                                                                                                                                                                                                                                                                                                              Membrane_helix_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outside_region_4
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                                                                                                                                                                                                   . .55
|abel= Signal_peptide
                                                                                                                                                                                         ocation/Qualifiers
AAE11906 standard; protein; 314 AA
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2000US-0256399P.
2000US-0256524P.
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2000US-0258828P.
2001US-0259659P.
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2000US-0199960P.
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/label= 0
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/label= T-
45
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/label= Mr
96
                                                                                                                                                                                                                                                                                                                                                      /label= Mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263. .277
'label= Our
                                                                                                                                                                                                                                                                                                                                                                          .162
                                                                                                                                                                                                                                                                                                                                    99. .122
/label= Me
                                                                                                                                                                                                                                                                                                                  9. .98
label=
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28-DEC-2000;
28-DEC-2000;
04-JAN-2001;
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14-AUG-2000;
18-DEC-2000;
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                                     18-DEC-2001
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                                                                                                                                                                                                  Peptide
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The present sequence is human G-protein coupled receptor-12 (GPCR-12) protein. GPCR protein and DNA may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate GPCRX expression, obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain, atherosclerosis, neurodegenerative disorders (Alzheimer's disease, Parkinson's disease, Huntington's disease); bulimia, immune disorder, haematopoietic disorders, disorders related to cell signal processing and metabolic pathway modulation, retinal disorder (photoreception), bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm adenocarcinoma); angina pectoris, hypotension, hypertension, asthma, Crohn's disease, multiple sclerosis, ulcers, neurological disorders (dementia, mental retardation, schizophrenia, anxiety); acute heart failure, osteoporosis, myocardial infarction and urinary retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                             G-Protein coupled receptor polypeptides and NAs useful for preventing, diagnosing and treating cardiomyopathy, atherosclerosis, cancers and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                         Padigaru M, Mishra V, Spytek KA, Grosse WM, Szekeres ES;
Alsobrook JP, Burgess CE, Casman SJ, Lepley DM, Gangolli EA;
Macdougall JR, Smithson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human olfactory receptor polypeptide, SEQ ID NO: 1518.
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Pred. No. 5.5e+02;
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                                                                                                                                                                                                                 Claim 1; Page 46; 242pp; English
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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(YEDA ) YEDA RES & DEV
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(CURA-) CURAGEN CORP.
                                                                                               WPI; 2001-611739/70.
N-PSDB; AAD19143.
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New polynucleotides which encode polypeptides involved in olfactory

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 970-971; 1857pp; English.
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Best Local Similarity
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                                                                                                                                               The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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sensation for identifying olfactory agonists and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human olfactory receptor polypeptide, SEQ ID NO: 1520.
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                                                                                Claim 11; Page 968-969; 1857pp; English
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(YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, G-protein coupled receptor-4; GCREC-4; cytostatic; hepatotropic; virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; notroproje; cerebroprocective, hypotensive; transpantiliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspesia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; crohn's disease; acquired immune deficiency syndrome; AIDS; uveitis; infection; transgenic animal; gene therapy.
This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
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                                                                                                                                                         Length 314;
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| Tabbel = G-protein-coupled_receptor_motif
199. .218
| Jabel = Transmembrane_domain
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                                                                                                                                                         100.0%; Score 25; DB 4; 1 100.0%; Pred. No. 5.5e+02;
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/label= Transmembrane_domain
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N-PSDB; AAD12947.
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Matches 5; Conserv
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The present sequence is human G-protein coupled receptor-4 (GCREC-4)

protein. The present invention relates to GCREC protein and nucleic acids

cc encoding them. GCREC protein, its agonist or antagonist are useful for

treating diseases or conditions associated with decreased expression or

cc reating diseases or conditions associated with decreased expression or

cc encerpression of functional GCREC in a patient, where the disorder is

selected from cell proliferative disorders such as actinic keratosis,

cancer, neurological disorders such as epilepsy, stroke, Alzheimer's

cc ancer, neurological disorders such as epilepsy, stroke, Alzheimer's

cd disease, Huntington's disease, Parkinson's disease, cardiovascular

cd disorders such as dysphadia, dyspepsia, anorexia, nausea,

cl intestinal disorders such as dysphadia, dyspepsia, anorexia, nausea,

cc intestinal disorders such as dysphadia, dyspepsia, anorexia, nausea,

cc intestinal disorders such as dysphadia, dyspepsia, anorexia, nausea,

cc intestinal disorders such as dysphadia, dyspepsia, anorexia, nausea,

cc intections, trauma and metabolic disorders such as disease,

cuvetitis, viral, bacterial, fungal, parasitic, protozoal, helminthic

contections, trauma and metabolic disorders such as diabetes, obesity,

categorosis. GCREC proteins and their cDNAs are used to assesse the

cf fects of exogenous compounds on the expression of GCREC sequence.

cc fransgenic animals (mice or rate) to model human disease, for therapputic

cr transgenic animals (mice or rate) to model human disease, for therapputic

cr transgenic animals (mice or rate) to model human disease, for therapputic

cor diagnostic purposes, for somatic or germinally occurring genomic

cc sequence, and in molecular biological techniques
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food additive; cosmetic; fragrance; pharmaceutical additive.
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12-APR-2000; 2000US-0199474P.
24-APR-2000; 2000US-019933F.
26-MAY-2000; 2000US-0207702P.
23-JUN-2000; 2000US-0213849F.
16-AUG-2000; 2000US-0226534F.
07-SEP-2000; 2000US-0332P.
07-FEB-2001; 2001US-0266662P.
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Nucleic acids encoding human olfactory G protein-coupled receptors,

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useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customize odors.
                                                                                                                         The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and fragrances. The present sequence is a human olfactory receptor of the
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100.0%; Pred. No. 5.5e+02;
ive 0; Mismatches 0;
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Best Local Similarity
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Job time : 42.1698 secs
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US-09-252-991A-25984
US-09-586-719-10
US-09-586-719-10
US-09-564-466-29
US-09-566E-8
US-08-44-189-8
US-08-444-189-8
US-08-468-54-8
US-08-969-644-8
US-08-468-240-1
US-08-468-240-1
US-08-468-240-1
US-08-468-240-1
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US-09-228-986-79
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US-08-476-900A-6
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US-09-208-716-4
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US-08-411-119A-2
US-08-411-119A-3
US-08-411-43-43
US-08-41-43-43
US-08-118-270-86
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US-08-871-355A-264
US-08-10-945-264
US-08-118-270-227
PCT-US93-0852B-227
US-08-118-270-197
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S-08-488-546A-29
S-08-404-531B-6
S-08-476-900A-6
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US-08-118-270-203
PCT-US93-08528-203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      September 24, 2004, 01:53:42; Search time 8.49057 Seconds (without alignments) 30.402 Million cell updates/sec
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/cgn2_6/ptcdata/2/iaa/RCCOMB.pep:*
/cgn2_6/ptcdata/2/iaa/PcTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-934-551-2

US-10-224-414-3

US-09-134-000C-4515

52.08144-37

US-08-134-000C-4515

52.08148-27

US-08-134-001C-4615

US-09-334-551-4

US-10-224-414-4

US-09-334-551-4

US-09-441-502B-6

US-09-441-502B-6

US-09-441-502B-6

US-09-441-502B-6

US-09-41-502B-6

US-09-32B-35-596B

US-09-32B-35-596B

US-09-32B-35-4307

US-09-489-033A-13210

US-09-252-991A-19132

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25
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Maximum Match 100%
Listing first 150 summaries
                                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Score

Result Š.

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NSGUENCE 2, Application US/09934551
; Sequence 2, Application US/09934551
; Sequence 2, Application US/09934551
; Sequence 2, Application US/09934551
; Patent No. 6464806
; Patent No. 6464806
; APPLICANT: BEASLEY, Ellen M.
; APPLICANT: Li, Zhenya
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION NUMBER: (0/226,903
; PRIOR PELICATION NUMBER: 60/226,903
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 144;
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COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
ATTORNEY/AGENT INFORMATION:
NAWE: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 61/499
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100: 7091:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 7091:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 7091:
SEQUENCE CHARACTERISTICS:
ILENGEN E CHARACTERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...144; SEQUENCE DESCRIPTION: SEQ ID NO: 7091:US-09-107-532A-7091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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; ORGANISM: HUMAN
US-09-934-551-2
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US-09-107-532A-7091
; Sequence 7091, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                               Sequence 200, App
Sequence 47, Appl
Sequence 49, Appl
Sequence 4904, Appl
Sequence 5884, Appl
Sequence 277, Appl
Sequence 777, Appl
Sequence 71414, Appl
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 39, Appl
Sequence 45, Appl
Sequence 5, Appl
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Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
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Sequence 2, Appli
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Sequence 143, App
Sequence 868, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 10, Appl
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Sequence 3,
Sequence 8,
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CORRESPONDENCE ADDRESS:
STREET: 100 Beaver Street
CITY: Waltham
STATE: Maseachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
               US-08-118-270-200
US-07-741-4534-47
US-07-741-453A-49
US-07-741-453A-49
US-07-741-453A-49
US-09-621-976-88
US-07-741-453A-49
US-09-621-976-88
US-09-621-976-7735
US-08-99-106A-9
US-08-399-106A-9
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US-08-433-105A-9
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US-08-434-644-45
US-08-433-105A-1
US-08-434-644-1
US-08-434-644-3
US-08-434-869A-1
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Gaps

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Сарв

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NAME/KEY: MISC_FEATURE
1 LOCATION: (477)...(500)
2 OTHER INFORMATION: Amino acid 477 & 500 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-4515
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Patent No. 5608384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.;

TITLE OF INTENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION NUMBER: US/07/396,697
; PILING DATE: 22-MG-1989
; PRIOR APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 22-FEB-1989
; PRIOR APPLICATION NUMBER: 235,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAKTIMA; NILES, JOHN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 726;
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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STREET: 419 Seventh Street, N.W., Suite 300
CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
CURRENT APPLICATION NUMBER: US/09/134,000C
                  CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4515
LENGTH: 517
TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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STATE: D.C.
COUNTRY: USA
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                                                    Sequence 2, Application US/10224414

Sequence 2, Application US/10224414

Patent No. 6638751

GENERAL INPORMATION:

APPLICANT: Elsanya

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REPREBENCE: CLOO0757 DIV

CURRENT PILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: 60/226,903

PRIOR PILING DATE: 2001-08-23

PRIOR PILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12736, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR RELIGING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12736
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 2.8
ative 0; Mismatches
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US-09-489-039A-12736
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Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-224-414-2
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                  RESULT 3
US-10-224-414-2
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Gaps

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Sequence 4, Application US/09934551

Sequence 4, Application US/09934551

Fatent No. 6461850

GENERAL INFORMATION:

APPLICANT: BRASLEY, Bllen M.

APPLICANT: Li Zhenya

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CLOO0757

CURRENT APPLICATION WURBER: 2001-08-23

PRIOR APPLICATION WURBER: 2001-08-23

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASLESC for Windows Version 4.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10224414

Sequence 4, Application US/10224414

Sequence 4, Application US/10224414

Sequence 4, Application US/10224414

Sequence 10. 6638751

GENERAL INFORMATION:

APPLICANT: BASALEX, Ellen M.

TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000757 DIV

CURRENT FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: 60/226,903

PRIOR APPLICATION NUMBER: 60/226,903

PRIOR APPLICATION NUMBER: 09/934,551

PRIOR PLINE PRIOR PRIOR DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

DENGRIF: 268
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                                                                                                5; Length 23;
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Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                             Score 24; DB
Pred. No. 29;
                                                                                                                                             1; Mismatches
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80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                             Conservative
; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US93-08528-93
                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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219 SSIMH 223
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13 SSIMH 17
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CRGANISM: HUMAN
US-09-934-551-4
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNED #4,033
REFERENCE/DOCKET NUMBER: #4,033
REFERENCE/DOCKET NUMBER: #4,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELEEPHONIS: 202-628-5197
TELEEPHONIS: 202-628-5197
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMBUTER: IBM PC compatible

COMBUTER: BRANCH PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.0%; Scur.
80.0%; Pred
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 4; Conservative
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STRANDEDNESS: si
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PCT-US93-08528-93
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Gaps

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Length 268;

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GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                     Score 22; DB 4; Length 19;
Pred. No. 67;
1; Mismatches 0; Indels
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNESSE: BROWDY AND NEIWARK STREET: 419 Seventh Street, N.W., Suite 300 STATE: D.C. COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 232, Application US/08118270 Patent No. 5508384
               NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-441-5028-7
 1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                   88.0%;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 35 amino acids
amino acid
                                                                                                                                                                                                          4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 4; Conservative
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CURRENT FILING DATE:
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                                                                                                                                                                     Query Match
Best Local Similarity
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Matches
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                                                                                                                                                                                            TITLE OF INVENTION: DUCCETE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/065,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09441502B
Sequence 6, Application US/09441502B
Patent No. 6455041
GENERAL INFORMATION:
APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: IMMUNGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN FILE REPERBNCE: 12231.2031.
CURRENT APPLICATION NUMBER: US/09/441,502B
CURRENT PILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 104
SOFTWARR: Patentin version 3.1
SEQ ID NO 6
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TITLE OF INVENTION: INMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
FILE REFERENCE: 12231.20801
CURRENT APPLICATION NUMBER: US/09/441,502B
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Pred. No. 7.1e+02;
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67;
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Pred. No. 6
                                                                                                                                           Sequence 4615, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09441502B Patent No. 6455041
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                     1|:||
219 SSIMH 223
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Best Local Similarity
Matches 4; Conserv
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283 SSIMH 287
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               1 SSVMH 5
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                                                                                                                         US-09-134-001C-4615
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US-09-441-502B-6
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Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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71 NSVMH 75
                                                                                                                                     38 SSVLH 42
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                                                                                            1 SSVMH 5
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US-09-107-532A-7054
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US-09-328-352-5968
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Sequence 232, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
ITILE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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; Sequence 5485, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REPERENCE: GENSET: 054PR2; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 5485
; LENGTH: 71
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATONNEY/AGENT INFORMATION:

NAME: TOWNESM KEVIN G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

TELEPHONE: 202-629-5197

TELEPHONE: 202-629-5197

TELEFRANE: 202-737-3528
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80.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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ORGANISM: Homo sapiens
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; LOCATION: -56..-1
US-09-621-976-5485
                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-621-976-5485
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Sequence 7054, Application US/09107532A
Sequence 7054, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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Score 22; DB 4; Length 71; Pred. No. 2.4e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7110
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
PILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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LOCATION: (B) LOCATION 1...86

; SEQUENCE DESCRIPTION: SEQ ID NO: 7054:

US-09-107-532A-7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7054:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 86 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
    88.0%;
80.0%;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Gaps
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JEACHT NO. 6573068

JEACHT NO. 6573068

JEACHT INCOMATION:

JEAPLICANT: Dunas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

JAPLICANT: Duclert, Aymeric

JAPLICANT: BOUGUELET, Lydie

JILE REFERENCE: 31.US3.CIP

JUNEAUT APPLICATION NUMBER: US/09/663,600A

CURRENT APPLICATION NUMBER: 09/191,997

PRIOR APPLICATION NUMBER: 09/191,997

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-17

PRIOR PILING DATE: 1998-04-13

PRIOR PILING DATE: 1998-04-13
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                                                        CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 562 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 30
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
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Matches 4; Conservative
                    03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 SSVLH 212
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NAME/KEY: SIGNAL
LOCATION: -21..-1
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US-09-663-600A-190
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Patent No. 6562958

GENERAL INFORMATION:

PAPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NOS: 9688

LENGTH: 201
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Patent No. 6562958
GENERAL INFORMATION:
FOR THILL OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REPRESENCE:

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Sequence 27, Application US/07857224B
Sequence 27, Application US/07857224B
Sequence 27, Application US/07857224B
Sequence 27, Application US/07857224B
Sequence 27, Application US/0785724B
Sequence 27, Application U
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COUNTRY: Switzerland
COUNTRY: Switzerland
ZIF (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 4; Length 201; Pred. No. 6.6e+02;
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80.0%; Pred. No. 7.2e+02;
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OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.0%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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US-09-328-352-4307
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LENGTH: 220
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Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-21306
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US-09-489-039A-13210
; Sequence 13210, Application US/09489039A
; Patent No. 6610810
; GRENERAL INFORMATION:
    APPLICANT: Gary Ereton et. al
    TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT PILING DATE: 1999-01-29
; RIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13210
. LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19132, Application US/09252991A
Sequence 19132, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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                                                                         0;
                                 88.0%; Score 22; DB 4; Length 267; 80.0%; Pred. No. 8.8e+02;
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Pred. No. 9.1e+02;
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                                                                         0; Indels
                                                                       1; Mismatches
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US-09-252-991A-19132
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SEQ ID NO 19132
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Best Local Similarity 80.v.
Fra 4; Conservative
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Best Local Similarity 80.v.
Best Local 4; Conservative
                                                                         4; Conservative
                                   Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-19132
US-09-663-600A-190
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RESULT 24 US-09-134-000C-4441

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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PALLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: OS 60/094,190

PRIOR FILING DATE: 1999-07-27

NUMBER: OS 21306

LENGTH: 318
; Sequence 4441, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
    APPLICANT: Lynn Doucette-Stamm et al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
    TITLE OF INVENTION: BYTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; PRIOR PAPLICATION NUMBER: US 60/055,778
; PRIOR PILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4441

LENGTH: 216
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Pred. No. 1e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21306, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%;
80.0%;
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Best Local Similarity 80.0.
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Sequence 2 Sequence 1 Sequence 1

Sequence 1 Sequence 8 Sequence 8

Sequence:

Run on:

Searched:

Database

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3 US-10-343-650A-162

4 US-10-312-166-10

4 US-10-012-166-10

4 US-10-012-166-10

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1 US-09-864-76-14-686

1 US-09-864-76-14-898-18

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1293
4660
   Sequence 182859,
Sequence 37, Appl
Sequence 51, Appl
Sequence 2, Appli
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Sequence 2, Appli
Sequence 24, Appl
Sequence 85, Appl
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Sequence 43019, A
                                                                                                       September 24, 2004, 01:54:43; Search time 28.9623 Seconds (without alignments) 55.513 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S US-10-276-74-2118
S US-10-437-963-182859
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2 US-10-167-555-2
4 US-10-143-26-4
4 US-10-143-375-2
1 US-09-844-861A-24
US-10-143-575-2
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Listing first 150 summaries
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                                                                             protein search, using sw model
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Perfect score:
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sequence 162, App Sequence 754, App Sequence 758, App Sequence 20, Appl Sequence 20, Appl Sequence 73027, A Sequence 714, Appl Sequence 10822, A Sequence 10822, A Sequence 37219, A Sequence 37219, A Sequence 15601, Sequence 25601, Sequence 15501, A Sequence 25601, Sequence 25601, Sequence 25601, A Sequence 25601, A Sequence 15900, Sequence 25601, A Sequence 25601, A Sequence 25601, A Sequence 25601, A Sequence 15900, A Sequence 20318, Sequence 20318, Sequence 20318, Sequence 20318, A Sequence 208508, Sequence 218314, A Sequence 208508, Sequence 218314, A Sequence 218314, A Sequence 218314, A Sequence 218314, A Sequence 218314, Sequence 215314, Sequence 2552, Appl

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99 84 14 US-10-072-349-85 90 22 88.0 85 16 US-10-437-951-199497 91 22 88.0 86 11 US-09-864-408A-7902 92 88.0 89 16 US-10-437-953-182752 95 22 88.0 99 16 US-10-437-953-182752 96 22 88.0 99 16 US-10-437-953-182752 96 22 88.0 99 16 US-10-437-953-182752 96 22 88.0 98 12 US-10-424-993-1831584 96 22 88.0 10 US-09-976-39-7484 97 22 88.0 10 US-09-925-29-7484 98 10 US-09-925-29-7484 10 99 10 US-10-424-599-20-8644 90 10 US-09-925-29-7484 98 10 US-10-424-4599-10-8692 99 10 US-10-424-4599-10-8692 90 10 U	nence 85, Appl puence 199497, puence 199487, puence 174887, puence 183752, puence 18315, puence 19692, puence 19692, puence 135184, puence 749, App puence 749, App puence 783, App	Junice 745, App Thence 29432, A Thence 29432, A Thence 210695, Thence 210691, Thence 21691, Thence 21691, Thence 21691, Thence 21644, Thence 24441, Thence 24441, Thence 22470, Thence 22470, Thence 22470, Thence 22470, Thence 3163, App Thence 4313, App Thence 4313, App Thence 4313, App Thence 4315, App Thence 4315, App Thence 4315, App Thence 3550, App Thence 4365, App Thence 5302, App Thence 5302, App Thence 5302, App Thence 5302, App Thence 54045, Thence 54045, Thence 54045, Thence 54045, Thence 54045, Thence 54045, Thence 54045, Thence 54045,	quence 61750, A quence 65124, A quence 625, App quence 2524, Ap quence 250163, quence 2510, Ap quence 2170, Ap quence 28, App quence 20215, A quence 1816, Ap quence 1816, Ap quence 1816, Ap quence 1817, A quence 1811, App quence 1811, App quence 1811, App quence 1811, App
22 88.0 84 14 US-99 93 22 88.0 85 11 US-99 94 22 88.0 85 11 US-99 95 22 88.0 87 16 US-99 95 22 88.0 87 16 US-99 96 22 88.0 87 16 US-99 96 22 88.0 87 16 US-99 96 22 88.0 97 16 US-99 96 22 88.0 97 16 US-99 96 22 88.0 102 US-99 US-99 US-99 96 22 88.0 102 US-99 US-99 US-99 96 22 88.0 102 US-99 US-99 US-99 97 25 88.0 109 US-99 US-99 US-99 98 25 88.0 1	-		•
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ALIGNMENTS

US-09-864-408A-5172; Sequence 5172, Application US/09864408A; Publication No. US20040009474A1; GRNEAL INFORMATION: APPLICANT: Leach, Martin D.

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APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Encoc
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 69
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BERGER OF USOLOGO 1049763A1

BERGER NO. USOLOGO 1049763A1

PRICARET REPRESENCE: ACCORDING AND SERVER SER
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-864-408A-5172
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APPLICANT: Kekuda et al.

TITLE OF INVENTION: No. US20040005656Alel GPCR-like Proteins and Nucleic Acids Encodir
TITLE OF INVENTION: Same
FILE REFERENCE: 21402-163
CURRENT APPLICATION UNMER: US/09/981,566A
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT Alexandra Glucksmann, Maria
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: M. Galvin, Katherine
APPLICANT: Weich, Nadine
APPLICANT: Weich, Nadine
APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory B.J.
APPLICANT: Curtis, Rory B.J.
APPLICANT: Applicant: Rapaleler-Libermann, Rosana
APPLICANT: Bandaru, Rapasekhar
APPLICANT: MEMBERS,
TITLE OF INVENTION: NUMBER GPOTEIN COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY ME
FILE REFERENCE: 10449-188001
CURRENT APPLICATION NUMBER: US/10/145,586
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       TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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COTHER INFORMATION: Clone ID: PAT_MRT4530_80004C.1.pep US-10-437-963-182859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 5.2e+02;
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OTHER INFORMATION: ungure at all Xaa locations
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                                                CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 182859
LENGTH: 147
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; Sequence 51, Application US/09981566A
; Publication No. US20040005656A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT · ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
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NAME/KEY: unsure
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LENGTH: 252
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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ITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18

PRIOR PILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SEQ ID NO 2118

LENGTH: 96
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OTHER INFORMATION: EXPRESED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 0.92
OTHER INFORMATION: SWISSPROT HIT: A1138213.1, EVALUE 4.00e-25
OTHER INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
OTHER INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 9; Length 76; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43019
LENGTH: 76
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0;
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Publication No. US20040123343A1
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Www. Wei
APPLICANT: Www. Wei
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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US-10-276-774-2118
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Best Local Similarity
Matches 5; Conser
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; LOCATION: 13
US-09-864-761-43019
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US-10-640-326-2

US-10-640-326-2

US-10-640-326-2

Sequence 2. Application US/10640326

Publication No. US20040038896A1

GENERAL INFORMATION:
APPLICANT: BRASLEY, Ellen M.
APPLICANT: LI, Zhenya

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CLOO757 D1V2

CURRENT APPLICATION NUMBER: US/10/640,326

CURRENT PILING DATE: 2001-08-25

PRIOR FILING DATE: 2001-08-23

PRIOR PLLING DATE: 2001-08-23

PRIOR PLLING DATE: 2001-08-21

PRIOR PLLING DATE: 2001-08-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2.
                               Sequence 2, Application US/10167555

| Publication No. US2003002212A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: 65649, A Human Metalloprotease Family Member and Uses
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: WIMBER: US/10/167,555
| CURRENT APPLICATION NUMBER: US/10/167,555
| CURRENT FILING DATE: 2001-06-13
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 14; Length 282; 100.0%; Pred. No. 5.8e+02; ive 0; Mismatches 0; Indels
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Publication No. US20030036167A1
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M.
APPLICANT: Li, Zhenya
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-167-555-2
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; ORGANISM: HUMAN
US-10-640-326-2
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US-10-224-414-2
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Sequence 966, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAKIKO

APPLICANT: ARIVA, XIVORAL

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED

CURRENT APPLICATION NOWBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR PLING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: Patentin Ver. 2.1

LENGTH: 261
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100.0%; Pred. No. 5.4e+02;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/240,704
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR PRILING DATE: 2001-01-27
PRIOR PELING DATE: 2001-01-15
PRIOR PELING DATE: 2001-10-11
PRIOR FILING DATE: 2001-10-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-22
PRIOR PELING DATE: 2001-11-22
PRIOR PELING DATE: 2001-01-22
PRIOR PELING DATE: 2001-01-21-2
PRIOR PELING DATE: 2001-01-21-2
PRIOR PELING DATE: 2001-01-21-2
PRIOR PELING DATE: 2001-01-21-2
PRIOR PELING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 209
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-10-017-161-966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-981-566A-51
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Best Local Similarity
Matches 5; Conserv
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| Sequence 85, Application US/09886055
| Patent No. US20020132273A1
| GENERAL INCRAMION:
| APPLICANT: STRYER, LUBERT
| APPLICANT: ZOZULYA, SERGEY
| TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
| TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
| FILE REFERENCE: 0780031-0277150
| CURRENT APPLICATION NUMBER: US/09/886,055
| CURRENT APPLICATION NUMBER: 60/213,812
| PRIOR FILING DATE: 2000-06-22
| NUMBER OF SEQ ID NOS: 5.22
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 85
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Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.5e+02;
ive 0; Mismatches 0;
              Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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US-09-886-055-85
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TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REPERRNCE: CLOO0757 DIV
CURRENT APPLICATION NUMBER: US/10/224,414
CURRENT APPLICATION NUMBER: 00/226,903
PRIOR PILING DATE: 2001-08-23
PRIOR PLING DATE: 2001-08-23
PRIOR PRIOR PLING DATE: 2001-08-23
PRIOR PRIOR PRIORS: HUMANS
CSCTWARE: PRESECT OF Windows Version 4.0
SEQ ID NOS: 4
SOFTWARE: PRESECT OF WINDOWS VERSION 4.0
CROMISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10143575
Publication No. US2030166072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USCATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCATED WIGHTER ADD TITLE OF INVENTION: USCATED WIGHTER SECRETED PROTEINS, AND TITLE OF INVENTION: USCATED WIGHTER SECRETED PROTEINS, AND CURRENT APPLICATION NUMBER: US/10/143,575
CURRENT PILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 3
SEQ ID NO 3
TYPE: PRT
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100.0%; Pred. No. 6.2e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Padigaru, Muralidhara APPLICANT: Mishra, Vishnu APPLICANT: Spyrek, Kimberly APPLICANT: Burgess, Catherine APPLICANT: Lepley, Denise APPLICANT: Grosse, William APPLICANT: Szekeres, Góward APPLICANT: Alsobrook, John
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Smithson, Glennda
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Gangolli, Esha
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100
Matches 5; Conservative
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260 SSVMH 264
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                                                                      US-09-804-291-89
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TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
FILE REPERENCE: P 0278005
FILE REPERENCE: P 0278005
CURRENT APPLICATION NUMBER: 60/188,914
PRIOR PILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/189,913
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-24
PRIOR FILING DATE: 2000-06-24
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-09-17
PRIOR FILING DATE: 2000-09-17
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/266,862
| Sequence 89, Application US/09886055 |
| Patent No. US2002013227341 |
| GENERAL INCRMATION: |
| APPLICANT: STRYER, LUBERT |
| TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSORY PERCEPTION, AND |
| TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS |
| TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS |
| FILE REFERENCE: 078003-0277150 |
| CURRENT APPLICATION NUMBER: US/09/886,055 |
| CURRENT FILING DATE: 2000-06-22 |
| PRIOR FILING DATE: 2000-06-22 |
| NUMBER OF SEQ ID NOS: 522 |
| SOFTWARE: PatentIN Ver. 2.1 |
| SEQ ID NO 89 |
| LENGTH: 314 |
| TYPE: PRT |
| US-09-886-055-89 |
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100.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 0;
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; Publication No. US20030088059A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
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; ORGANISM: Homo sapiens
US-09-804-291-85
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Matches 5; Conserv
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260 SSVMH 264

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Sequence 25 - Application UB/09604291

Publication No. USCOINOBERSAL
APPLICATION NO. USCOINOBERS
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Gaps
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Publication No. US20020155473A1

GENERAL INFORMATION:

APPLICANT: Peng Zaoyuan

APPLICANT: Wiley, Andrew

APPLICANT: Wiley, Andrew

APPLICANT: Hu, Qianjin

TITLE OF INVENTION: METHODS FOR IDENTIFYING G-PROTEIN

TITLE OF INVENTION: COUPLED RECEPTORS ASSOCIATED WITH DISEASES

FILE REFERENCE: 433112000700
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; Pred. No. 6.5e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
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                                APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REPERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR PRICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2001-02-13
NUMBER: OF SEQ ID NOS: 694
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT PILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-00-63
PRIOR PILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PATCHIN UNEX. 2.1
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/258,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-343-650A-162
; Sequence 162, Application US/10343650A
; Publication No. US20040067499A1
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-343-650A-162
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LENGTH: 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R. APPLICANT: AU-YOUNG, Janice; YUE, Henry TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS FILE REPERSUES: PI-0032 USN CURRENT APPLICATION NUMBER: US/10/182,822A CURRENT FILING DATE: 2001-02-01
PRIOR PELICATION NUMBER: PCT/US 01/03455
PRIOR APPLICATION NUMBER: US 60/180,093
PRIOR APPLICATION NUMBER: US 60/180,093
PRIOR APPLICATION NUMBER: US 60/182,045
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 11;
Pred. No. 6.5e+02;
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US-10-182-822A-4
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/256,399
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-10-14
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-03-13
SOFTWARE: PATENTING DATE: 2011-03-13
SOFTWARE: PATENTING DATE: 2011-03-13
LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/10182822A
; Publication No. US20030211493A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-343-650A-160
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; Sequence 160, Application US/10343650A; Publication No. US20040067499A1

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Gaps

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100.0%; Score 25; DB 14; Length 314; 100.0%; Pred. No. 6.5e+02; ive 0; Mismatches 0; Indels

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Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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US-10-387-629-164
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100.0%; Pred. No. 6.5e+02;
rative 0; Mismatches 0; Indels
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PUBLICATION NO. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, WAKION:

APPLICANT: AKIYAWA, YUTAKA

APPLICANT: ARIYAWA, YUTAKA

APPLICANT: ABURATION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: US/201/246789

PRIOR FILING DATE: 2002-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARRE PATENTIN VET. 2.1

SEQ ID NO 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ASMINA, TICORA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US 2001/246789
PRIOR APPLICATION NUMBER: US 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 978
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 314
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                     US-10-017-161-878
; Sequence 878, Application US/10017161
; Publication No. US20030143668A1
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
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; ORGANISM: Homo sapiens
US-10-017-161-880
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CRGANISM: Homo sapiens
US-10-017-161-878
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US-10-032-106-10
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RESULT 24
US-10-387-629-162
is Sequence 162, Application US/10387629
is Publication No. US2003021205A1
is GENERAL INFORMATION:
is APPLICANT: Chemicon S.A.
is APPLICANT: Chemicon S.A.
is APPLICANT: Veithen, Alex
is TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
is FILE REFERENCE: 9409/2192
is CURRENT APPLICATION NUMBER: US/10/387,629
is CURRENT FILING DATE: 2003-03-13
is NUMBER OF SEQ ID NOS: 254
is SEQ ID NO 162
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Publication No. US20030221205A1

GENERAL INFORMATION:
APPLICANT: ChemCom S.A.
TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
FILE REFERENCE: 9409/2192
CURRENT APPLICATION NUMBER: US/10/387,629
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.1
SECTION 0.164
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Matches 5; Conservative
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US-10-387-629-164
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US-10-387-629-162
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 150 summaries
                                                - protein search, using sw model
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A;Map position: circular chromosome
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(Species: Mus musculus (house mouse)

(Species: Mus musculus (house mouse)

(Spacession: A30502

R) Eilat, D.; Webster, D.M.; Rees, A.R.

A) Immunol. 141, 1745-1753, 1988

A) Immunol. 141, 1745-1753, 1988

A) Fitle: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m

A) Reference number: A30502; MUD:88315787; PMID:2457627

A) RASCHAUS: PREILIMINARY

A) Molecule type: mRNA

A) Residues: 1-112 < EIL>
C) Superfamily: immunoglobulin V region; immunoglobulin homology

C) Superfamily: immunoglobulin homology < INMA

F)15-98/Domain; immunoglobulin homology < INMA
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Pred. No. 17;
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                                                                                                                                                  A41361
A39128
C86180
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S41096
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T40508
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Best Local Similarity
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Dates: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: AF2871
R; Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellé; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metalloproteinase (EC 3.4.24.-) - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 28-Jul-2000
R;Elaroussi, M.A.; DeLuca, H.F.
Biochim. Biophys. Acta 1217, 1-8, 1994
A;Title: A new member to the astacin family of metalloendopeptidases: a novel 1,25-dihyd;
A;Reference number: S41055; MUID:94114563; PMID:8286408
A;Accession: S41055
A;Accession: S41055
A;Residues: 1-310 < ELAA
A;Residues: 1-310 < ELAA
A;Cross-references: GB:U12642; GB:S68488; NID:g530065; PIDN:AAA20842.1; PID:g530066
A;Rosidues: 1-310 < ELAA
A;Cross-references: GB:U12642; GB:S68488; NID:g530065; PIDN:AAA20842.1; PID:g530066
A;Cross-references: GB:U12642; GB:U1264; PID:MAA20842.1; PID:G530065; PID:MAA20842.1; PID:G550065; PID:MAA20842.1; PID:G500666
A;Cross-references: GB:U12642; G
conserved hypothetical protein Atu2400 [imported] - Agrobacterium tumefaciens (strain C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AF2871
A,Status: preliminary
A,Rolecule type: DNA
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100.0%; Pred. No. 35;
iive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 52;
Conservative 0; Mismatches
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A pescription: the net reaction catalyzed by the ubiquinol-cytochrome-c reductase complexith two hydrogen ions taken up from the mitochondrial matrix and four hydrogen ions relegant two hydrogen ions taken up from the mitochondrial matrix and four hydrogen ions relegant two hydrogen ions taken up from the mitochondry; cytochrome b, cytochrome b homology; cytochrome be homology; cytochrome be homology complexity. The state of the complexity of the complexity of the composition of the complexity of the composition of the c
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C;Dacies: mitochondrion Petromyzon marinus (sea lamprey)
C;Dacession: S54999
R;Lee, W.J.; Kocher, T.D.
Genetics 139, 873-887, 1995
A;Fitle: Complete sequence of a sea lamprey (Petromyzon marinus) mitochondrial genome: et A;Reference number: S54999; MUID:95229067; PMID:7713438
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AjGenome: mitochondrion
AjGenome: mitochondrion
AjGenome: SCI
Cyderfaily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol-Cjkeywords: electron transfer; heme; iron; metalloprotein; mitochondrion; oxidative phosy F;15-343/Domain: cytochrome b homology <CBH>
F;15-343/Domain: cytochrome b6 homology <CBH>
F;25-343/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;87,186/Binding site: heme iron (His) (axial ligands) (low potential) #status predictef F;101,200/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
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A;Readidues: 1-396 c-LEE>
A;Cross-references: EMBL:U11880; NID:g515484; PIDN:AAB08737.1; PID:g515485
A;Note: the authors translated the codon ATA for residue 21 as 11e
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68;
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100.0%; Pred. No. 66;
iive 0; Mismatches
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                                                                       Cross-references: EMBL:X12631
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Best Local Similarity 100.
Matches 5; Conservative
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A,Genetic code: SGC8
A,Start codon: ATA
C,Function:
A,Description: the net re
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molybdenum transport ATP-binding protein ModC STY0816 [imported] - Salmonella enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0595
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Croni, A: Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S.; Moule, S; O'Gaora, P; Croni, A: Davis, P; Davies, R.M.; Skelton, J; Stevens, K.; A; Huthors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: AE0595
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-352 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD05231.1; PID:g16502001; GSPDB:GN00176
C; Genetics:
A; Gene: STY0816
C; Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
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C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Sep-1999
C;Accession: A43697
R;Rushlow, C.; Doyle, H.; Hoey, T.; Levine, M.
Genes Dev. 1, 1268-1279, 1987
A;Title: Molecular characterization of the zerknuellt region of the antennapedia gene cc
A;Reference number: A43697; MUID:88112803; PMID:2892759
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R; Jacobs, H.T.; Elliott, D.J.; Math, V.B.; Farquharson, A.
J. Nol. Biol. 202, 185-217, 1988
J; Noleotide sequence and gene organization of sea urchin mitochondrial DNA.
A; Reference number: S01499; MUID:89011951; PMID:3172215
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;91-147/Domain: homeobox homology <HOX>
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Pred. No. 60;
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100.0%; Pred. No. cc...
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325 SSVMH 329

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

SSVMH 329

325

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1 SSVMH 5

A;Residues: 1-417 <RES>

A; Molecule type: mRNA

Rhesus-like protein - gorilla

Molecule type: mRNA Residues: 1-417 <RES>

SSVMH 329 1 SSVMH 5

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C,Accession: 137003
R,Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, i. Biochem. Genet. 32, 201-221, 1994
A,Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the FA,Reference number: 137003; MUID:95085595; PMID:7993375
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 08-Feb-1996
C;Accession: A57410
R;HO, S.N.; Thomas D.J.; Timmerman, L.A.; Li, X.; Francke, U.; Crabtree, G.R.
A;Title: NFATC3, a lymphoid-specific NFATC family member that is calcium-regulated and example of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T49849
S;Schulte, U.; Ajgn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
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                                                                                                                                                                                                           Rhesus-like protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Experimental source: BAC clone B24P11; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 417;
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N,Alternate names: protein B24P11.50
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100.0%; Score 25; DB 2;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-538 < SCH>
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Matches 5; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
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C;Species: Gorilla gorilla (gorilla)
C;Species: Gorilla gorilla (gorilla)
C;Species: Gorilla gorilla (gorilla)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
C;Accession: 137076
R;Salvignol, 1: Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Accession: 137076
A;Accession: 137076
A;Accession: 137076
A;Molecule type: mRNA
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R;Salvignol, I:; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Reference number: 137003; MUID:95085595; PMID:7993375
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rans-like protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
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C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
C;Accession: 137075
R;Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin,
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A;Cross-references: GB:L37052; NID:g607009; PIDN:AAA65626.1; PID:g607010
C;Superfamily: human erythrocyte membrane protein RhD
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A;Cross-references: GB:L37053; NID:g607011; PIDN:AAA65627.1; PID:g607012
C;Superfamily: human erythrocyte membrane protein RhD
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C;Superfamily: human erythrocyte membrane protein RhD
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Hypothetical protein T6A9.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Adra-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Adra-2001 #sequence_revision 02-Mar-2001
C;Accession: G86154
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Arubbors: Hunter, J.L.; Johnizar, L.; Conway, A.B.; Conway, A.R.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Eraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tules: Saquence and analyais of chromosome 1 of the plant Arabidopsis.
A;Rcference number: A86141; MUID:21016719; PMID:11130712
A;Rccession: G86154
A;Status: preliminary
A;Rccession: G86154
A;Rccession: G86154
A;Rccession: G86154
A;Rccession: G86154
A;Rccession: G86154
A;Rccession: GB6164
A;Rccession: GB6172; NID:g9857537; PIDN:AAG00892.1; GSPDB:GN00141
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: H86154
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conn, L.; Conn, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudbes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C. C.A.; Li, J.H.; Li, Y.; Liu, S.Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Exaser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: H86184
A;Accession: H86184
A;Accession: H86184
A;Accession: H86184
A;Accession: H86184
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-199 <STO>
A;Coss-references: GB:AE005172; NID:99972392; PIDN:AAG10642.1; GSPDB:GN00141
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96.0%; Score 24; DB 2; Length 199;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 4; Conservative 1; Mismatches 0; Indels
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C,Superfamily: ADP-ribosylation factor
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C,Superfamily: ADP-ribosylation factor
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Best Local Similarity 80.0°
Matches 4; Conservative
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S57548
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DNA-directed RNA polymerase, omega subunit VC2709 [imported] - Vibrio cholerae (strain N C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: A82044
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477+483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82044
A; Status: preliminary
A; Molecule type: DNA
A; Status
A; Molecule type: DNA
A; Residues: 1-90 <HEI>A; Cross-references: GB:AE004336; GB:AE003852; NID:G9657296; PIDN:AAF95849.1; GSPDB:GN001
A; Experimental source: serogroup O1; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-4660 <5A1>
A;Residues: 1-4660 <5A1>
A;Cross-references: EMBL:134049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A;Experimental source: strain Sprague-Dawley; kidney
C;Superfamily: alpha-2-macroglobulin receptor; BGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gp330 protein precursor - rat
NiAlternate names: megalin
C;Species atatus norvegicus (Norway rat)
C;Decies atatus norvegicus (Norway rat)
C;Date: 11-7an-2000 #sequence_revision 11-7an-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of A;Reference number: AS8173; MUID:95024033; PMID:7937880
A;Reference number: AS8173; MUID:95024033; PMID:7937880
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                                                                                                  100.0%; Score 25; DB 2; Length 1065; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 2; Length 4660; 100.0%; Pred. No. 1.1e+03; ative 0; Mismatches 0; Indels (
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C,Superfamily: DNA-directed RNA polymerase omega chain
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Molecule type: mRNA
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                                                                  Query Match
Best Local Similarity 100...
5; Conservative
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Best Local Similarity 100.0
Matches 5; Conservative
A;Residues: 1-1065 <HOA>
A;Cross-references: GB:U28807
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Best Local Similarity
Matches 4; Conserv
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A;Cross-references: GRM96170; NID:g213501; PIDN:AAA49438.1; PID:g213502
A;Cross-references: GRM96170; NID:g213501; PIDN:AAA49438.1; PID:g213502
A;Experimental source: orange red variety, embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:114769, NCBIP:114770)
A;Note: part of this sequence, including the amino end of the mature protein, was determid substantly: astacin; astacin; hydrolase; metalloproteinase; zinc
E;1-20/Domain: sityal sequence #status predicted <SIG>
F;21-70/Domain: stacin homology <AST>
F;88-270/Domain: astacin homology <AST>
F;58 -270/Domain: astacin homology <AST>
F;58 -270/Domain: astacin homology share (Asn) (covalent) #status predicted
F;169,173;179,225/Binding site: zinc (His, His, His, Tyr) #status predicted
F;170/Active site: Glu #status predicted
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69416
E;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F;Klenk, H.P.; Clayton, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
Shith, H.O.; Woese, C.R.; Venter, J.C.
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A;Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching er A;Reference number: A48826; MUID:93012471; PMID:1397682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high choriolytic hatching proteinase (BC 3.4.24.-) HCB21 precursor - Japanese medaka C, Species: Oryzias latipes (Japanese medaka)
C, Species: Oryzias latipes (Japanese medaka)
C, Date: O8-Feb-1996 #sequence_revision O8-Feb-1996 #text_change 03-Dec-1999
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                                   A; Reference number: A48826; MUID:93012471; PMID:1397682
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                                                                                                                 A; Molecule type: mRNA; protein A; Residues: 1-270 <YAS>
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Matches 4; Conservative
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229 SSIMH 233
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A; Status: not compar
                                                                                  A;Accession: B48826
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B69416
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High choriolytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka (Species Oryzias latipes (Japanese medaka)

C;Species Oryzias latipes (Japanese medaka)

C;Date: 01-Dec-1993 Hsequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: B48826

K; Assaaka, K; Akasaka, K; Mitsunaga, K; Iuchi, I; Shimada, H; Yamagami, Dev. Biol. 153, 250-258, 1992

A;Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching e
                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-247 <BON>
A,Cross-references: EMBL:Z49919; NID:g887584; PID:g887592; MIPS:YPR015c
A,Cross-references: EMBL:Z49919; NID:g887584; PID:g887592; MIPS:YPR015c
A,Experimental source: strain AB972
R,Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Vc
submitted to the EMBL Data Library, July 1995
A,Description: The sequence of Saccharomyces cerevisiae chromosome XVI right arm.
A,Reference number: S59746
A,Accession: S59759
NiAlternate names: hypothetical protein LPZ14c; hypothetical protein YP9531.08c C; Species: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae C; Accession: S57548; S59759 R; Bowman, S.
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Ryindsay, S.
Ryindsay, S
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| Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
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Pred. No. 78;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                  R;Bowman, S. submitted to the EMBL Data Library, June 1995 A;Reference number: 857541 A;Accession: 857548
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A,Map position: 3
A,Introns: 63/3; 94/1; 134/2; 169/1; 225/3
C,Superfamily: astacin homology
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Similarity 80.0%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A;Residues: 1-247 <WAN>
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SSIMH 51
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36 SSIMH 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable transmembrane transport protein ML2279 [imported] - Mycobacterium leprae Cispecies: Carry Mycole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho R.; Dauthes, R.M., Beltherford, K.M. Mat. Rutherford, K.M. Mat. Mycobacterium leprae Mycob
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69416
                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-330 <KLE>
A;Cross-references: GB:AE001012; GB:AE000782; NID:g2689335; PIDN:AAB89926.1; PID:g264925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter ATP-binding protein BMEI1258 [imported] - Brucella melitensis (strain 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: AD3409
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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A;Gene: ML2279
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A;Cross-references: GB:AE008917; PIDN:AAL52439.1; PID:g17983243; GSPDB:GN00190
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1e+02;
1; Mismatches 0; Indels
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80.0%; Pred. No. 1.6e+02;
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Best Local Similarity 80.0-
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Best Local Similarity 80.0°
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conser
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A;Molecule type: DNA
A;Residues: 1-496 <STO>
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A,Cross-references: EMBL:U46668; PIDN:AAA93348.1; CESP:F38E9.2
C,Genetics:
A,Gene: CESP:F38E9.2
A,Introns: 13/1; 37/3; 62/1; 89/1; 127/1; 164/2; 182/1; 235/3; 269/3; 321/2; 360/1; 455/3
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                                                                                                                                                                                         C'Species: Caenorhabditis elegans
C'Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C'Accession: T30018
R;Wu, X.; Gattung, S.
submitted to the EmBL Data Library, January 1996
A;Description: The sequence of C. elegans cosmid F38B9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 767;
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                                                                                                                                                                   - Caenorhabditis elegans
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Pred. No. 2.6e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             A,Accession: T30018
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,MOJecule type: DNA
A,Residues: 1-767 <WUX>
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                     hypothetical protein F38E9.2
                                             224 SSIMH 228
1 SSVMH 5
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Scoring table:

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Database

Perfect score:

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Sequence:

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INSPOOS D
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Human G-P
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                                                                                                                                                                                                                                                                                                                                                                                               mouse, anti-idiotypic antibody; 14C12; Factor VIII inhibitory antibody; C2 domain, Factor VIII; procoagulant; bleeding disorder; haemophilia; B cell apoptosis; antibody; heavy chain; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New monoclonal anti-idiotypic antibodies against human Factor VIII inhibitory antibodies, useful for treating or preventing bleeding disorders of hemophilia patient.
          Adq26167
Adq26171
Aae11905
                                           Aag71840
Aac11836
Aag71830
Aag71839
Aau24560
Aau24568
Aau2458
Aau2458
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AAE06754
AAU24550
AAU24550
AAU24550
AAU24550
AAU95703
AAU95703
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AAG71837
                                             AAG71840
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                                                                                                                                                                                                                                                                                                          ADL73176 standard; peptide; 12
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Mus musculus.
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 ADL73176;
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 Add73176 CDR1 of h
Add26158 INSP005B
Add26138 INSP005A
Abp33613 Human ORF
Abb11748 Human odo
Aae12026 Human Go
Aae12026 Human Go
Aag77494 Human OR-
Agg77795 Human OR-
Abg17755 Human Olf
Abg17755 Human Olf
Abg17755 Human PM
Abg6095 Amino aci
Abr37777 Ani-idio
Adc97464 E. faeciu
Adc97464 E. faeciu
Adb6086 Amino aci
Abg6087 An anti-a
Abg6695 Novel G-p
Adb47277 Novel hum
Adh42271 Novel hum
Adh42271 Novel hum
Adh42273 Novel hum
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                                                                                        (without alignments)
51.354 Million cell updates/sec
                                                                           April 28, 2005, 17:57:45; Search time 37.6562 Seconds
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          5.1.6
Compugen Ltd.
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     2105692 segs, 386760381 residues
           version 5
                                                                                                                         US-10-088-639A-2_COPY_158_162
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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ADQ26158
ADQ26138
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AAM57202
ABG51202
ABG512026
AAG72494
AAG71795
ADC77464
AAG7173173
ADC97464
AAB68087
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ADB47696
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AAO23391
ADB47698
ABB07687
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Gapop 10.0 , Gapext 0.5
          GenCore (c) 1993
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geneseqp1990s:*
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Maximum DB seq length: 2000000000
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                                                                                                                                               1 SSVMH 5
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Match
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Score

Result No.

ADQ26138 standard; peptide; 27 AA.

24

SSVMH

20

RESULT 3 ADQ2613

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g or treating diseases associated with metalloproteases, e.g., cystic fibrosis, metabolic disorders, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                       choriolysin/astacin-like metalloprotease; respiratory disorder; emphysema; cystic fibrosis; metabolic disorder; oardiovascular disorder; bacterial infection; hypertension; proliferative disorder; cancer; aucoimmune; inflammatory disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSP005B. This protein is a metalloprotease, specifically a choriolysin/astacin-like metalloprotease. The INSP005 polypeptides and nucleic acid molecules of the invention are useful in the therapy or diagnosis of diseases or in the manufacture of a medicament for the treatment of a disease, such as a respiratory disorder, including emphysema and cystic fibrosis, a metabolic disorder, a cardiovascular disorder, a bacterial infection, hypertension, a proliferative disorder, including cancer, an autoimmune/inflammatory disorder, including rheumatoid arthritis, a neurological disorder, a developmental disorder, a reproductive disorder or other pathological condition in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological disorder; developmental disorder; reproductive disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a fragment of a new secreted polypeptide,
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                             100.0%; Score 25; DB 8; Length 12; 100.0%; Pred. No. 23; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boschert U,
                                                                                                                                                                                                                                                                                                                                                                         secreted; INSP005A; INSP005B; metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitter RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 28; 101pp; English
                                                                                                                                                                                                                                ADQ26158 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                     INSP005B protein sequence exon 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Power C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metalloproteases are implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-2003; 2003WO-GB005664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-2002; 2002GB-00030006
                                                                                                                                                                                                                                                                                                    23-SEP-2004 (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARES-) ARES TRADING SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fagan RJ, Phelps CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-507715/48.
                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                     SSVMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADQ26157.
                                                                                                     1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              emphysema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer
                                                                                                                                         9
                                                                                                                                                                                                                                                                   ADQ26158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing or treating diseases associated with metalloproteases, e.g. emphysema, cystic fibrosis, metabolic disorders, cardiovascular disorders
                                                                                                                                                                                                                                                    choriolysin/astacin-like metalloprotease; respiratory disorder; emphysema; cystic fibrosis; metabolic disorder; cardiovascular disorder; bacterial infection; hypertension; proliferative disorder; cancer; autoimmune; inflammatory disorder; rheumatoid arthritis; neurological disorder; developmental disorder; reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSPOOSA. This protein is a metalloprotease, specifically a choriolysin/astacin-like metalloprotease. The INSPOOS polypetides and conclete acid molecules of the invention are useful in the therapy or diagnosis of diseases or in the manufacture of a medicament for the treatment of a disease, such as a respiratory disorder, including emphysema and cystic fibrosis, a metabolic disorder, a cardiovascular disorder, a bacterial infection, hypertension, a proliferative disorder, including cancer, an autoimmune/inflammatory disorder, including rheumatoid arthritis, a neurological disorder, a developmental disorder, a reproductive disorder or other pathological condition in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chvatchko Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               new metalloprotease proteins (INSPO05a or INSPO05b) for diagnosing, purkenting or treating diseases associated with matallocated but matallocated with matallocated but matallocated by the matallocated but matallocated by the matallocated but matallocated by the mata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a fragment of a new secreted polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                            secreted; INSP005A; INSP005B; metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 100.0%; Pred. No. 55;
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                                                                                                                                                            INSP005A protein sequence exon 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metalloproteases are implicated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2002; 2002GB-00030006.
                                                                                           (first entry)
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ses 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phelps CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARES-) ARES TRADING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-507715/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                           23-SEP-2004
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                              ADQ26138;
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Matches
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ID ABP3
XX
AC ABP3
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ABP33613

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Gaps

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Indels

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Local Similarity les 5; Conser

Best Loca Matches

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Leach MD,
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888888 ઠે 셤 Human; ORF; open reading frame; ORPX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; dimune modulation; hamanacopoiseis regulation; tissue growth; angiogenesis; activin; inhibhi; chemocactic; chemokinetic; fertility; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytostatalc; noctropic; neuroprotective; antiaherosclerotic; anticogulant; thrombolytic; cardiant; hypotensive; antithyroid; antinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Human ORF2586 protein, SEQ ID NO:5172. (first entry) 08-JUL-2002

Homo sapiens.

WO200190366-A2

29-NOV-2001.

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Shimkets RA;

WPI; 2002-106200/14.

N-PSDB; ABN77639.

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 10; Page 1545; 2508pp; English.

designated ORF (open reading frame) 1-454, and sequences ABN75054ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORFT-ORF4534 (collectively referred to as ORFX) proteins, polymcleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polymcleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies opportific for ORFX proteins, methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, timmune modulation, haematopoiesis regulation, cell differentiation, immune modulation, haematopoiesis regulation, cissue growth anglogenesis, activin, haematopoiesis regulation, cemokinetic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, on the coll of cancers, on the coll of and antinfective activity, and may also be involved in the treatment of cancers, on the coll of t ester other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. OREX nucleic acids may also be used as a source of primers and probes, in the detection of OREX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The OREX nucleic acids may additionally be used to produce transgenic animals Sequences ABP31028-ABP35561 represent 4534 novel human proteins

35 SSVMH 39

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                                                                                                                                                                                                                                                                                                                                                                                                       Human, brain expressed exon, gene expression analysis, probe, microarray, Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe encoded protein SEQ ID NO: 29307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases
                                                                                                                                          Gaps
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                                                                                                           Length 69;
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                                                                                                                                        0; Indels
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                                                                                                                      pred. No. 1.5e+02;
0; Mismatches 0;
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                                                                                                         100.0%; Score 25; DB 5; 100.0%; Pred. No. 1.5e+02
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                                                                                                                                                                                                                                                                                AAM57202 standard; protein; 76 AA.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the probes of the invention
                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                        5; Conservative
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Best Local Similarity
Local 5; Conserve
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                                                                                                                           Local Similarity
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                                                                                                                                                                        1 SSVMH 5
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                                                                              Sequence 69 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                           Query Match
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Matches
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cytokine; cell proliferation; cell differentiation; growth factor;

Human odorant receptor S18 homologue, SEQ ID NO:2118.

11-JAN-2002 (first entry)

haematopoieeis regulation, tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; matesatesis; cancer; tumoun; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; chronic inflammatory condition; proliferative retinopathy; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; antiathure; drug screening; gene therapy; antinflammatory; antiathmatic; antiathritic; haemostatic; cardiant; virucide; antibacterial;

antifungal; vulnerary; antiulcer.

WO200157188-A2

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhoosis, hyperlipideaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at from Letp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                            Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 4; Length 76; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                  Human liver peptide, SEQ ID No 29930.
                                 ABG51282 standard; peptide; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000664
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488898/53.
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                                                                                                                                                                                                                                                   WO200157273-A2
                                                                                                                                                                                                                      Homo sapiens
                                                                                                 25-FEB-2003
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                                                                  ABG51282;
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             RESULT 6
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xx sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The sequences ABA08225-ABA09574 represent nucleic acids encoding them. The sequences ABA08225-ABA09574 represent nucleic caids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of identifying compounds which bolypeptides against the polypeptides, methods of identifying compounds which bolypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activities, and hence cytomeration activities; stem cell growth factor activities; core chemology to crementated activities; chemology core chemology activity; activity; itsue growth activity; including cytokine, cell proliferation or cell functions or chemology activities, hemostactic or may be comparated activities; corporated activities; corporated activities; corporated activities; corporated activities; corporated activities; corporated activities, polypeptides and nucleotides of the involution are useful for preventing, treating or amelicating cell conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions in admining cell and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound immunomodulatory activities may be used in the treatment of viral, immunomodulatory activities may be used in the treatment of viral, immunomodulatory activities may be used in cell cultures to belypeptides with growth factor activity may be used in cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 238; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US003800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABA08992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
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Gaps

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5; Conservative

SSVMH 39 1 SSVMH 5

Sest Local Similarity

Matches

à d ABB11748 standard; peptide; 96 AA.

RESULT 7
ABB11748
ID ABB1
XX
AC ABB1

ABB11748;

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                              manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protection and years and an arterior protection and arterior classis; cancer; neurological disorder; Huntington's disease; Parkinson's disease; cardiovascular disorder; atherosclerosis; congestive heart failure; gastrointestinal disorder; agentritis; nausea; autoimmune; anaemia; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                          Gaps
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ייי J, Hafalia A;
      such polypeptides may be used to
                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Visual pigments retinal binding site"
                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 4; Length 96; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= G-protein_coupled_receptor_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; G-protein coupled receptor; GCREC; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tribouley CM, Tang YT, Baughn MR, Graul
Patterson C, Lal P, Au-Young J, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Mature human GCREC-5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .23
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein coupled receptor, GCREC-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .27
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE12026 standard; protein; 112 AA.
promote cell growth. For example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2000, 2000US-0193051P.
06-APR-2000; 2000US-0195155P.
20-APR-2000; 2000US-0199084P.
28-APR-2000; 2000US-020551P.
05-MAY-2000; 2000US-0202278P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001; 2001WO-US010436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .112
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Das D;
                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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N-PSDB; AAD19581.
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 SSVMH 43
                                                                                                                                                                                                                                                                                                                                                                                                             1 SSVMH 5
                                                                                                                                                                                                                                        Sequence 96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200172836-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001
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Walia NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12026;
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protein. The GCRECs are used for treating or preventing disorders associated with decreased expression of functional GCREC, and for identifying specific agonists and antagonists, also binding agents and outleters. Also binding agents and outleters. They can also be used for generating specific antibodies and for proteosome analysis. Disorders that can be treated include cell proliferative disorders, e.g., arteriosclerosis and cancer, neurological disorders, e.g., atherosclerosis and congestive heart cardiovascular disorders, e.g., atherosclerosis and congestive heart failure, gastrointesfinal disorders, e.g., acquired immunofintlammatory disorders, e.g., acquired immunodeficiency syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and obesity and viral infections. Nucleic acids that encode GCREC are used to identifying agents that alter its expression, for assessing toxicity of test compounds, and as sources of primers and probes for diagnostic detection of GCREC DNA and of therapeutic antisense and riboscme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
              New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                        sequences. They can also be used in gene therapy, for chromosomal mapping, and for recombinant production of GCREC. The antibodies are useful for diagnosis and monitoring of diseases associated with GCREC expression, for detecting and purifying GCREC, and as therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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                                                                                                                    present sequence is a human G-protein coupled receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human OR-like polypeptide query sequence, SEQ ID NO: 2175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 4; I Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG72494 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lancet D,
                                                                                 Claim 1; Page 106; 111pp; English.
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100.0%;
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24-FEB-2000; 2000US-0184809P.
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(YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
5; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200127158-A2
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New polynucleotides which encode polypeptides involved in olfactory

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour
                                                                                                                                                                                                                                                                                                              Claim 11; Page 934-935; 1857pp; English.
                                         63
                                                                                         AAG71795;
Query Match
                                                             Matches
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The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory agonists and antapolists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of elfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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sensation for identifying olfactory agonists and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuchs T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human olfactory receptor polypeptide, SEQ ID NO: 1476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                       Example 6; Page 1464-1465; 1857pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG71795 standard; protein; 117 AA
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290713/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200127158-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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The invention relates to isolated polymucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polymucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
c in diagnostics as expressed sequence tags for identifying expressed
c extivity of (II) is useful in gene therapy techniques to restore normal
c useful for generating antibodies against it, detecting or quantitating a
c useful for generating antibodies against it, detecting or quantitating a
c useful for supplement. (II) and its binding partners are useful in medical imaging
c supplement. (II) and its binding partners are useful for treating disorders
involving aberrant protein expression or biological activity. The
c polypeptide and polymucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
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receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                            100.0%; Score 25; DB 4; I
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 41124; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #10756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG10765 standard; protein; 133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS74952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                              SSVMH 67
                                                                                                                                                                                                                                                                                                                          1 SSVMH 5
                                                                                                                                                                                                          Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG10765;
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG10765
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                              and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain; variable region; mouse; anti-idiotypic antibody; 14Cl2; Factor VIII inhibitory antibody; C2 domain; Factor VIII; procoagulant; bleeding disorder; haemophilia; B cell apoptosis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal anti-idiotypic antibodies against human Factor VIII inhibitory antibodies, useful for treating or preventing bleeding disorders of hemophilia patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 4; Length 133; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-idiotypic antibody 14C12 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saint-Remy JR, Jacquemin MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL73173 standard; protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3A; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2002; 2002EP-00447150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-158719/16.
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVMH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-158719/
N-PSDB; ADL73172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSVMH 5
                                                                                                                                                                                                                                                             Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1388544-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL73173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                              Query Match
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ADL73173
XX
AC ADL73173
XX
DX ADL73173
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XX
Heavy
XW Heavy
XX
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The invention relates to an isolated nucleic acid derived from Enterococcus faecium monoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid operably linked to chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for disagnosing pathological conditions of resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans on nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid ace useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                ö
apoptosis of B cells carrying anti-C2 inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                ö
                                                                                            Length 137;
                                                                                           Score 25; DB 8; Length 13
Pred. No. 3e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 7091; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                       E. faecium protein sequence SEQ ID 7091.
               antibodies in a haemophilia patient
                                                                                                                                                                                                                                                                                                      ADC97464 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0051571P.
98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                5; Conservative
patients, or to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-799836/75.
                                                                                                              Similarity
                                                                                                                                                                                                       31 SSVMH 35
                                                                                                                                                                      1 SSVMH 5
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                                                       Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection
                                                                                                                                                                                                                                                                                                                                            ADC97464;
                                                                                            Query Match
Best Local &
                                                                                                                              Matches
                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                      ADC97464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 167
/note= "residues Xaa are encoded by internal stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine; cervical; stomach; rectal; cytostatic; vaccine; cell function regulator; human; prostate homologue of olfactory receptor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel gene designated PHOR-1, a G-protein-coupled receptor up-regulated in prostate cancer, useful as diagnostic marker and therapeutic target for cancers of prostate, kidney, uterus.
                                                                  Gaps
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Length 144;
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                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of AI138218, a PHOR-1 family member.
                               . 3.2e+02;
100.0%; Score 25; DB 7; 100.0%; Pred. No. 3.2e+02
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     AAB85005 standard; protein; 167 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Afar DEH, J., Saffran DC;
                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-367230/38.
Query Match
Best Local Similarity
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                                                                                                                                                                                                    SSVMH 98
                                                                                                                                 1 SSVMH 5
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Mitchell SC,
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                                                                  Matches
                                                                                                                                                                                                                                                                                                      RESULT 14
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ID AABB

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antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC59959 to ACC59989 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated PMMM-1 to PMMM-31 (1). (1) have cytostatic, antiarteriososlerotic, antiallergic, antialtarteriososlerotic, antiallergic, antiallergic and thyromimetic activities, and can be useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of PMMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. applepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cubhing's syndrome) disorders, or infections. They are also useful in assessing the effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramkumar J,
                                                                                                                                                                                                                                              Human; protein modification and maintenance molecule; PMMM;
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Yang J, Lu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NK, Warren BA, Tang YT,
Griffin JA, Gietzen KJ,
BM, Richardson TW, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swarnakar A, Tran UK, Kable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 213-214; 270pp; English.
                                                                                                                 ABR43245 standard; protein; 248 AA.
                                                                                                                                                                                                                 Human PMMM-6 protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002; 2002WO-US029221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0322196P
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N-PSDB; ACC59964.
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 SSVMH
                               58 SSVMH
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09-NOV-2001; 2
16-NOV-2001; 2
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Marquis JP,
Emerling BM,
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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05-OCT-2001;
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                                                                                 RESULT 15
ABR43245
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Gaps

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100.0%; Score 25; DB 4; Length 167; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

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of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMMM. The PMMMMs or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or medulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles
88888888888
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Sequence 248 AA;

Query Match 100.0%; Score 25; DB 6; Length 248; Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels

°; Gaps .; 0

[|||| 234 SSVMH 238 1 SSVMH 5

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Search completed: April 28, 2005, 18:17:27 Job time : 40.6562 secs

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27, Appl 190, App 958, App 13210, A 17082, A

4441, Ap 21306, A 13907, A 2, Appli

625, App 5968, Ap 4307, Ap 14773, A

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Sequence 7091, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                        Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                         US-09-270-767-54547
US-10-101-464A-625
US-09-328-325-5968
US-09-328-32-5968
US-09-902-540-14773
US-07-857-224B-27
US-09-638-092-958
US-09-638-092-958
US-09-248-795A-13210
US-09-248-795A-17082
US-09-134-000C-4441
US-09-252-991A-13106
US-09-252-991A-13106
US-09-252-991A-13107
US-08-688-988-2
US-08-252-991A-13907
US-08-688-988-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05151
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
NAME/KEY: misc_feature
;
LOCATION: (B) LÖCATION 1...144
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7091:
US-09-107-532A-7091
                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 144 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7091:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
RESULT 1
US-09-107-532A-7091
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                                                                                                                                                                                                                                                                                                                                    Sequence 4, Appli
Sequence 1104, Ap
Sequence 4615, Ap
Sequence 6, Appli
Sequence 7, Appli
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Sequence 7, Appli
Sequence 12352, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 12736, A
Sequence 12736, A
Patent No. 5208144
Patent No. 5208144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50611, A
Sequence 24525, A
Sequence 4, Appli
Sequence 4, Appli
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Sequence 232, App
Sequence 7885, Ap
Sequence 7054, Ap
Sequence 48353, A
Sequence 48353, A
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Sequence 93, Appl
Sequence 35394, A
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                                                                                                                   (without alignments)
36.750 Million cell updates/sec
                                                                                                   April 28, 2005, 18:06:50; Search time 10.1562 Seconds
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                                                                                                                                                                                                                                                                                                      513545
                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-680-728-7

US-10-017-066A-7

US-09-902-540-12352

US-09-934-551-2

US-09-134-000C-4515

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US-09-134-000C-4515

5208144-37

US-08-118-270-93

PCT-US33-08528-93

US-09-270-767-35394

US-09-270-767-35394

US-09-270-767-355394

US-09-270-767-3528

US-09-241-5028-7

US-09-114-010-4615

US-09-114-010-4615

US-09-441-5028-7

US-09-441-5028-7

US-09-441-5028-7

US-09-441-5028-7

US-09-441-5028-7

US-09-441-5028-7

US-09-114-010-4615

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US-09-110-328-332

US-09-621-976-5485

US-09-270-767-35513
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                          US-10-088-639A-2_COPY_158_162
25
1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                           Scoring table:
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Database :

Result

Sequence:

Run on:

Searched:

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APPLICANT: BEASLEY, Ellen M.
APPLICANT: BEASLEY, Ellen M.
APPLICANT: Li, Zhenya
APPLICANTON: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TILE REPERENCE: CLO00757
CURRENT APPLICATION NUMBER: US/09/934,551
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/226,903
PRIOR PILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                              Patent No. 6833447;
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12352
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                                               Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                            100.0%; Score 25; DB 4; 100.0%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                         Sequence 12352, Application US/09902540 Patent No. 6833447
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; Sequence 2, Application US/09934551
: Patent No. 6461850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Myxococcus xanthus
US-09-902-540-12352
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                    US-09-902-540-12352
US-10-017-066A-7
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: UV-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REPERENCE: 129.24U5U1
CURRENT APPLICATION NUMBER: US/09/680,728
CURRENT PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 6/157,902
PRIOR APPLICATION NUMBER: 6/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mary Faris
APPLICANT: Rene S. Hubert
APPLICANT: Reve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REPERENCE: 511582002410
CURRENT APPLICATION NUMBER: US/10/017,066A
CURRENT FILING DATE: 2002-05-29
                                                                         .
0
                  Query Match 100.0%; Score 25; DB 4; Length 144; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity 100.0%; Score 25; DB 4; Length 163; Similarity 100.0%; Pred. No. 1.6e+02; 5; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10017066A
Patent No. 6838258
                                                                                                                                                                                                                                                                            US-09-680-728-7; Sequence 7, Application US/09680728; Patent No. 6790631
                                                                                                                                                                                                                                                                                                                                                                             Arthur B. Raitano
Daniel E.H. Afar
Aya Jakobovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mary Faris
Rene S. Hub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                           94 SSVMH 98
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PAPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.

TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA

CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/396,697

FILING DATE: 22-MG-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 225,211

FILING DATE: 23-WG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR NO. 5208144

PAPLICATION STATES, JOHN A.; RAYCHOWDHURY, RAKTIMA, NILES, JOHN L.

TITLE OF INVENTION BETHOD FOR DETECTION OF HUMAN DNA

CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/396,697

FILING DATA:

APPLICATION NUMBER: 313,682

FILING DATA:

PRIOR APPLICATION NUMBER: 22-FRB-1989

FILING DATE: 22-FRB-1989

RILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IOMDHURY, RAKTIMA; NILES, JOHN L. DETECTION OF HUMAN DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 726;
                                                                                                                                                                                                                                                                                                                                                                                    Length 517;
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 4; I 100.0%; Pred. No. 4.8e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.7e+02;
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CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 4515 LENGTH: 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25;
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                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                          FEATURE: NAME/KEY: MISC_FEATURE
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                                                               Sequence 2, Application US/10224414

Patent No. 6638751

GENERAL INFORMATION:
THE CAN INVESTION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNMBER: US/10/224,414
CURRENT APPLICATION NUMBER: US/226,903
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6617156
GRNERAL INFORMATION:
APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
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100.0%; Score 25; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 4; I
100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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APPLICANT: Gary Bre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-000C-4515
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LENGTH: 300
                                                   US-10-224-414-2
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                                                                                   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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Pred. No. 94;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                 MURPHY=2 PCT
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US-09-270-767-50611
; Sequence 50611, Application US/09270767
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                               NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                          COMPUTER READABLE FORM:
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                      D.C.
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                                                     20004
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
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                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNBER: 34,033
REGISTRATION NUMBER: 34,033
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
 100.0%; Pred. No. 6.7e+02; ative 0; Mismatches 0;
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                  Sequence 93, Application US/08118270 Patent No. 5508384
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 Best Local Similarity 100.
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Sever
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Matches 4; Conserv
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SSIMH 17
                                                                                           82 SSVMH 86
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Sequence 24525, Application US/09248796A

Batent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE

1. LOCATION: (1011)

1. TOPER INFORMATION: Identity of amino acid sequences at the above locations are unknoted us-09-248-796A-24525
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5611
LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
PEATURE:
                                                                                                                                                                                                                                                                                                                                            96.0%;
80.0%;
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80.0%;
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Best Local Similarity 80...
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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108 SSIMH 112
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24 SSIMH 28
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Search completed: April 28, 2005, 18:28:08 Job time : 12.1562 secs

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Sequence 24, Appl Sequence 85, Appl Sequence 85, Appl Sequence 89, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 102, Appl Sequence 162, Appl Sequence 756, Appl Sequence 756, Appl Sequence 756, Appl Sequence 160, Appl Sequence 120, Appl Sequence 120, Appl Sequence 21, Appl Sequence 22, Appl Sequence 20, Appl Sequence 5005, A Sequence 73021, A Sequence 75011, A

Sequence 74, Appl Sequence 37219, A

Run on:

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Sequence 5172, Application US/09864408A

Sequence 5172, Application US/09864408A

Publication No. US20040009474A1

GENERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Encoc FILE REFERENCE: 21402-012

CURRENT APPLICATION NUMBER: US/09/864,408A

CURRENT FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-05-24
               US-09-886-055-85
US-09-886-055-85
US-09-886-055-89
US-09-844-861A-26
US-10-804-291-85
US-10-107-161-878
US-10-017-161-880
US-10-107-161-880
US-10-107-161-880
US-10-107-161-880
US-10-107-629-164
US-10-107-629-164
US-10-387-629-164
US-10-387-629-164
US-10-387-629-164
US-10-292-798-756
US-10-292-798-756
US-10-292-798-756
US-10-293-798-756
US-10-144-566-720
US-10-144-861A-20
US-10-282-122A-5085-015
US-10-282-122A-75081
US-10-282-122A-75081
US-10-282-122A-75081
US-10-282-122A-75081
US-10-282-122A-75081
US-10-282-122A-75081
US-10-283-122A-75081
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
US-10-144-9618-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 25; DB 11; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5172
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43019, Application US/09864761 Patent No. US/00020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5172
SSVMH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSVMH 5
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 23
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5172, Ap Sequence 43019, A Sequence 2118, Ap Sequence 51, Appli Sequence 17, Appli Sequence 51, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                     (without alignments)
53.700 Million cell updates/sec
                                                                                                                             April 28, 2005, 18:24:46; Search time 31.0156 Seconds
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1. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US09_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

1. (cgn2_6)ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 US-09-864-408A-5172
US-09-864-761-43019
US-09-864-761-43019
1 US-09-980-049-5
6 US-10-437-963-182859
4 US-10-145-586-37
1 US-09-981-56A-51
4 US-10-167-555-2
US-09-934-551-2
US-09-934-551-2
4 US-10-143-575-2
5 US-10-640-326-2
                                                                                                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             1426032 segs, 333106140 residues
                                                                                                                                                                                                   US-10-088-639A-2_COPY_158_162
25
1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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                                                                                             protein
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Gaps

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Length 69; Indels

Result

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CURRENT APPLICATION VUMBER: US/09/980,049
CURRENT APPLICATION VUMBER: 2001-11-28
PRIOR APPLICATION VUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR APPLICATION VUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR APPLICATION VUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR APPLICATION VUMBER: 60/193,051; 60/193,051; 60/200,04-20; 2000-04-20; 2000-05-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SEQ ID NO 5
LENGTH: 112
TYPE: PRT
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                                                                             APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REPERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276, 774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560, 875
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496, 914
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 25; DB 15;
; Pred. No. 2.1e+02;
0; Mismatches 0;
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0072 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 4585651CD1
US-09-980-049-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: GRAUL, Richard
APPLICANT: KHAN, Farrah A.
APPLICANT: KHAN, Farrah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/09980049; Publication No. US20040220092A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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HAFALIA, April
WALIA, Narinder K.
Publication No. US20040053245A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATTERSON, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAL, Preeti
AU-YOUNG, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-10-276-774-2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 SSVMH 43
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        APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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INFORMATION: SWISSPROT HIT: Q95156, EVALUE 6.00e-05
INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
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EXPRESSED IN BRAIN, SIGNAL = 0.92
                                                                                                                                                                                                                             FILE REFERENCE: 1001-05-23

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR PELING DATE: 2001-05-24

PRIOR PELING DATE: 2000-05-04

PRIOR PELING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-05

PRIOR PILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-05

PRIOR PILING DATE: 2000-05-05

PRIOR PILING DATE: 2000-06-03

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2001-01-01

PRIOR PILING DATE: 2001-01-07

PRIOR PILING DATE: 2001-01-30

PRIOR PILOR DATE
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US-10-276-774-2118
; Sequence 2118, Application US/10276774
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MOTHER INFORMATION: EQUHER INFORMATION: EQUHER INFORMATION: S
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55 SSVMH 59

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| PUBLICARION NO. US20040005656A1
| PUBLICARIN KARDA EL A. |
| APPLICAMIN KARDA EL A. |
| TITLE OF INVENTION: Same |
| FILE OF INVENTION NUMBER: US /09/981,566A |
| FRIOR APPLICATION NUMBER: 00/240,704 |
| FRIOR FILING DATE: 2000-10-16 |
| FRIOR PILING DATE: 2001-01-25 |
| FRIOR APPLICATION NUMBER: 00/24,118 |
| FRIOR PILING DATE: 2000-10-25 |
| FRIOR PILING DATE: 2000-10-25 |
| FRIOR FILING DATE: 2000-10-21 |
| FRIOR FILING DATE: 2000-10-3 |
| FRIOR FILING DATE: 2001-02-12 |
| FRIOR FILING DATE: 2000-10-3 |
| FRIOR FILING DATE: 2001-02-12 |
| FRIOR FILING DATE: 2000-10-3 |
| FRIOR FILING DATE: 2001-03-12 |
| FRIOR FILING DATE: 2001-03-13 |
| FRIOR 
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APPLICANT: ASAL, KIYOSHI
APPLICANT: ASAL, KIYOSHI
APPLICANT: ASURATANI, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
ITILE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
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                                                                                                                                                                                  US-09-981-566A-51; Sequence 51, Application US/09981566A; Publication No. US20040005656A1
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Publication No. US20030143668A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-09-981-566A-51
                                                            218 SSVMH 222
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1 SSVMH 5
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Brabazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICANTON NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 182859
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Weich, Nadine
APPLICANT: Weich, Nadine
APPLICANT: Weich, Nadine
APPLICANT: Experiment, Rajasekhar
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: HUMAN THIOREDOXIN PAMILY MEMBERS,
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, HUMAN LIUGINE-RICH
TITLE OF INVENTION: UNMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 252
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Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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US-10-437-963-182859
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100.0%; Pred. No. 3.3e+02;
ttive 0; Mismatches 0;
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LOCATION: (1)..(147)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                  Sequence 182859, Application US/10437963
Publication No. US20040123343A1
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Best Local Similarity luv...
S; Conservative
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ORGANISM: Oryza sativa
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US-10-145-586-37
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Sequence 2; Application US/10143575
Publication No. US20030166072A1
GENERAL INFORMATION:
TUDICATION TO. US20030166072A1
GENERAL INFORMATION:
TITLE OF INVENTION: LOGICATED HOAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION NUMBER: US/10/143,575
CURRENT FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                  APPLICANT: BEASLEY.

APPLICANT: BEASLEY.

APPLICANT: Li, Zhenya

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: USES THEREOF

FILE REPERENCE: CLOOOTS DIV

CURRENT APPLICATION NUMBER: 05/26,903

PRIOR APPLICATION NUMBER: 06/226,903

PRIOR APPLICATION NUMBER: 09/334,551

PRIOR FILING DATE: 2001-08-23

NUMBER: 09/334,551

NUMBER: PROTEING DATE: 2001-08-23

NUMBER: OF SEQ ID NOS: 4

SOFTWARE: FASTERO FOR Windows Version 4.0

SEQ ID NO 2
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                                                                                                                                    US-10-224-414-2

; Sequence 2, Application US/10224414

; Publication No. US20030036167A1

; GENERAL INFORMATION:
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Matches 5; Conservative
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ORGANISM: Homo sapiens
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Matches 5; Conserv
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  1 SSVMH 5
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ORGANISM: HUMAN
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US-10-640-326-2
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Sequence 2, Application No. US20020072106A1
GENERAL INFORMATION:
APPLICANT: Li, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL000757
CURRENT PELLING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
FRICH REPERENCE: CL000757
FRICH REPERENCE: C.001-08-23
FRICH FILING DATE: 2001-08-23
FRICH FILING DATE: 2001-08-23
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Publication No US20030022212A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therefor
FILE REFERENCE: WRIO1-089PIRM
CURRENT APPLICATION UNMBER: US/10/167,555
CURRENT FILING DATE: 2002-06-12
PRIOR PILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 300
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 966
LENGTH: 261
TYPE: PRT
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Best Local Similarity luv...
Lag 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-10-167-555-2
                                                                                         ; ORGANISM: Homo sapiens
US-10-017-161-966
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; ORGANISM: HUMAN
US-09-934-551-2
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LENGIH: 282
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APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
TILLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PEI
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: 078003-0277150
CURRENT APPLICATION NUMBER: 00/213,812
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 85
                                                                                                                                                                                 100.0%; Score 25; DB 10;
100.0%; Pred. No. 6.9e+02;
iive 0; Mismatches 0;
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Pred. No. 7.1e+02;
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Best Local Similarity 100.
Matches 5; Conservative
       SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-09-886-055-85
                                                                                 TYPE: PRT CORGANISM: Homo sapiens US-09-844-861A-24
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                       APPLICANT: LI, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/640,326
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/934,551
PRIOR PILING DATE: 2001-8-23
PRIOR APPLICATION NUMBER: 09/24,414
PRIOR APPLICATION NUMBER: 09/24,414
PRIOR PILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 300
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: No. US20030216304A1el Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 15966-789 US
CURRENT APPLICATION WHERE: US/99/844,861A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 300;
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100.0%; Pred. No. 6.8e+02;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/199, 947

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-08-27

PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/255, 226

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR PELICATION NUMBER: 60/256, 524

PRIOR PELICATION NUMBER: 60/256, 524

PRIOR APPLICATION NUMBER: 60/258, 159

PRIOR APPLICATION NUMBER: 60/258, 511

PRIOR APPLICATION NUMBER: 60/258, 511

PRIOR PILING DATE: 2000-12-28

PRIOR PILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: 60/258, 511

PRIOR PILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: 60/258, 511

PRIOR PILING DATE: 2000-12-28

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PRIOR PILING DATE: 2000-12-28

PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09844861A Publication No. US20030216304A1 GENERAL INFORMATION:
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Mishra, Vishnu
Spytek, Kimberly
Burgess, Catherine
Lepley, Denise
Grosse, William
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Alsobrook, John
Gangolli, Esha
Casman, Stacie
APPLICANT: BEASLEY, Ellen M.
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: HUMAN
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UNC8_CABEL
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K685 HUMAN
KIN1 YEAST
DPYD CAEEL
N124 SCHPO
HAIR RAT
 052538 erwinia car

P42662 coturnix co

08ngk4 homo sapien

08ngk4 homo sapien

08zg46 salmonella

08zg46 darosophila

024648 drosophila

024648 drosophila

024648 drosophila

02461 percopsis t

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026177 gorilla gor

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095716 crotalus vi

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009469 cryctolagus
09768 oryctolagus
095614 homo sapies
014248 plasmodium
003133 saccharopol
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P3199 1 genome pc
P26541 human papil
P76248 escherichia
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P6249 anguilla an
P0219 cryrinus ca
O98480 nororhynchu
P6219 cryrinus ca
O98480 mororhynchu
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O98480 mororhynchu
O99480 methanococc
P6463 canis famil
P7525 sescherichia
Q10528 mycobacterii
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MEDLINE=99030316; PubMed=9811652;
Beach M.B., Osuna R.;
"Identification and characterization of the fis operon in enteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Carbonic anhydrase precursor (EC 4.2.1.1) (Carbonate dehydratase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=554;
                             Q9dgn1
Q00449
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Q98936
Q05909 r
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P87416
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-!- FUNCTION: Reversible hydration of carbon dioxide.
-!- CATALYICS ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- COPACTOR: Zinc (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AA
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ACCB CRICR
ACCB CRICR
SUIS_SUNMU
SUIS_RABIT
MIBA_HUMAN
MS 3_SCHPO
RPB1 PLAFD
POLG LAWO
HEBB CACR
HEBB CARCR
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NEUU_RAT
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C56I_ECOLI
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052538;
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 CAH ERWCA

ID CAH B

AC 15-523

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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01-NoV-1995 (Rel. 32, Last sequence update)
01-NoV-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Astacin like metalloendopeptidase (EC 3.4.24.-).
Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Crainata; Vertebrata; Euteleostomi;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elaroussi M.A., Deluca H.F.;
"A new member to the astacin family of metalloendopeptidases: a novel
1,25-dihydroxyvitamin D-3-stimulated mRNA from chorioallantoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Biochim. Biophys. Acta 1217:1-8(1994).
-!- FUNCTION: May play a role in the degradation of eggshell matrix.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- INDUCTION: By 1,25-dihydroxyvitamin D-3.
-!- SIMILARITY: Belongs to peptidase family M12A.
-!- SIMILARITY: Contains 1 CUB domain.
SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBONIC ANHYDRASE.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 20;
; Mismatches
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ProDom; PD000865; Buk COanhd; 1.
PROSITE; PS00162; BUK CO2_ANHYDRASE; 1.
Lyase; Zinc; Periplasmic; Signal.
1 19 POTENTIAL.
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TISSUE=Chorioallantoic membrane;
MEDLINE=94114563; PubMed=8286408;
                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q50940; 1KOQ.
InterPro; IPR001148; Euk_COanhd.
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.P42662;
                                       family.
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-- FUNCTION: Putative odorant receptor.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
-- WWW-"http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcel
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Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
8045963357FAB634 CRC64;
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                                                             2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 27; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AA
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InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF0001; 7tm 1; 1.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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or send an email to license@isb-sib.ch).
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OR52K2.
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DOMAIN 1 27
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56
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101
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative odcraft receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR ELOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Hydrolase; Metalloprotease; Zinc.
METAL
ACT_SITE 85 85 BY SIMILARITY.
METAL 88 88 ZINC (CATALYTIC) (BY SIMILARITY).
METAL 94 ZINC (CATALYTIC) (BY SIMILARITY).
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InterPro; IPR000276; GPCR Rhodpsn.
FRAM; PR00001; 7tm 1; 1.
PROSITE: PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE: PS0262; G-PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; DOMAIN; DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2ACE1EAC96366A1 CRC64;
                                            InterPro; IMR00899; CUB.
InterPro; IPR008059; CUB.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006026; Peptidase_M.
InterPro; IPR001506; Peptidase_M.
InterPro; IPR001506; Peptidase_M.
Pfam; PF00410; Astacin; 1.
Pfam; PF00480; ASTACIN.
SMART; SM00042; CUB; I.
PR05ITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS01180; CUB; 1.
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10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52Kl.
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HSSP; P07584; 1IAE
MEROPS; M12.UPA; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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OBNGK4:
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SEQUENCE
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-1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-1- SUBLERITY: Belongs to the ABC transporter family. ModC subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRARIT-TY2 / ATCC 700931;
STRARIT-TY2 / ATCC 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland W., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol: 185:2330-2337(2003).
-!- FUNCTION: Part of the ABC transporter complex modABC (TC 3.A.1.8)
involved in molybdenum import. Responsible for energy coupling to
the transport system (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Churcher C., Mungall K.L., Bentley S.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebathia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                      .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 314;
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10-OCT-2003 (Rel. 42, Last annotation update)
Molybdenum import ATP-binding protein modC (EC 3.6.3.29)
MODO OR STY0816 OR T2104.
                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (PC 56D56A898904BC58 CRC64;
                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) 7 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                          (POTENTIAL).
                                                                                                           CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCN
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  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                              314 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21534948; PubMed=11677669; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + molybdate(In).
--- SUBNIT: The complex is composed of two ATP-binding proteins (mod0), two transmembrane proteins (mod8) and a solute-binding protein (modA) (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00211; ABC_TEANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PHOSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATPACATAGE; Transport; Molybdenum; Membrane; Inner membrane; ATP-binding; Complete protecome.
ATP-binding; Complete protecome.
NP_BIND 31 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 352; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Molybdenum import ATP-binding protein modC (EC 3.6.3.29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP BIND 31 38 ATP (By similarity).
SEQUENCE 352 AA; 39111 MW; 30E56C25FD1D6683 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                  EMBL; AE016841; AA069721.1;
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR008995; MoP_like.
InterPro; IPR008995; MoP_like.
InterPro; IPR005116; TOBE.
Pfam; PP00405; ABC_tran; I.
SWART; SM00382; AAA; I.
TIGRFAMS; TIGR00638; MOP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                EMBL; AL627268; CAD05231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 SSVMH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MODO OR STM0783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODC SALTY
Q8ZQR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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MODC_SALTY
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RESULT 8
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                (See http://www.isb-sib.ch/announce/
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MEDLINE-Z0196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutron G.G., Wortman J.R., Yandell M.D., Zhanp Q., Chen L.X.,

Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendal J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A., Palazzolo M.J.;
   and for
                                                                                      R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR004666; Mop.
R InterPro; IPR00816; TOBE.
R InterPro; IPR00816; TOBE.
R Pfam; PF00045; ABC_tran; 1.
R Pfam; PF004459; TOBE; 1.
R Pfam; PF004459; AAA; 1.
R TIGRPAMS; ITGR00638; Mop; 1.
R PROSITE; PS00911; AAA; 1.
R PROSITE; PS00911; AAA; 1.
R PROSITE; PS00911; ABC_TRANSPORTER_2; 1.
R PROSITE; PS00911; ABC_TRANSPORTER_2; 1.
R PROSITE; PS0093; ABC_TRANSPORTER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence of the Antennapedia complex of Drosophila.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; Length 352; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88112803; PubMed=2892759;
Rushlow C., Doyle H., Hoey T., Levine M.;
Rushlar characterization of the zerknullt region of the Antennapedia gene complex in Drosophila.";
Genes Dev. 1:1268-1279(1987).
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
   Usage by
                                                                                                                                                                                                                                                                                                       31 38 ATP (By similarity).
352 AA; 39055 MW; 65137E645711AAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWZ1_DROME STANDARD; PRT; 353 AA. P09089; Q9VI45; 01-NOV-1988 (Rel. 09, Created) 10-NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Zerknuellt protein 1 (ZEN-1). ZEN OR ZEN1 OR Z1 OR CG1046.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. ...
                  entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
                                                            EMBL; AE008732; AAL19721.1; -.
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 SSVMH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSVMH 5
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                                                                                                                                                                                                                                                                                                       NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       Query Match
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HM21 DROME
ID HM21 DROME
DAC 01-NOV.
DT 01-NOV.
DT 10-NOV.
DT 10-NOV.
DT 10-NOV.
DE ZErKNUM
GN ZEN OR
OC BURATY.
OC NEOPTE
OC BURATY.
OC NEOPTE
OC BURATY.
OC NEOPTE
OC STRAIN
RA RUBBLIN
RA PALECE
RI Genes
RY Adams
RA ADATI
RY MBLII
RY BENES
RA ADATI
RA ADATI
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B. Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M., RA Dogeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., B. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosier C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Krafc C., Kravitz S., Kulp D., Lai Z., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lia X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Nelson D.K., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Reinert K., Remington K.A., Nusskern D.R., Pacleb J.M., RA Reinert K., Saunders R.D.C., Scheeler F., Shen H., Shier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q., Zheng X.H., Mohiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng X.H., Zhong F.M., Worley K.C., Wu D., Yang S., Yao Q., Zheng X.H., Globs R.A., Myers E.W., Rubin G.M., Venter I., Stapleton R., Shong S., Yao Q., Zheng X.H., Globs R.A., Myers E.W., Rubin G.M., Venter I., Ships R.A., Myers E.W., Rubin G.M., Venter I., Stapleton R., Shong G., Zhao G., Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- FUNCTION: Required for the differentiation of the dorsal-ventral pattern, and does not appear to be involved in the process of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA; 39302 MW; 1FA64031C160CE2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Nuclear.
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FlyBase; FBgn0004053; zen.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
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DNA BIND 90 149 HOMEOR
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PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X68347; CAA48416.1; -.
EMBL; AE001572; AAD19800.1; -.
EMBL; AE003674; AAP54087.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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PDB; 1KZ2; 19-JUN-03
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2 SSVMH

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Mammalia; Eutheria; Rodentia; Sciurognathi; Geomyidae; Cratogeomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesoplodon peruvianus (Peruvian beaked whale).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR005798; Cytb_b6_C.
Interpro, IPR005797; Cytb_b6_N.
Pfam; PP00032; Cytochrome_b_C; I.
Pfam; PP00033; Cytochrome_b_N; I.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF302162; AAL69575.1; -. EMBL; AF302182; AAL69595.1; -. EMBL; AF302183; AAL69596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
97
182
196
266
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97
182
196
196
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SSVMH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=27617;
               NCBI_TaxID=13463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYB_MESPE
Q35066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heme.
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
CYB_MESPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cratogeomys tylorhinus (Naked-nosed pocket gopher).
Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                       Chromosoma 103:613-624(1995).

-!- FUNCTION: Required for the differentiation of the dorsal-venting pattern, and does not appear to be involved in the process of segmentation (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000010; Homeobox; 1.

PRART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

Transcription regulation; Homeobox; DNA-binding; Nuclear protein; Developmental protein.

HOMEOBOX: HOMEOBOX DNA-binding; Nuclear protein; Homeobox; DNA-BIND 88 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                     Drosophila subobscura (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 373; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                   Terol J., Perez-Alonso M., de Frutos R.; "Molecular characterization of the zerknullt region of the Antennapedia complex of D. subobscura.";
                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha.
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX.
7D647EA2241045F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08WDU1; 08W7F3;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0015180; Dsub\zen.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                      MEDLINE=96088375; PubMed=7587584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA; 40602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X78058; CAA54976.1; -. HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox;
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochrome b. MTCYB OR COTB.
                                                                              Zerknuellt protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSVMH 6
                                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7241;
                 DROSU
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                           024648;
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CYB_CRATY
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                                                                                                                                                                                                                                MOI. Phylogenet. Evel. 22:144-154 (2002).

Phylogenet. Evol. 22:144-154 (2002).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or b660) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B DO: 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukammālia; Butheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae; Mesoplodon.
SEQUENCE FROM N.A.
STRAIN=Isolate G30, and Isolate G31;
MEDLINE=21655508; PubMed=11796037;
Demastes W., Spradling T.A., Hafner M.S., Hafner D.J., Reed D.L.;
"Systematics and phylogeography of pocket gophers in the genera Cratogeomys and Pappogeomys.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBMUNT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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IRON 2 (HEME BS66 AXIAL LIGAND)
IRON 1 (HEWE BS62 AXIAL LIGAND)
IRON 2 (HEME BS66 AXIAL LIGAND)
P -> S (in isolate G30).
F3EEDFICAFABFAD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 1; Length 379;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Acanthomorpha; Paracanthopterygii; Percopsiformes; Percopsoidei;
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MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
97
182
196
380 AA;
                                                                                                    SEQUENCE FROM N.A.
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                                                    NCBI_TaxID=143327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=27708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
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Q9B2C4;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00157; 1BE3.
InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005798; Cytb b6 C.
Pfam; PF00032; Cytochrome b C; 1.
Pfam; PF00033; Cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B D8; 1.
PROSITE; PS00192; CYTOCHROME B D8; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                     Millinkovitch M.C., Mayer A., Powell J.R.;
"Phylogeny of all major groups of cetaceans based on DNA sequences
from three mitochondrial genes.";
Mol. Biol. Evol. 11:339-948(1994).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562, and heme 2 (or b
cor b566), is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
SEQUENCE FROM N.A.
MEDLINE=20481910; PubMed=11027333;
Cassens I., Vicario S., Waddell V.G., Balchowsky H., Van Belle D.,
Cassens I., Vicario S., Wadell V.G.,
Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
Stanhope M.J., Milinkovitch M.C.;
"Independent adaptation to riverine habitats allowed survival of
ancient cetacean lineages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percopsis transmontana (Sand roller).
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 379; 100.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA; 43066 MW; 1BE8AC9AAE5D2050 CRC64;
                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                            MEDLINE=95115542; PubMed=7755710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF304074; AAC48451.2; -.
                                                                                                                                                                                 SEQUENCE OF 1-134 FROM N.A.
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97
182
196
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MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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TO CYB_P
TO CYB_P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP002928; BAB70156.1; -.
InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005799; Cytb b6 C.
InterPro; IPR005799; Cytb b6 N.
Pfam; PF00032; cytochrome b C; N.
Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B QO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPACTOR: Binds two home groups non-covalently. Heme 1 (or BL or D5562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.
                                                                                                                           MEDLINE=21519020; PubMed=11606696;
MAYA M., Kawaguchi A., Nishida M.,
"Mitya M., Kawaguchi A., Nishida M.,
"Mitya moderate-scale evolutionary genomics with 38 newly
study for moderate-scale evolutionary genomics with 38 newly
determined complete mitochondrial DNA sequences.";
Mol. Biol. Evol. 18:1993-2009(2001).
-I- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity)

similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
SIMILARITY: Belongs to the cytochrome b family.

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97 IRON 2 (HEME BS66 AXIAL LIGAND)
182 IRON 1 (HEME BS62 AXIAL LIGAND)
196 IRON 2 (HEME BS66 AXIAL LIGAND)
42233 MW; 3CEBBCBA74271968 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380;
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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MEDLINE=21097364; PubMed=11161760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Conservative 0
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Percopsidae; Percopsis.
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          SOUTH TEXT TO THE 
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                                                                                                                                                                                                                                                                                                                                H
Machordom A., Doadrio I.;

"Evidence of a cenozoic Betic-Kabilian Connection based on freshwater lish phylogeography (Luciobarbus, Cyprinidae).";

Mol. Phylogenet. Evol. 18:252-263(2001).

-! FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (Complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!-COPACTOR: Binds two heme groups non-covalently. Heme I (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b552) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSTE; PS00192; CYTOCHROME_b HEME; 1.
PROSITE; PS00193; CYTOCHROME_b_Q0; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial DNA.";
J. Mol. Biol. 202:185-217(1988).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential
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CON 2 (HEME B566 AXIAL LIGAND).
CON 1 (HEME B562 AXIAL LIGAND).
CON 2 (HEME B566 AXIAL LIGAND).
7AFA02ECC599306A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 1; Length 380; 100.0%; Pred. No. 33; ive 0; Mismatches 0; Indels
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MEDILIBE=89011951; DubMed=3172215; Barquharson A.; Jacobs H.T., Elliott D.J., Math V.B., Farquharson A.; "Nucleotide sequence and gene organization of sea urchin
                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytoc
cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus (Purple sea urchin)
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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IRON 2
IRON 1
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42732 MW;
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380 AA;
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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PIR, S01511; S01511.

InterPro; IPR005799; Cytb b6 C.

InterPro; IPR005797; Cytb b6 N.

Pfam; PF00032; cytochrome b C; 1.

Pfam; PF00033; cytochrome b N; 1.

PROSITE; PS00192; CYTOCHROME B DE HEME; 1.

ELECTION transport; Mitochondrion; Respiratory chain; Transmembrane;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
631ycylpeptide N-tetradecancyltransferase (BC 2.3.1.97) (Peptide N-myristoyltransferase) (Myristoyl-CoA:protein N-myristoyltransferase)
coupled to ATP synthesis (By similarity).

COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                            cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 IRON 1 (HEME B562 AXIAL LICAND)
98 IRON 2 (HEME B566 AXIAL LIGAND).
11 IRON 1 (HEME B562 AXIAL LIGAND).
117 IRON 2 (HEME B566 AXIAL LIGAND).
42733 MW, B151A26B55A214F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                   similarity).
SUBUNIT: The main subunits of complex b-cl are: cyto cytochrome cl and the Rieske protein (By similarity) SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; 100.0%; Pred. No. 33;
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-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: Belongs to the NMT family.
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98
183
197
380 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=20206853; PubMed=10742044; Delarbre C., Escriva H., Gallut C., Barriel V., Kourilsky P., Janvier P., Laudet V., Gachelin C.; The complete nucleotide sequence of the mitochondrial DNA of the agnathan Lampetra fluviatilis: bearings on the phylogeny of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Biol. Evol. 17:519-529 (2000).
FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
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SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
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Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBF518F24CECECOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
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InterPro; IPR000903; Nmt.
Ffam; PF01233; NMT; 1.
Ffam; PF01233; NMT c; 1.
PROSITE; PS00975; NMT c; 1.
PROSITE; PS00976; NMT 2; 1.
TVANISERS ASVILTANISERSE; Membrane.
SEQUENCE 387 AA; 45121 MW; 0BF518F24C]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lampetra fluviatilis (River lamprey).
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InterPro; IPR005798; Cytb_b6_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                  EMBL; AF053725; AAC08578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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المال Si Conservative أ
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10-OCT-2003 (Rel. 42,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytochrome b. MTCYB OR COTB.
                                                                                                                                                                                                                                                                                                 P30418; 1NMT
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Mol. Biol. E
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InterPro; IPR005797; Cytb b6 N.

Pfam; PF00032; cytochrome b c; 1.

Pfam; PF00033; cytochrome b N; 1.

PROSTE; PS00193; CYTOCHROME B O: 1.

PROSTE; PS00193; CYTOCHROME B O: 1.

Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_REME; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics 139:873-887(1995).

-!-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or expochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!-COPACTOR, Binds two heme groups non-covalently. Heme I (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
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                                                                                                                  IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
                                                                                                                                                                                                                 Score 25; DB 1; Length 396; Pred. No. 34; 0; Mismatches 0; Indels
                                                                                                                                                                                    B2E69A5CB1C3304C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     396 AA
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petromyzon marinus (Sea lamprey).
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                                                                                                                                                                                    44541 MW;
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                                                                                                                                                                                                                                                     5; Conservative
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186
200
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MTCYB OR COB OR CYTB.
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101
186
200
396 AA;
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  68 SSVMH 72
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE. SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the Rh family.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB=Bone marrow;
MEDLINE=9508555; PubMed=7993375;
Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
Colin Y., Ruffie J.;
"Molecular genetics of chimpanzee Rh-related genes: their
"elationship with the R-C-E-F blood group system, the chimpanzee counterpart of the human rhesus system.";
Biochem. Genet. 32:201-221(1994).
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                    (HEME B562 AXIAL LIGAND).
(HEME B566 AXIAL LIGAND).
(HEME B562 AXIAL LIGAND).
(HEME B566 AXIAL LIGAND).
                                                                                                                                             DB 1; Length 396;
                                                                                                                                                                                   0; Indels
                  IRON 1 (HEME B562 AXIAL LIGGIRON 2 (HEME B566 AXIAL LIGGIRON 1 (HEME B562 AXIAL LIGGIRON 2 (HEME B565 AXIAL LIGGIRON 3) A7983DA248A0767D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NH-like protein IA (Rhesus-like protein IA).
Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                  416 AA.
                                                                                                                                         100.0%; Score 25; DB
100.0%; Pred. No. 34;
Live 0; Mismatches
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InterPro; IPR002229; RhesusRHD.
Pfam; PF00909; Ammonium transp; 1.
PRINTS; PR00342; RHESUSRHD.
                    87 IRC
101 IRC
186 IRC
200 IRC
44551 MW; i
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                                                                                                                                                                                 5; Conservative
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396 AA;
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                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                          1 SSVMH 5
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Q28813;
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SEQUENCE
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DB 1; Length 416;

Score 25;

100.08;

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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE=Bone marrow;

MEDLINE=508555; PubMed=7993375;

MEDLINE=1085555; PubMed=7993375;

Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,

Colin Y., Ruffie J.;

"Molecular genetics of chimpanzee Rh-related genes: their

"Molecular genetics of chimpanzee Rh-related genes: their

relationship with the R-C-E-F blood group system, the chimpanzee

counterpart of the human rhesus system.";

Biochem. Genet. 32:201-221(1994).

- FRANCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO

- FRANCTION: Integral membrane protein.

- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
8H-11ke protein IC (Rhesus-1ike protein IC).
Gorilla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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0F3B623F9908E087 CRC64;
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Pred. No. 36;
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PIR; 137075; 137075. I37075. InterPro; IPR001905; Ammonium transpt.
InterPro; IPR002229; RhesusRHD.
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PRINTS; PR00342; RHESUSRHD.
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100.0%;
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                                                                                                                                              STANDARD;
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416 AA;
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Best Local Similarity
Matches 5; Conserv
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                                       324 SSVMH 328
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1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9595;
                                                                                                                                            RHLC_GORGO
Q28426;
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                                                                                                    RESULT 18
RHLC GORGO
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1 SSVMH 5
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                                           SEQUENCE
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                                                                                                                                        Gaps
                                                                 Gorilla gorilla gorilla (Lowland gorilla).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Gorilla.
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                                                                                                                  SEGURAL TRESURE BONDE MAIRON;
TISSUE=BONDE MAIRON;
MEDLINE=95085599; PubMed=7993375;
Calvionol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 1; Length 416; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398877F2B7BEE802 CRC64;
                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Rhesus-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RH-like protein IIF (Rhesus-like protein IIF)
               416 AA
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InterPro, IPR002229, RhesusRHD.
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00909; Ammonium transp; 1.
PRINTS; PR00342; RHESUSRHD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44838 MW;
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              STANDARD;
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                                                                                                            SEQUENCE FROM N.A.
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                                                                                            NCBI_TaxID=9595;
              GORGO
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Q28812;
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RHLF_PANTR
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                                                                                                        Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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15-MAR-2004 (Rel. 43, Last annotation update)
Nuclear factor of 43, Last annotation update)
transcription factor NPAT4) (NF-ATG) (NF-ATA) (NFATX).
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Pred. No. 36;
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PIR; 137003, 137003.

InterPro; 1PR001905; Ammonium transpt.

InterPro; 1PR002229; RheeusRHD.
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PRINTS; PR00342; RHESUSÄHD.
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TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFC3 MOUSE STANDARD,
P97305, Q60896,
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythrocyte; Transmembrane
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416 AA;
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Best Local Similarity
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                                                                                                                                                                                  TISSUB=Thymic lymphoma;
MEDLINE=97170074; PubMed=9017603;
Liu J., Koyano-Nakagawa N., Amasaki Y., Saito-Ohara F., Ikeuchi T.,
Imai S.-I., Takano T., Arai N., Yokota T., Arai K.-I.
"Calcineurin-dependent nuclear translocation of a murine transcription factor NFATX: molecular cloning and functional characterization.";
Mol. Biol. Cell 8:157-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Member of the multicomponent NFATC transcription complex that consists of at least two components, a pre-existing oypoplasmic component NFATCs and an inducible nuclear component NFATC1. Other members such as NFATC4, NFATC3 or members of the activating protein-1 family, MAF, GATA4 and Cbp/p300 can also bind the complex. NFATC proteins bind to DNA as monomers. SUBCELLULAR LOCATION: Cytoplasmic for the phosphorylated form and nuclear after activation that is controlled by calcineurinmediated dephosphorylation. Rapid nuclear exit of NFATC is thought to be one mechanism by which cells distinguish between sustained and transient calcium signals. The subcellular localization of NFATC play a key role in the gene transcription.
                                                                                          calcium-regulated and exhibits distinct DNA binding specificity."; J. Biol. Chem. 270:19898-19907(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mosco, Medicas, Medicas, GO:0045333; P:cellular respiration; IMP. GO:0007507; P:heart development; IGI. GO:000555; P:regulation of transcription, DNA-dependent; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Plays a role in the inducible expression of cytokine genes in \Gamma cells, especially in the induction of the \rm Lb\text{-}2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=p97305-3; Sequence=VSP_005603;
-!- TISSUE SPECIFICITY: Expressed in thwnus. Weakly expressed in muscle, spleen and kidney. Also expressed in lymph node.
-!- DOWAIN: Rel Similarity Domain (RSD) allows DNA-binding and cooperative interactions with API factors (By similarity).
-!- PTM: Phosphorylated by NFATC-kinase; dephosphorylated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Generic signals and specific outcomes: signaling through Ca2+, calcineurin, and NF-AT.";
Cell 96:611-614(1999).
                                                                                                                                                                 SEQUENCE OF 12-1075 FROM N.A. (ISOFORMS X1; X2 AND DELTA-X).
                   Ho S.N., Thomas D.J., Timmerman L.A., Li X., Francke U., Crabtree G.R.;
                                                                    "NFATC3, a lymphoid-specific NFATc family member that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcineurin (By similarity).
-!- SIMILARITY: Belongs to the Rel/Dorsal family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P97305-2; Sequence=VSP_005604;
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                                                                                                                                                                                                                                                                                                                                                                              REVIEW.
MEDLINE=99189746; PubMed=10089876;
MEDLINE=95378239; PubMed=7650004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; IG-11ke.
InterPro; IPR002909; IPT TIG.
InterPro; IPR00451; NF Rel_dor.
InterPro; IPR008366; NFAT.
InterPro; IPR008967; P53-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D85612; BAA12833.1; -. EMBL; U28807; AAA93249.1; -.
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/FTIG=VSP 005604.
LDFKLVFGEDGAPAPPEGRPA -> PRRVLFSVSAQLPS
RTREDGSDL (IN REF. 2).
TTPLC -> NSSLG (IN REF. 2).
P -> LQ (IN REF. 2).
SH -> GY (IN REF. 2).
CEIP -> GIP -> GY (IN REF. 2).
F -> I (IN REF. 2).
F -> I (IN REF. 2).
F -> I (IN REF. 2).
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G -> S (IN per ...)
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-> DQLISDLEHQPSGSTEKWSNHSEFSCPVPFWRI (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330) (gp330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                           PROSITE; PS01204; REL 1; FALSE NEG.
PROSITE; PS50254; REL 2; 1
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito A. Pietromonaco S. Loo A.K.C., Farquhar M.G.; and complete cloning and sequencing of rat gp330/'megalin,' a distinctive member of the low density lipoprotein receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1075;
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REDTDLPSVPSLPVPHSAQAQRPSSETG
                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL.
DNA-BINDING.
                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL. NUCLEAR EXPORT SIGNAL.
                                                                                                                                                                                                                                                                                                    Missing (in isoform Delta-X)
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                                                                                                                                                   CALCINEURIN-BINDING
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F -> Y (IN REF. 2).
G -> R (IN REF. 2).
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1;
100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> S (IN REF. 2)
-> Q (IN REF. 2)
                                                                                                                    Alternative splicing; Repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                       FTIG=VSP 005603
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MEDLINE=95024033; PubMed=7937880;
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01-OCT-1996 (Rel. 34, Last seq
                             PRINTS; PR01789; NUCFACTORATC.
SMART; SM00429; IPT; 1.
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Best Local Similarity الاست
الا الاستفادية Si Conservative
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68
83
1124
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Pfam; PF00554; RHD; 1.
Pfam; PF01833; TIG; 1.
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CALCIUM-BINDING (POTENTIAL).
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                 CYTOPLASMIC (POTENTIAL).

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 7.

EGF-LIKE 1.

EGF-LIKE 2.

LDL-RECEPTOR CLASS B 1.

LDL-RECEPTOR CLASS B 6.

LDL-RECEPTOR CLASS B 6.

LDL-RECEPTOR CLASS B 9.

EGF-LIKE 4.

LDL-RECEPTOR CLASS B 9.

EGF-LIKE 4.

LDL-RECEPTOR CLASS B 9.

EGF-LIKE 4.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS B 11.
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B 16.
B 17.
B 18.
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LDL-RECEPTOR CLASS B
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RGR-LIKE 11.
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LDL-RECEPTOR C
LDL-RECEPTOR C
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LDL-RECEPTOR C
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    \begin{array}{c} 444 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\ 447 \\
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  WEDLINE-9417242; PubMed=7510321;
Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,
Zheng G., McClusky R.T.;
Andres G., McClusky R.T.;
To morgan distribution in rats of two members of the low-density
Ilipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
Treceptor-associated protein (RAP).
Thistochem. Cytochem. 42:531-891.
Thistochem. Cytochem 42:531-891.
Thistochem. Cytochem 42:531-891.
Thistochem. Cytochem activator-plasminogen activator inhibitor type I
Dlasminogen activator-plasminogen activator inhibitor type I
Complex. apolipoprotein B-enriched beta-VLDL, lipoprotein lipase,
Iactoferrin, clusterin and calcium.
FWNTION: Receptor-mediated uptake of polybasic drugs such as
aprotinin, aminoglycosides and polymyxin B.
Trustonin, aminoglycosides and polymyxin B.
Subunit: Forms a multimeric complex together with a receptor-
associated protein (RAP). Binds to ankyrin-repeat family A protein
Colathin-coated pite; a soluble form is possibly derived by
Clathin-coated pite; a soluble form is possibly derived by
Clathin-coated pite; a soluble form is possibly derived by
Clathin-coated pite; Bitherace.
Clathin-coated pite; Bitherace.
Clathin-coated pite; Bitherace.
Clathin-coated pite; a soluble form is possibly derived by
Clathin-coated pite; Bitherace.
Clathin-coated pite; Bitherace.
Clathin-coated pite; Bitherace.
Clathin-coated pite; Spithin-coated pite; Similarity:
Contains 37 LDL-receptor class & domains.
Collaboration SIMILARITY: Contains 17 EGF-like domains.
Collaboration SIMILARITY: Contains 17 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               FUNCTION.

MUBDILINE-95386696; PubMed=7544804;

Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,

Norris K., Gliemann J., Christensen E.I.;

Evidence that epithelial glycoprotein 330/megalin mediates uptake of polybasic drugs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
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EXTRACELLULAR (POTENTIAL)
Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994)
                                                                                                                                                                 J. Clin. Invest. 96:1404-1413(1995).
[3]
TISSUE SPECIFICITY.
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CYB_CROWV
Q95776;
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CYB CROVV
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STRAINEL TOT NIG961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
MEDLINE=20406833; PubMed=10952301;
MEDLINE=20406833; PubMed=10952301;
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                          CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
-!- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase omega chain (EC 2.7.7.6) (Transcriptase omega chain) (RNA polymerase omega subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of both chromosomes of the cholera pathogen Vibrio
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0
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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ENDOCYTOSIS SIGNAL (POTENTIAL).
ENDOCYTOSIS SIGNAL (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 4660; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                         SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
                                                                                                                                                                                                                                        LDL-RECEPTOR CLASS B 35.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 37.
EGF-LIKE 13.
LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
                                                                                                                                                                                                                                                                                            EGF-LIKE 16.
EGF-LIKE 17.
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Les 5; Conservative
   954 SSVMH 958
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DT 26-FEB
DE DNA-di
DE COMEGGA
CO VIDNIO
CO BACTER
CO VIDNIO
CO NACEL
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RN [1]
RN SEGUEN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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0
                                                                                                                                                                                  SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1 omega chain (By similarity).
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytcochrome c reductase complex (complex III or cytcochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b565) is high-potential and absorbs at about 566 (By
terminal regions of the beta' subunit thereby facilitating its interaction with the beta and alpha subunits (By similarity). CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity)
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the RNA polymerase omega chain family.
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HAMAP; MF_00366; -; 1.

InterPro; IPR003116; RNA_pol_omega.

InterPro; IPR006110; RNA_poly_Rpb6.

Pfam; PF01192; RNA_pol_Rpb6; 1.

TIGRPAMs; TIGR00690; rpoZ; 1.

Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 1; Length 90;
Pred. No. 13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AA; 10054 MW; DB701616D02657F6 CRC64;
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MTCYB OR COB OR CYTB.
Crotalus viridis viridis (Prairie rattlesnake).
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15-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Best Local Similarity 80.0
Matches 4; Conservative
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               (See http://www.isb-sib.ch/announce/
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                                                       EMBL, U65377; AAB06740.1; -.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam, PF00033; cytochrome_B N.
PROSTTE; PS00192; CYTOCHROWE B N. EMER.
PROSTTE; PS00193; CYTOCHROME B QO; PARTIAL.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vidal N., Lecointre G.; "Weighting and congruence: a case study based on three mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex.";
C. R. Acad. Sci., III, Sci. Vie 320:95-101(1997).
C. R. Acad. Sci., III, Sci. Vie 320:95-101(1997).
C. PUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
COPACTOR: Binds two heme groups non-covalently. Heme I (or BL b562) is low-potential and absorbs at about 562, and heme 2 (or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Atractaspididae; Atractaspis.
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   and for
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                                                                                                                                                                                             IRON 1 (HEME B562 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 1 (HEME B562 AXIAL LIGAND)
                                                                                                                                                                                                                                                                                        Score 24; DB 1; Length 128; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBUNIT: The main subunits of complex b-cl are: cytocytochrome cl and the Rieske protein (By similarity) SIMILARITY: Belongs to the cytochrome b family.
   Usage by
                                                                                                                                                                                                                                                          14602 MW; 993267807EB97550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AA
                                                                                                                                                                                                                                                                                                                      1; Mismatches
                 entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes in pitvipers.";
Mol. Phylogenet. Evol. 9:366-374(1998)
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MEDLINE=98334559; PubMed=9667984;
                                                                                                                                                                                                                                                                                        96.0%;
80.0%;
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Best Local Similarity
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SSIMH 60
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or send an email to license@isb-sib.ch)
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IRON 2 (HEME B566 AXIAL LIGAND)
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62 SSIMH 66
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Q17637
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Q95SY6
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Q9T4Q1
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Q8XJV8
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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      GenCore version (c) 1993 - 2004
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Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

Bol. Zool. 61:331-331(1994).

C. I. SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, X79111; CAA55728.2; -.

RO, GO:0016021; C:integral to membrane; IEA.

RO, GO:0016021; C:integral to membrane; IEA.

RO, GO:0016191; F:oxidoreductase activity; IEA.

RO, GO:0016191; F:oxidoreductase activity; IEA.

RO, GO:0016191; P:exansport; IEA.

RO, GO:0016191; P:exansport; IEA.

RO, GO:0016191; C:transport; IEA.

RO, GO:0016191; P:exansport; IEA.

RO, GO:0016191; P:exansport; IEA.

RECTON transport; Heme; Transmembrane; Transport.

MON_TER 100031

SEQUENCE 90 AA; 10103 MW; AAAED2A254889404 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacea; Pseudomonas.
NCBI_TaxID=303;
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Similarity 100.0%; Score 25; DB 13; Length 90;
Similarity 100.0%; Pred. No. 73;
5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 2; Length 78; 100.0%; Pred. No. 63; cive 0; Mismatches 0; Indels
                                                                                                                                     SEQUENCE FROM N.A.

Greated A., Lambertson L., Williams P.A., Thomas C.M.;

"Complete nucleotide sequence of IncP-9 plasmid pWW0.";

Submitted (AUG-201) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ34668; CAC86770.1;

GO: GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                          Hypothetical protein; Plasmid.
SEQUENCE 78 AA; 8805 MW; 8762D76ACESFF30A CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2003 (TrEMBLrel. 24, La
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
      Hypothetical protein.
                      Pseudomonas putida.
Plasmid pwwo.
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AC Q9Y07
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Q9mih2 crotalus vi
Q7y929 azemiops fe
Q7y94 lachesis mu
Q85xr5 crotalus du
Q12531 saccharcmyc
Q97318 sulfolobus
O13116 oryzias lat
G62243 caenorchabdi
Q98120 rhizobium l
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Q98120 rhizobium l
Q98121 lampetra l
G98121 lampetra l
G98121 lampetra l
Q98121 plasmodium
Q9124 arabidopsis
Q9chal arabidopsis
Q9chal mus musculu
Q80139 bacillus an
Q81397 oryza sativ
Q89232 variola vir
Q89232 variola vir
Q89232 variola vir
Q86233 homo sapien
Q8011 brucella su
Q8011 brucella me
Q70115 oryza sativ
Q89130 karodopirell
Q90130 homo sapien
Q91977 homo sapien
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09jf90 vaccinia vi
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09jf30 leptospira
020176 caenorhabdi
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020171 occupium
08x79 zea mays (m
08x70 bacillus an
08715 vibrio para
039303 brassica na
070xx9 rhodopirell
07uxy rhodopirell
07uxy rhodopirell
03eu09 bacteroides
08x604 yerssinia pe
08m620 bacteroides
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Q870s0 neurospora
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Q86tj8 homo sapien
Q9ylu5 schistosoma
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Q53419 streptomyce
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      Q8VML9
Q8VML9;
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01-MAR-2002 (
01-OCT-2003 (
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Created) Last sequence update)

90 AA

PRT;

O9Y072 PRELIMINARY; O9Y072; 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,

Last sequence update)
Last annotation update)

Created)

20, 20, 25,

(TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2

RESULT 1 Q8VML9 ID Q8VMI AC Q8VMI DT 01-MG DT 01-MG

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GO:0006810; P:transport; IEA.
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Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 SSVMH 36
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                                                                                       Electron transp
Mitochondrion.
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01-JUN-2003
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SEQUENCE
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Matches
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-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAINT THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COPACTOR: TWO HEME GROUPS (BSES AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,
CYTOCHROME CI AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL: M64997; AAB01609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                         Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G., "Mitochondrial DNA sequences in three genera of Italian lampreys."; Boll. Zool. 61:331-333(1994).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92130804; PubMed=1663569;
Normark B.B., McCune A.R., Harrison R.G.;
"Phylogenetic relationships of neopterygian fishes, inferred from mitochondrial DNA sequences.";
Mol. Biol. Evol. 8:819-834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha,
Osteoglossiformes, Pantodontidae, Pantodon.
                                                           Lampetra planeri (Brook lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NGBI_TaxID=7750;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 13; Length 90; 100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 AA; 10112 MW; AC0C7153062B63F4 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron transport; Heme; Transmembrane; Transport.

NON TER 1 1 1 1 NON TER 90 90
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Last annotation update)
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:001618; P:electron transport; IEA.
GO:0006810; P:electron transport; IEA.
InterPro; IPR005797; Cvth hf v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR065797; Cytb b6 N.
Pfam; PF00033; cytochrome D N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X79110; CAA55727.2;
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Matches 5; Conservative
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                               Cytochrome b (Fragment).
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   TISSUE=Muscle;
                                                        CYTB OR CYT B.
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01-JUN-2003
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Q35383;
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DT 01-V

DT 01-J

DD 01-V

DD 00-V

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InterPro; IPR005797; Cytb b6 N. Pfam; PF00033; cytochrome_b\overline{\rm N}; 1. Blectron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Perseon A.E., Lundeberg J., Uhlen M.;

"EU-IMAGE: Full-insert length sequencing of human cDNA clones.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF143328; AAD33911.1; -.
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Tinti F., Nadiani M., Tommasini S., Piccinetti C., Stagni A.M.;
Tinti F., Nadiani M., Tommasini S., Piccinetti C., Stagni A.M.;
"Phylogeny and Evolution of Mediterranean Soles (Soleidae,
Pleuronectiformes) Based on Mitochondrial DNA Sequences.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
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                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                93 93 93 93 93 93 93 P32F96584CDF43F0 CRC64;
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Hypothetical protein.
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5; Conservative
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SEQUENCE 102
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NON TER
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COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-1- COMPLEX TWO HEME GROUPS (BESC AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-1- SUBMINIT: THE MAIN SUBMINIS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME CI AND THE RIESER PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF113706; AAD23435.1; --
RG0; G0:0016211; C:integral to membrane; IEA.
GO; G0:0005746; C:mitochondrion; IEA.
GO; G0:0005739; C:mitochondrion; IEA.
GO; G0:0006109; P:electron transport IEA.
GO; G0:0006109; P:electron transport; IEA.

InterPro; IRROGS797; Cytb b6 N.
RG0; G0:0006109; Cytochrome b N.
RG0; G0:0006109; CYTOCHROME B HEME; 1.
RPGM; PF00033; CYTOCHROME B HEME; 1.
RRG1FF0; IRROGS797; Cytb b6 N.
RRG2FT0; IRROGS797; CYTOCHROME B HEME; 1.
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-1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AND ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-1- COFACTOR: TWO HEME GROUPS (BS-C2 AND BS-G6) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
-1- SUBMINIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
C-1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CO GO:0016021; C:integral to membrane; IEA.
GO; GO:0016746; C:mitcchondrial electron transport chain; IEA.
RO; GO:0016491; F:oxidoreductase activity; IEA.
RO; GO:0016418; P:electron transport; IEA.
RO; GO:0016810; P:transport; IEA.
RO; GO:0016810; P:transport; IEA.
RIHGEPPC; IPR005991; GYtb b6, N.
RIHGEPPC; IPR005991; GATASE-1.
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Matches 5; Conservative
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REQUENCE FROM N.A.

RA Gilles A., Lecointre G.;

Ra dilles A., Lecointre G.;

Ra dilles A., Lecointre G.;

Ra maner accurate phylogeny of european cyprinids based on the mitochondrial control region.";

Rubmitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

C. EUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III OR CYTOCHROME B.-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. C. SUBDINIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CANDONS C1 C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CANDONS C1 C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.-C1 ARE: CYTOCHROME B, CANDONS C1 C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE PROTEIN (BY SIMILARITY).

C. C. CORPLEX CANDONS C1 AND THE RIBSKE CANDONS C1 AND THE CYTOCHROME B FAMILY.

C. C. C. CORPLEX CANDONS C1 AND THE CANDONS C1 AND THE CANDON C1 AND THE C
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Pfam; PF00033; cytochrome b N; 1.
PROSTIE; PS00192; CYTOCHRONE B HEME; 1.
PROSTIE; PS00442; GATASE TYPE I; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.
NCBI_TaxID=27708;
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110 AA; 12598 MW; FAA7FE8EDDA70AC3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 8;
100.0%; Pred. No. 82;
iive 0; Mismatches 0
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100.0%; Pred. No. 89;
iive 0; Mismatches 0
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Puntius conchonius (Rosy barb).
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Best Local Similarity 100.v.
Best Local Similarity 5; Conservative
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Cyprinodontiformes; Aplocheilidae; Aplocheilinae; Fundulosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
               NCBI_TaxID=60304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                 sednences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Q9TB72
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                                                                                                                                                                                                                                                                                               MOÎ. Phylogenet. Evol. 11:351-360(1999).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GRAPATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00033; cytochrome D N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Cyprinodontiformes, Aplocheilidae, Aplocheilinae, Pronothobranchius.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                     STRAIN=Aquarium strain;
MEDLINE=99214037; PubMed=10196077;
Murphy W.J., Collier G.E.;
"Phylogenetic relationships of African killifishes in the genera Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                        щ
                                                                                                                                                                                                                                                                                                                                                                      BOUND TO THE PROTEIN (BY SIMILARITY).

-1-SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME I CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-1-SIMILARITY: BLOONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF002285, AAD00946.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016739; C:mitochondrial electron transport chain; IEA.
GO, GO:0016491; F:oxidoreductage activity; IEA.
GO; GO:0006810; P:electron transport; IEA.
GO; GO:0006810; P:electron transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AA; 13591 MW; 54D1F7D50C1538CE CRC64;
                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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                                                  Created)
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                                                                                                             Pronothobranchius kiyawensis.
                                             01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24,
                        PRELIMINARY;
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                                                                                   Cytochrome b (Fragment).
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                                                                                                                                                                                     NCBI_TaxID=60306;
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                                                                                                                       Mitochondrion.
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RESULT 9
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EMBL; AF002284; AAD00345.1; --
GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 0016719; C: integral to membrane; IEA.
GO; GO: 0016719; C: mitochondrion; IEA.
GO; GO: 0016491; F: oxidoreductage activity; IEA.
GO; GO: 0016810; P: transport; IEA.
InterPro; IPR05797; Cytb_b6 N.
Pfam; PF00031; CYTCCHROME B. HEA.
ELECTON transport; Hea.
ELECTON transport; Heae; RespIratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                    MOÎ. Phylogenet. Evol. 11:351-360(1999).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERALES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
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"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
cytochrome b and ND3 gene sequences.",
can. J. Fish. Aguat. Sci. Sci. 26.2140-2149(1999).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

"RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-Aquarium strain;
MEDLINE-99214037;
Murphy W.J., Collier G.E.;
"Phylogenetic relationships of African killifishes in the genera
Aphyosemion and Pundulopanchax inferred from mitochondrial DNA
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Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOUND TO THE PROTEIN (BY SIMILARITY).
SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 8; Length 120; 100.0%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 AA; 13600 MW; EECADA4FE9B9639B CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lampetra fluviatilis (River lamprey).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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Gaps

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minima.";

Copeia 2000:1019-1028(2000).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

-:- FUNCTION: COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COMPLED TO ATP SYMTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HENE GROUDS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBDUIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME CI AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROWE B FAMILY.
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PROSITE; PS00192; CYTOCHROME_B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ORE 07, CAL 01, and ORE 01;
Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";
Can. J. Fish. Aquat. Sci. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
NCBI_TaxID=104636;
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EMBL, AF257123; AGG13274.1; —
GO; GO: 0016621; C: integral to membrane; IEA.
GO; GO: 0005739; C: intochondrial electron transport chain; IEA.
GO; GO: 00016491; F: oxidoreductase activity; IEA.
GO; GO: 00066119; P: electron transport; IEA.
GO; GO: 00066119; P: electron transport; IEA.
GO; GO: 0006610; P: transport; IEA.
InterPro; IPR005797; Cytb_b6.
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
  Indels
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                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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  Mismatches
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AF177955; AAF01002.1; -.
AF177956; AAF01003.1; -.
AF257134; AAG13284.1; -.
                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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  5; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Entosphenus similis.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                       64 SSVMH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 SSVMH 72
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                                                   1 SSVMH 5
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  Matches
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Mar. Mamm. Sci. 18:0-0(2002).

C. 1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO AFP SYNTHESIS (BY SIMILARITY).

C. 1- COPACTOR: TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

C. 1- SIBMILT: THE MAIN SUBBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C. 1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL, AF49144; AAM74073.1;

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
RO; GO:0006189; P:electron transport; IEA.
RO; GO:00061810; P:transport; IEA.
RO; GO:00061810; P:transport; IEA.
RO; GO:00061810; P:transport; IEA.
RO; GO:00061810; P:transport; IEA.
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PROSITE; PS00192; CYTOCHROME_B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                         InterPro; IPR065797, Cytb b6 N.
Pfam; PF00031, cytoChrome b N.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
-1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF177994) AAF00996.1, -..

GO; GO:0016021; C:initegral to membrane; IEA.

GO; GO:0005746; C:initechondrial electron transport chain; IEA.

GO; GO:0005739; C:mitechondrion; IEA.

GO; GO:0016419; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006810; P:transport; IEA.
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SEQÜENCE 128 AA; 14301 MW; BBCCB1BB1EEC494A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 1e+02;
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Mesoplodon peruvianus (Peruvian beaked whale).
Mitochondrion.
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100.0%;
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Best Local Similarity
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.",
can. J. Fish. Aquat. Sci. 56:2340-2349(1999).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY)
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Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.", 1900 Can. J. Fish. Aquat. Sci. 56:2340-2349(1999).

-I. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzonțidae; Lampetra.
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Petromyzontiformes, Petromyzontidae, Lampetra.
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-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME CYTOCHRO
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EMBL; AR17948; AAF00995.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrian; IEA.
GO; GO:000619; F:oxidoreductase activity; IEA.
GO; GO:0006119; P:electron transport; IEA.
GO; GO:0006119; P:electron transport; IEA.
GO; GO:0006119; P:electron transport; IEA.
GO; GO:000610; P:transport; IEA.
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SEQUENCE 128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                     Lampetra richardsoni (Western brook lamprey).
    128 AA
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                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
                                                                                                                                                                                           Cytochrome b (Fragment).
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Matches 5; Conserv
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01-OCT-2003
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(BS62 AND BS66) WHICH ARE NOT COVALENTLY
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Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-i- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
-i- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
-i- SIMILARITY: AAPOLOGO 1.;
--- SIMILARITY: ABOLOGO 1.;
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"Phylydeny of the lamprey genus Lampetra inferred from mitochondrial
cytochrome b and ND3 gene sequences ";
Can. J. Fish. Aguat. Sci. 0:0-0(1999).
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                                     COUPLED TO THE NATIONAL OF STATEMENTS OF STATEMENTY).

C. !- COFACTOR: TWO HENE GROUPS (B562 AND B566) WHICH ARE NOT COVALEN BOUND TO THE PROTEIN (BY SIMILARITY).

C. !- SUBBALT: THE MAIN SUBBALTS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C. !- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF177947; AAF00994.1; -- CATOCHROME B FAMILY.

R G0; G0:0016021; C:integral to membrane; IEA.

G0; G0:0016021; C:integral to membrane; IEA.

G0; G0:0016491; F:oxidocaductase activity; IEA.

G0; G0:0006810; P:coxidocaductase activity; IEA.

R G0; G0:0006810; P:coxidocaductase activity; IEA.

R G0; G0:0006810; P:transport; IEA.

R HTCHPRO; IPRO05797; CYLD_66.N.

R PFam; PF00003; cytochrome b N; 1.

R PROSITE; PS00192; CYTOCHROME B HEME; 1.
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
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EMBL; AF257129; AAG13279.1; -.
EMBL; AF257124; AAG13275.1; -.
EMBL; Of0160010101; Cnintegral to membrane; IEA.
GO; GO:0005746; Cnintednondrial electron transport chain; IEA.
GO; GO:0005739; Cnitochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Copeia 2000:1019-1028(2000).
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SEQUENCE FROM N.A.
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01-JUN-2003
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                                      09T656
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Matches
               RESULT 18
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GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005797; Cyto_b6 N.
Pfam; PF00033; cytochrome D N; 1.
PROSITE; PS00192; CYTOCHRŌME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPETA 2000:1019-1028(2000).

-!- FUNCTION! COMPURENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUNDED TO APP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUDS (1856 AND 8566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBLUIT: THE MAIN SUBDATIS OF COMPLEX B-C. TARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Lorion C.M., Markle D.F., Reid S.B., Docker M.F.;
"Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
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EMBL; AF257132; AG13280.1; ...
EMBL; AF257130; AAG13280.1; ...
EMBL; AF257130; AAG13280.1; ...
EMBL; AF257130; AAG13280.1; ...
GO; GO:0016021; C:initegral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0016919; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                         100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 8; Length 128, 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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SEQÜENCE 128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                        128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  Entosphenus minimus.
                                                                                                                                    Local Similarity
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                                                                                      128
                                                                           Mitochondrion.
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                                                                                     NON TER
SEQUENCE
                                                                                                                          Query Match
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Matches
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COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";
Can. J. Fish. Aquat. Sci. 56:2340-2349(1999).
-I. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GRIBEATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
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Loriton C.M., Markle D.F., Reid S.B., Docker M.F.;
"Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
minima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-!-SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!-SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AF177959; AAF01006.1; --
G0, G0.016021; C.integral to membrane, IEA.
G0, G0.010619; C.integral to membrane, IEA.
G0, G0.010619; F.cmitochondrial electron transport chain; IEA.
G0, G0.016491; F.cxidoreductase activity; IEA.
G0, G0.016491; F.exidoreductase activity; IEA.
G0, G0.0006118; P.electron transport; IEA.
G0, G0.0006118; P.electron transport; IEA.
InterPro, IPR005797; Cytb_b6_N.
                                                                                                                                                                                                                                                       Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Betromyzontiformes; Petromyzontidae; Lethenteron.
NCBI_TaxID=94989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
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                                                                                                                                                                                                                             Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                  01-JUN-2003 (TrEMBLrel. 13, Last sequence update)
Cytochrome b (Fragment).
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Last annotation update)
      128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                          OT656;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                             128 AA;
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                                                                                                                                                                                                                                                                                                                                68 SSVMH 72
                                                                                                                                                                                                                                                                         1 SSVMH 5
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                                       Mitochondrion.
NON TER 128
SEQUENCE 128
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Q9TB70;
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Matches
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09TB71
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COPPEIA 2000:1019-1028(2000).

COPPEIA COMPLEX (COMPLEX III OR CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A REPERTATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO AND THE RIESKE PROTEIN (BY SIMILARITY).

COUPLED TO COUPLED TO MEMBRANE TO THE CYTOCHROME B FAMILY.

COUPLED TO COUPLED TO MEMBRANE TO THE CYTOCHROME B FAMILY.

COUPLED TO COUPLE TO THE STAND T
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COMPLEX (COMPLEX II OR CYTCCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNWHESIS (BY SIMILARITY).

C. 1- COPACTOR: TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

C. 1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
C. 1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL, AR177961; AAPO1008.1; -
R GO; GO:0005746; C:mitcchondrion; IEA.

GO; GO:0005746; C:mitcchondrion; IEA.

GO; GO:0006718; P:electron transport; IEA.

GO; GO:0006118; P:electron transport; IEA.

R INTERPRO; IRROGESOFT; C:mitcchondrion; IEA.

R GO; GO:0006810; P:transport; IEA.

R INTERPRO; IRROGESOFT; IEA.

R INTERPRO; IRROGESOFT; IEA.

R INTERPRO; IRROGESOFT; IEA.
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";
can. J. Fish. Aquat. Sci. 56:2340-2349(1999).
-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petromyzon marinus (Sea lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR005797; Cytb_b6_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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GO; GO:000
GO; GO:000
InterPro;
Pfam; PF00
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Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
cytochrome b and ND3 gene. sequences.";

Can. J. Fish. Aquat. Sci. 56:2340-2349 [1999].

Complex (COMPLEX III OR CYTOCHROME B.C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUND TO THE PROTEIN (BY SIMILARITY).

COUND TO THE PROTEIN (BY SIMILARITY).

CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CYTOCHROME C1 AND THE CYTOCHROME B FAMILY.

EMBL; AF117953; AAF01000.1;
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Blectron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                   Gaps
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Petromyzontiformes; Petromyzontidae; Entosphenus.
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GO; GO:0005746; C:integral to membrane; IEA.
GO; GO:0005739; C:inticochondrian; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006181; F:electron transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
                                                                           Length 128;
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                                                                     100.0%; Score 25; DB 8; Length 12
100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
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                      BEACB618195C4D4A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                           128 AA.
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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128
14318 MW;
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                                               Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Entosphenus macrostomus.
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NCBI_TaxID=104632;
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NON TER 128
SEQUENCE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- FUNCTION: COMPLEX III OR CYTOCHROWE B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-:- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
-:- SUBDUNIT: THE MAIN SUBUNITS OP COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                        Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.; "Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences."; Can. J. Fish. Aquat. Sci. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=104630;
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
                                                                                      Lampetra tridentata (Pacific lamprey) (Entosphenus tridentatus).
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(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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BWBL, AF25713, AAG13283.1, --
EWBL, AF257121, AAG13271.1, --
EWBL, AF257121, AAG13272.1, --
EWBL, AF257122, AAG13273.1, --
EWBL, AF257125, AAG13273.1, --
EWBL, AF257125, AAG13277.1, --
EWBL, AF257126, AAG13277.1, --
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Best Local Similarity 100.
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                              Cytochrome B (Fragment).
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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01-JUN-2003
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Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Thylogeny of the lamprey genus Lampetra inferred from mitochondrial

Cytochrome b and ND3 genus eaquences.";

Can. J. Fish. Aquat. Sci. 56:2340-2349(1999).

Can. J. Fish. Aquat. Sci. 56:2340-2349(1999).

COUPLEX (COMPLEX III OR CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BS SIMILARITY).

COUPLED TO THE PROTEIN (BY SIMILARITY).

COUPLEX COMPLEX BELONGS TO THE RIESER PROTEIN (BY SIMILARITY).

CYTOCHROME C1 AND THE RIESER PROTEIN (BY SIMILARITY).
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GO; GO:0016041; C:integral to membrane; IEA.
GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
GO; GO:0006431; F:oxidoreductase activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
GO; GO:0006119; P:transport; IEA.
InterPro; IPR005797; Cytb A6 N.
Fram; PP00033; Cytochrome b N; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.",

"I Fish. Aguat. Sci. Sci. 240-2349 (1999).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COPACTOR: TWO HEME GROUPS (BSSC AND BSSG) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Petromyzontiformes; Petromyzontidae; Entosphenus.
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-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME CTYOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AR177958, AAR71005.1; -..

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0005746; C:mitochondrial electron transport chain; IEA.

GO, GO:0016491; F:oxidoreductase activity; IEA.

GO, GO:0016491; F:oxidoreductase activity; IEA.

GO, GO:0006118; P:electron transport; IEA.
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA
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Search completed: September 24, 2004, 02:18:40 Job time : 30.9623 secs

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11. MOL. Biol. Evol. 14:883-891(1997).

12. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B.C. COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES WELCTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

12. COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
13. COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
14. COPACTOR: TWO HEME GROUPS (BSCS AND BSS6) WHICH ARE NOT COVALENTLY
15. SOUND TO THE PROTEIN (BY SIMILARITY).
16. SIBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
17. C. I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
18. SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
18. SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
19. GO: GO: 00106214; C: mitcochondrial electron transport chain; IEA.
18. GO: GO: 0016491; P: electron transport; IEA.
18. GO: GO: 0016491; P: electron transport; IEA.
18. GO: GO: 0016491; P: electron transport; IEA.
18. InterPro; IRROBS-77; CYLD-L.
18. CAMPLE TO THE THE TREATH TO THE TRANSPORT; IEA.
18. COMPLEX TRANSPORT; IEA.
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                  InterPro; IPR065797; Cytb_b6 N.
Pfam; PF00033; cytcotrome_b N.
PROSITE; PS00192; CYTCOTROME B HEWE; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport; Mitochondrion.
Mitochondrion.
SEQÜENCE 128 A3; 14287 MW; 40BCA119C947802D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00033; cytochrome D N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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MEDLINE=97398713; PubMed=9254927;
Jackman T.R., Applebaum G., Wake D.B.;
"Phylogenetic relationships of bolitoglossine salamanders: a demonstration of the effects of combining morphological and molecular
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
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Local Similarity 100.0%; Pred. No. 1.5e+02;
les 5; Conservative 0; Mismatches 0; Indels
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185 AA; 20851 MW; 471DB2B09ECF251A CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
GO:0006810; P:transport; IEA.
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Best Local Similarity 100.
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Mol. Biol. E
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51 SSVMH 55

SSVMH 5

8 8

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SEQUENCE FROM N.A.
TISSUE=Muscle;
Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;
Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;
"Mitochondrial DNA sequences in three genera of Italian lampreys.";
Boll. Zool. 61:331-333(1994).
GO: 0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
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26,
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01-WAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2)
Hypothetical protein.
Pseudomonas putida.
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01-MAY-2000 (TrEMBLrel. 1
01-MAY-2004 (TrEMBLrel. 2
Cytochrome b (Fragment).
Name=cyt b;
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QBVML9;
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Q9PW02
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Q8VML9
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0997072 lampetra pl
03538 pantodon bu
095347 homo sapien
095718 dicologloss
095070 fundulosoma
099071 proncthobra
09071 proncthobra
09155 entosphenus
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                                                                                   (without alignments)
79.162 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       ; Search time 32,3438 Seconds
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Q676s1
Q21661
Q7gf68
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          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                            fotal number of hits satisfying chosen parameters:
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25
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Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                       April 28, 2005, 17:57:45
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Gapop 10.0 , Gapext 0.5
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Q6Y4CB
Q6Y4D1
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Q9T3E3
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Q9Y072
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1: uniprot_sprot:*
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Maximum DB seq length: 200000000
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Greated A., Lambertson L., Williams P.A., Thomas C.M.;
"Complete sequence of the InCP-9 TOL plasmid pWW0 from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pWW0.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=303;
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                                         Q8uct3
Q33739
Q6sms2
Q6smx4
Q6sm31
Q6sn31
Q6sn96
Q6sn92
Q6sn92
Q6sn92
Q6sn15
            Q8rj29
Q6w236
Q7v858
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EMBL, AJ344068; CAC86770.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 78 AA; 8805 MW; 8762D76ACE5FF30A CRC64;
                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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            Q8RJZ9
Q6W236
Q8UCT3
Q8UCT3
Q6SWS2
Q6SWZ4
Q6SWZ4
Q6SW31
Q6SWB6
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Q6SWB6
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
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Homo sapiens (Human).
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Best Local Similarity 100.
Matches 5; Conservative
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nes 5; Conservative
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Mitochondrial DNA sequences in three genera of Italian lampreys.";
Boll. Zool. 61:331-333(1994).
EMBL; X79110; CAASS727.22: -.
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Petromyzontiformes, Petromyzontidae, Lampetra.
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                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 2; Length 90; 100.0%; Pred. No. 72; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 2; Length 90; 100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                 90 AA; 10103 MW; AAAED2A254889404 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA; 10112 MW; AC0C7153062B63F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
1-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Cytochrome b (Fragment).
Pantodon buchholtzi (Butterflyfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:nembrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
InterPro; IFR005797; Cytb b6. N.
Pfan; PF00033; Cytochrom E N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; UNKNOWN_1.
GO, GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro. IPROG5797; Cytb De N.
Emi, PE00033; Cytcohrom B N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=cyt b;
Lampetra planeri (Brook lamprey).
                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSVMH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVMH 33
                                                                                                                                                                                                                                                                                                                                                                                                   1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                             Query Match
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NON TER
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(9970)

AC (9970)

DD (01-N)

CYLOO

CO (01-N)

CYLOO

CO (01-N)

CYLOO

CO (01-N)

CO (0
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Persson A.E., Lundeberg J., Uhlen M.;

Persson A.E., Lundeberg J., Uhlen M.;

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF14328; AAD33911.1;

Genew; HGNC:15224; OR52K3P.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004984; F:olfactory receptor activity; IEA.

GO; GO:000186; P:olfact_receptor oupled receptor protein signalin. .; IEA.

InterPro; IPR01036; PH related.
MEDLINE=92130804; PubMed=1663569;
Normark B.B., McCune A.R., Harrison R.G.;
Normark B.B., McCune A.R., Harrison R.G.;
"Phylogenetic relationships of neopterygian fishes, inferred from mitochondrial DNA sequences.";
Mol. Biol. Evol. 8:819-834(1991).
-!-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (Complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!-COPACTOR: Binds two heme groups non-covalently. Heme I (or BL or b562) is low-potential and absorbs at about 566 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
EMBL; M64907; AAB01609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000574; C:intechondrial electron transport chain; IEA.

GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006119; P:transport; IEA.

InterPro; IPR005797; Cytb b6 N.

Pfam; PF00033; Cytochrom BN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 2; Length 100; 100.0%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 2; Length 93; 100.0%; Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 100 AA; 11028 MW; 34EAE445D3DBC50A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AA; 10689 MW; F32F96584CDF43F0 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 AA
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Gilles A., Lecointre G.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.
NCBI_TaxID=27708;
Lunaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Soleoidei; Soleidae; Buglossidium.
                                                                                                                                                                                                                        Mar. Biotechnol. 2:274-284 (2000).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL b562) is low-potential and absorbs at about 562 nm, and heme 2 BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                    similarity).
-!-SUBMUTT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
-!-SIMILARITY: Belongs to the cytochrome b family.
-!-SIMILARITY: Belongs to the cytochrome b family.
BEMBL, ARI12206, AAD23435.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016491; C:intcchondrial electron transport chain; IEA.
GO, GO:0016491; P:exidoreductase activity; IEA.
GO, GO:0016491; P:exidoreductase activity; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                            Tinti F., Piccinetti C., Tommasini S., Vallisneri M., "Mitochondrial DNA Variation, Phylogenetic Relationships, Evolution of Four Mediterranean Genera of Soles (Soleidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA; 11356 MW; 90F4444E2DD2E4E3 CRC64;
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Last annotation update)
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Pfam; PF00033; Cytochrom B N; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 10v...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                            Pleuronectiformes)."
                                                                                                                                FROM N.A.
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                                                                                                                             SEQUENCE FROM N. PubMed=10852807;
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NON TER
SEQUENCE
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COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (C BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, estinopterygii, Neoperygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes; Soleoidei, Soleidae, Dicologlossa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                  Cunha R., Caetano S., Castilho R.;
Submitted (JAN-2201) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGM; PF00033; Cytochrom B N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00442; GATASE TYPE I; UNRNOWN 1.
Electron transport; Heme; Mitochondrion; Respiratory chain; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 2; Length 102; 100.0%; Pred. No. 82; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AA; 11318 MW; C89116AD5009B699 CRC64;
                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochrome b (Fragment).
Name=cytb;
Buglossidium luteum.
                                                                                                                                                                                                           Cytochrome b (Fragment).
                                                                                                                                                                                                                                            Dicologlossa cuneata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                 |||||
SSVMH 47
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=153209
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVMH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSVMH 5
                                                                                                                                                                                                                                                         Mitochondrion.
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                                                                                                                                                                                                                             Name=cytb;
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                                                                                                                                              098378;
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09XLK3
1D 09XLK3
AC 09XLD
DT 01-NC
DT 01-NC
DT 01-MC
DE CYCO
GN Name:
OS Bugico
OG Mitoo
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01-MAY-1999
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                      Query Match
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b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, definiopterygii, Neopterygii, Teleostei, Meteleostei, Meteleostei, Meteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Cyprinodontiformes, Aplocheilidae, Aplocheilinae, Fundulosoma.
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FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
                                                          -!-SIGNUNT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
-!-SIMILARITY: Belongs to the cytochrome b family.
EMBL; AJ38845; CAB62077.1; --
GO; GO:0005746; Cintegral to membrane; IEA.
GO; GO:0005746; Cintcochondrial electron transport chain; IEA.
GO; GO:0005797; Cintcochondrial electron transport chain; IEA.
GO; GO:0006118; P:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
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--- SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
--- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Aquarium strain; MEDILINE=99214037; PubMed=10196077; DOI=10.1006/mpev.1998.0566; Murphy W.J., Collier G.E.; "Phylogenetic relationships of African killifishes in the genera Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
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                                                                                                                                                                                                                                                                                                                               Pfam, PF00033; Cytochrom B N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 2; Length 110;
Pred. No. 89;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA; 12598 MW; FAA7FE8EDDA70AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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100.0%;
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Transport, NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVMH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=60304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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ID 0990'
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c.i. SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).

c.i. SIMILARITY: Belongs to the cytochrome b family.

R EMBL; AF002285; AAD00946.1; -...

R GO; GO:0016716; Cimitochondrial electron transport chain; IEA.

R GO; GO:005739; Cimitochondrial electron transport chain; IEA.

R GO; GO:00189; F:cimitochondrial electron transport chain; IEA.

R GO; GO:001891; F:cimitochondrial electron transport; IEA.

R GO; GO:001891; F:cimitochondrial electron transport; IEA.

R GO; GO:001891; F:cimitochondrial electron transport; IEA.

R GO; GO:006810; F:transport; IEA.

R GO; GO:0006810; F:transport; IEA.

R GO; GO:0006810; F:transport; IEA.

R GO; GO:000831; Cytochrom E N. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOI. Phylogenet. Evol. 11:351-360(1999).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme I (or BL b562) is low-potential and absorbs at about 562 nm, and heme B. Hy or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Aquarium strain;
MEDLINE=992140131; PubMed=10196077; DOI=10.1006/mpev.1998.0566;
Murphy W.J., Collier G.E.;
"Phylogenetic relationships of African killifishes in the genera
Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                              ö
GO; GO:0006810; P:transport; IEA.
InterPro; IPR05797; Cytb b6 N.
Fam; PF00033; Cytochrom E N; 1.
PROSITE; PS00192; CYTOCHROME B HENB: 1.
Electron transport; Heme; Mitochondrion; Respiratory chain; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00033; Cytochrom B N; 1.
PROSITE; PS00192; CYTOCHROME B HEMB; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                2; Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                 120 120 120 120 NW; EECADA4FE9B9639B CRC64;
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26, Last annotation update)
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 100.0%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 10, (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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Query Match
Best Local Similarity
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SEQUENCE
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FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or B562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Van Helden A.L., Baker A.N., Dalebout M.L., Reyes J.C.,
Van Waerebeek K., Baker C.S.,
"Resurrection of Mesoplodon traversii (Gray, 1874), senior synonym of
M. bahamondi Reyes, Van Waerebeek, Cardenas and Yanez, 1995 (Cetacea:
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti, Ziphiidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mead L.S., Clayton D.R., Nauman R.S., Olson D.H., Pfrender M.E.; "Newly discovered populations of salamanders from Siskiyou County California represent a species distinct from Plethodon stormi."; Submitted (JUL.2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY688284; AAU21592.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
Plethodontinae; Plethodontini; Plethodon.
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   Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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Mesoplodon peruvianus (Peruvian beaked whale).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plethodon elongatus (Del Norte salamander).
Mismatches
                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
5; Conservative
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                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Cytochrome b (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                          SSVMH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=46761;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=27617;
                                                    1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RAF0245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=cytb;
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C-1-SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).

C-1-SIMILARITY: Belongs the cytochrome b family.

R GO; GO: 001674; ARM74073.1; --

R GO; GO: 001674; C: mitochondrial electron transport chain; IEA.

R GO; GO: 001673; C: mitochondrial electron transport chain; IEA.

R GO; GO: 001673; C: mitochondrial electron transport chain; IEA.

R GO; GO: 001673; C: mitochondrial electron transport chain; IEA.

R GO; GO: 0016118; P: electron transport; IEA.

R GO; GO: 0016118; P: electron transport; IEA.

R GO; GO: 0016118; P: electron transport; IEA.

R Pfam; PF00033; CYtoCHROME B INE.

R Pfam; PR0013; CYTOCHROME B INE.

R Blectron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coupled to ATP synthesis (By similarity),
COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
b562) is low-potential and absorbs at about 562 nm, and heme 2 (c
BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
Plethodontinae; Plethodontini; Plethodon.
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-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
--- SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome-cl and the Rieske protein (By similarity).
--- SIMILARITY: Belongs to the cytochrome b family.
EMBL; AY183769; AA063634.1; --
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GO; GO:0005746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005749; C:mitcochondrian; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006110; P:transport; IEA.
InterPro; IPR005797; Cytb b6_N.
Pfam; PF00033; Cytcochrom B N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEMB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA; 14611 MW; 5BF9B08C2A6CC991 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 2; I
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport.
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128 AA

Created)

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Copela (10:1019-1028(2000).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COPACTOR, Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (BH or b566) is high-potential and absorbs at about 560 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.

NCBI_TaxID=126726;
                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome b (Fragment).
                                                                                                                           Q9G155 PRELIMINARY;
Q9G155;
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                              Entosphenus minimus.
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                                                                 RESULT 15
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MOI. Ecol. 13:149-166(2004).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By constitutions).
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Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
Plethodontinae; Plethodontini; Plethodon.
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain; Transport.
Transmembrane; Transport.
1 1 1 1 NON TER 128
Electron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
NOW TER 128 128
NOW TER 128 128
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                                                                                                                                                                                            100.0%; Score 25; DB 2; Length 128; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
PubMed=14653796; DOI=10.1046/j.1365-294X.2003.02030.x;
Mahoney M.J.;
                                                                                                                                  128 AA; 14630 MW; F5485853845ADC2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plethodon elongatus (Del Norte salamander).
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Pfam: PF00033; Cytochrom B N;
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                                                                                                                              SEQUENCE
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AF257131; AAG13281.1;

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GO, GO:0016021, C:integral to membrane, IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005799, C:mitochondrian, IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006119; P:transport; IEA.
                                                                                                                                               InterPro; IPR005797; Cytb b6_N.
Paran, PR00033; Cytcothorm B N; 1.
PROSITE; PS00192; CYTCOTROME B HEWE; UNKNOWN 1.
Electron transport; Heme; MitoChondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                             Length 128;
                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Job time : 35.3438 secs
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Best Local
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58 SSVMH 62

1 SSVMH 5

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MS-R Fab/
Anti-Abet
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AAR30765
ADA90439
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AAU02547
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AAU00212
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ABG78204
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AAW08582
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 Aab68087 An anti-a
Aar47042 Sequence
Aau82607 Llama CDR
Ada91299 MS-R Fab/
Ada91291 MS-R Fab/
Ada91199 MS-R Fab/
Ada91199 MS-R Fab/
Ada91199 MS-R Fab/
Ada91199 MS-R Fab/
Ada90188 Anti-Abet
Ada91199 MS-R Fab/
Ada91191 MS-R Fab/
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Ada91191 MS-R Ab/
Ada90440 MS-Roche
Ada90484 Anti-Abet
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Ada90184 Anti-Abet
Ada90189 MS-R Fab/
Ada90189 MS-R Fab/
Ada90189 MS-R Pab/
Ada90580 MS-Roche
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  September 24, 2004, 01:32:26; Search time 109.377 Seconds (without alignments) 43.915 Million cell updates/sec
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                                                                                                                                                                                                1586107
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                             rotal number of hits satisfying chosen parameters:
                                                                                                                                                                            1586107 segs, 282547505 residues
                                                                                                    US-10-088-639A-2_COPY_177_193
85
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Maximum Match 100%
Listing first 150 summaries
                                               protein search, using sw model
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ADA91299
ADA91290
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ADA90186
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AAR47042
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Gapop 10.0 , Gapext 0.5
                                                                                                                             1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                      A_Geneseq_29Jan04:*
11: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2013s:*
6: geneseqp2013s:*
7: geneseqp2033s:*
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Maximum DB seq length: 2000000000
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Match
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No.
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.33
 note= "Complementarity determining region (CDR) 1 of the

ocation/Qualifiers

Key Region

note= "Complementarity determining region (CDR) 3 of the ight chain"

"Complementarity determining region (CDR) 2 of

note= "Comp. ight chain"

chain"

ight

Region

"Complementarity determining region (CDR) 1 of the

note= "linker"

Peptide

Region

Region

.162

seavy chain

note=

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Region

'note= "Complementarity determining region (CDR) 1 of neavy chain" 226. 238 /note="Complementarity determining region (CDR) 1 of Meavy chain!

Tordsson MJ,

Ohlsson LG,

Karlstroem PJ,

Brodin TN, Nilson BHK;

WPI; 2001-308619/32. N-PSDB; AAF84797.

(ACTI-) ACTIVE BIOTECH AB

26-OCT-2000; 2000WO-SE002082.

WO200130854-A2

Region

03-MAY-2001

99SE-00003895

28-OCT-1999;

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Human BLY
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CDR regio
SAC isola
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IgG kappa
Anti-Rh(D
Human MUC
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                      Abp46013
Abp46023
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Abp46002
Abp46002
Abp46002
Abp46002
Abp46002
Abp46002
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Ada90012
Abp67888
Abb61288
Abb61288
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Abb61288
Abb6002
Abp6002
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ABP45963
ABP45954
ABP45168
ABG77162
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ADA90438
ADA89993
ABP46009
ABP46029
ABP46099
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ABP46018
ABP45996
ABP46034
ABP46106
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ABU11254
                                                                           ABP46014
                                                                                                                               ABP46030
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ALIGNMENTS

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An anti-alpha6beta4 integrin light chain linked to a heavy chain.
       AAB68087 standard; protein; 249 AA
                                 (first entry)
                                 09-JUL-2001
                    AAB68087;
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셤 Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

ö The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal numan gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vitvo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells. Gaps ; 0 Length 249; 0; Indels Score 85; DB 4; Pred. No. 2e-06; Mismatches 0; Claim 1; Page 55-56; 75pp; English. Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 17; Conservative 0; 17 1 VISENGRIINYADSVKG tumour deposits in humans Seguence 249 AA;

8

RESULT 2 AAR47042 ID AAR47042 standard; peptide; 120 AA.

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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody cragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the lama heavy chain domain fragments of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                        New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 5;
Pred. No. 0.00025;
                                                                                                                                                                                                                                             Disclosure, Page 19a, 46pp, English
                                                                 (CANA ) NAT RES COUNCIL CANADA.
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LLSRSGRTTNYADSVKG 17
25-MAY-2001; 2001WO-CA000763.
                                  26-MAY-2000; 2000US-0207234P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.5%;
70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.5
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuronal disorder; aging
                                                                                                                                        WPI; 2002-083093/11.
                                                                                                     Dubuc G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 AA;
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                                                                                                   Tanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA91299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abundant sublasses in the sequence compilation of Kabat et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda MD (1987), namely, VL-Kappa subgroup I and VH group III. In such igG-gamma-1 human consensus sequences, the VI consensus domain has the AA sequence in AAR47041, and the VH consensus domain has the AA sequence in AAR47042. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The consensus variable domain sequences are derived from the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                            consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Llama; phage display library; variable heavy domain fragment; VHH; VH; sdAb fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
                                                                                                 Sequence of the consensus antibody variable domain of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of improved humanised antibodies - by comparison of con and import complementarity determining regions and framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                    Monoclonal antibody; heavy chain; variable domain; consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.8%; Score 67; DB 2; Length 120; 82.4%; Pred. No. 0.0012; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Llama CDR2 region variable heavy chain fragment #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 108; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences, e.g. to humanise murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU82607 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                              92US-00934373
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                                                                 (first entry)
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                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                   Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-083196/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 120 AA;
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                                                                                                                                                                                                                                                                            20-AUG-1993;
                                                                                                                                                                                                                                                                                                              21-AUG-1992;
                                                                                                                                                                                                       WO9404679-A1
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                                                25-MAR-2003
                                                                                                                                                                                                                                          03-MAR-1994
                                                                 02-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                   Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lama glama
                                                                                                                                                                     Synthetic.
              AAR47042;
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Matches
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Gaps

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Mismatches

Length 17; 2; Indels

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Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                               antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosig
                                                                                                                                                                                                                                                                                          MS-R Fab/antibody related peptide #347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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ADA91299 standard; peptide; 17
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Kretzschmar T;

Huber W, Rothe C;

Brockhaus M, Nordstedt C,

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Pha-Ang-His-Ang-Glu-Pha-Ang-His-Ang-Glu-Pha-Ang-His-Ang-His-Ang-Glu-Pha-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang-His-Ang
                                                                                                                                                                            New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                Example 13; Page 93; 312pp; English
                                                 Bohrmann B,
Loetscher H,
(MORP-) MORPHOSYS AG
                                                                                                                                WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                      (e.g. dementia).
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                                                    Bardroff M,
Loehning C,
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Gaps ; 74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056; 3; Indels 1; Mismatches 13; Conservative Local Similarity Query Match Matches ò

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ADA90004 standard; peptide; 17 AA. 20-NOV-2003 (first entry)

Anti-Abeta antibody related amino acid sequence SEQ ID NO:119.

antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; noctropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;

```
The present invention describes an antibody molecule (1) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Aag-His-Asp-Car-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA88987 or its fragment. Also described: (1) a muclaic acid molecule cencoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising the bost cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1), vector of (2) or host cell of (3); (7) optimising (1), or nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1) cultured (2) a kit comprising optimisation of (1), and formulating the captimised clones; (1) preparing a pharmaceutical composition prepared by method (8): (1) has characeutical composition prepared by method (8): (1) has characeutical composition prepared by method (8): (1) has characeutical composition of the antibody molecule of a disease associated with amyloid-plaque formation. The antibody molecule of the prevention and/or treatment of a disease associated with amyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the described antibody also beta-amyloid plaque formation. In particular, the disease is capainst beta-amyloid plaque formation. In particular, the disease is capainst beta-amyloid plaque formation of the disease, wherefitary cerebral hemotral composition.

Composition of sequence is 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
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Pred. No. 0.00056;
1; Mismatches 3; Indels
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Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 189-190; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                       Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                             Nordstedt
                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VISETGKNIYYADSVKG 17
                                                                                                                                                                                                                                                  20-FEB-2002; 2002EP-00003844.
                                                                                                                                                                                                           20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                       Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                       neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. dementia).
                                                                                                                           WO2003070760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 AA;
                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       Bardroff M,
Loehning C,
                                                                                                                                                                    28-AUG-2003.
                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADAB9886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lyg-Leu-Val-Phe-Aha-Glu-Abp-Val-Gly ADAB9887 or its fragment. Also described: (I) a nucleic acid molecule cording (I); (2) a vector comprising the nucleic acid of (I); (3) a host coll comprising the vector of (2); (4) preparing (I), comprising (I) coll comprising the vector of (2); (4) preparing (I), comprising (I) contributed molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) cor an antibody molecule produced by method (4); (6) a kit comprising (I) cor an antibody molecule produced by method (4); (6) a kit comprising (I) cordinated of (I), vector of (2) or host cell of (3); (7) optimising (I) cordinated of (I); and recovering (II) preparing a pharmaceutical composition, comprising optimisation of (I), and formulating the coptimised antibody/antibody molecule with a carrier; and (12) a composition, compresition, prepared by method (8). (I) has composition, prepared by method (8). (I) has composition prepared by method (8). (I) has controprotective, nootropic and antiparkinsonian activities, and can be used in preparing a disease associated with any also be used in preparing a disease associated with action of beter amyloid plaque formation. The antibody administration of dementia, Alzheimer's d
                                                                                                                                                                                                                                                         nootropic, antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; heraditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                     antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brockhaus M, Huber W,
Nordstedt C, Rothe C;
                                                                                                                                                                                    MS-R Fab/antibody related peptide #249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 13; Page 92; 312pp; English.
                                          ADA91201 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-PEB-2003; 2003WO-EP001759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2002; 2002EP-00003844.
                                                                                                                                     20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                neuronal disorder; aging.
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Loehning C, Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-663848/62
                                                                                                                                                                                                                                     antibody molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g. dementia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003070760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                           ADA91201;
RESULT 6
                        ADA9120
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                  amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                        Gaps
  amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kretzschmar T;
                                                                                                                                                        ö
                                                                                                             Score 63; DB 6; Length 17;
Pred. No. 0.00056;
!; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brockhaus M, Huber W,
Nordstedt C, Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS-Roche #3.4.H7 H-CDR2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOFFMANN LA ROCHE & CO AG F. MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 64; 312pp; English.
                                                                                                                                                                                                                                                                                                                                  ADA90434 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                 VISETGKNIYYADSVKG 17
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                                                                                                                 74.1%;
76.5%;
                                                                                                                                                                                            1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bohrmann B,
Loetscher H,
                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-663848/62.
                                                                                                               Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003070760-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. dementia).
                                                                           Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bardroff M,
Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                       ADA90434;
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                                                                                                                                                                                                                                                                                                              ADA90434
                                                                                                                                                                                                                                                                                          RESULT
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composition, comprising optimisation of (I), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a plarmaceutical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule amyloidogenesis and/or amyloid-plaque formation. The antibody molecule composition for the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeld Jacob disease, motor neuropathy, Down's syndrome, created the dementia, anyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis putent sequence is used in the exemplification of the present invention.
selected, optimised clones; (11) preparing a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
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Length 17;
Score 63; DB 6; Length 17;
Pred. No. 0.00056;
1; Mismatches 3; Indels
                                                      1 VISENGRTINYADSVKG 17
                                                                      1 VISETGKNIYYADSVKG 17
 74.18;
76.58;
                            13; Conservative
                Local Similarity
 Query Match
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Gaps

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ADA91199 standard; peptide; 17 AA. 20-NOV-2003 (first entry) ADA91199; RESULT 8 ADA91199

MS-R Fab/antibody related peptide #247.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque; formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creuzzfeldt Jacob disease; hereditary cerebral heemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging

Synthetic

Homo sapiens.

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844. (HOFF) HOFFMANN LA ROCHE & CO AG F.

(MORP-) MORPHOSYS AG.

Huber W, Kretzschmar T;

Rothe C;

Brockhaus M, Nordstedt C,

Bardroff M, Loehning C,

Loetscher H, Bohrmann B,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Example 13; Page 92; 312pp; English

20-FEB-2002; 2002EP-00003844. 20-FEB-2003; 2003WO-EP001759.

WO2003070760-A2.

28-AUG-2003.

Homo sapiens

Synthetic

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Gre-Gly-Tyx ADA89886 or list fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lya-Lpu-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or list fragment. Also described: (1) a nucleic acid molecule cancoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of (1); (1) and recovering (I) from the culture; (5) a composition comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or comprising (I), vector of (2) or host cell of (3); (7) optimising (I), or comprising optimisation library by panning of selected, optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (1) has composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a paramaceutical composition prepared by method (8). (1) has neutroprotective, noctropic and antiparkinsonian activities, and can be used in green therapy. The antibody molecule (I), nucleic acid molecule of the prevention and/or treatment of a disease associated with amy also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the antibody alsease, hareditary cerebral hammorrhage with anyloidosis butch type, Parkinson's disease, with anyloidosis butch type, Parkinson's disease, with resent sequence is used in the exemplification of the prevention. ö antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; Gaps ö 74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056; ive 1; Mismatches 3; Indels MS-R Fab/antibody related peptide #349. Ą. ADA91301 standard; peptide; 17 1 VISETGKNIYYADSVKG 17 1 VISENGRIINYADSVKG 17 (first entry) 13; Conservative neuronal disorder; aging Best Local Similarity Sequence 17 AA; 20-NOV-2003 ADA91301; Query Match Matches RESULT 9 ADA91301 ઠે

Huber W, Kretzschmar T; Rothe C;

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Agp-Sar-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Arg-His-Agp-CG Gly ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-CG Gly ADA898897 or its fragment. Also described: (1) a mucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host coll comprising the vector of (2); (4) preparing (1), comprising (I) contains the bost cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody antipody molecule proprimised clones; (10) expressing (1); (8) testing the resulting Pab optimisation library by panning against Abeta(Abeta(4); (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (I) has composition prepared by method (8). (I) has composition prepared by method (8). (I) has certor or host is useful in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a disease associated with entition of the disease mentioned above The antibody is used for the detection of the disease mentioned above The antibody is used for the detection of the disease mentioned above The antibody is used for the detection of the disease mentioned above The antibody is used for the detection of the disease mentioned above The antibody is used for the detection of the disease mentioned above The antibody is used to the disease mentioned ab
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                                                                                                                                                                                                                                                                 New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
                                                                                                                    Brockhaus M, F
Nordstedt C,
                         HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Page 93; 312pp; English
                                                                                                                    Bohrmann B,
Loetscher H,
                                                        MORPHOSYS AG.
                                                                                                                                                                                                        WPI; 2003-663848/62
                                                                                                                                                                                                                                                                                                                                                            (e.g. dementia).
                                                                                                                Bardroff M,
Loehning C,
                         (HOFF ) I
%XGCCCCCCCCCCCCCCCCCCCCCCCCX
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Sequence 17 AA;

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0
74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056; ive 1; Mismatches 3; Indels
                                                                          1 VISENGRIINYADSVKG 17
                                                                                               1 VISETGKNIYYADSVKG 17
                 Local Similarity 76.5
nes 13; Conservative
Query Match
                                     Matches
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Gaps

ADA90190 standard; protein; 120 AA.

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ADA90190;

(first entry) 20-NOV-2003 antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;

Anti-Abeta antibody related amino acid sequence SEQ ID NO:305.

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App. (C Ser-Gly-Tyr ADA89866 or its fragment, and the second region comprises the amino acid sequence val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Cly ADA89887 or its fragment, and the second region comprises the canoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host concoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (I) or nucleic acid of (1), vector of (2) or host cell of (3); (10) expressing (1); (8) testing the resulting Fab optimised clones; (10) expressing of selected, optimisation of (I), and formulating the optimised antibody antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (I) has compressing optimisation of (I), and formulating the composition and/or the antibody molecule with a carrier; and common for the prevention and/or reatment of a disease associated with a carrier; and can be used in preparing a disease associated with a carrier; and can be cused in preparing a disease associated with a carrier of candion of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned bove: The antibody is used for the disease mentioned bove: more of the disease mentioned bove: more of passive immunisation. The disease is more demential companion of perparing a disease is more demential solutions.
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Alzheimer's disease; motor neuropathy; Down's syndrome;
Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Page 272-273; 312pp; English.
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                    Œ,
                                                                                                                                                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.
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                                                                                                                                                                                                                                                                                      20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                                                                                                                                                     20-FEB-2002; 2002EP-00003844
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Loetscher H,
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                                                                   neuronal disorder; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-663848/62.
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hes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. dementia).
                                                                                                                                                                                          WO2003070760-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 120 AA;
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bardroff M,
Loehning C,
                                                                                                                                                                                                                                      28-AUG-2003
                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
  8
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dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp. Ser-Gly-Tyr ADAB9886 or its fragment, and the second region comprises the amino acid sequence val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host culturing the host cell of (3); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I); (8) testing the resulting Fab optimisation library by panning against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) reparing the composition, comprising optimisation of (I), and formulating the composition, comprising optimisation of (I), and (12) a composition of (2) or host cell (2) and (2) an
                                                                                                                                                                                                                                                               antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immuniaation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaques or for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                              Anti-Abeta antibody related amino acid sequence SEQ ID NO:303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 16; Page 271-272; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brockhaus M,
Nordstedt C,
                                 ADA90188 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003WO-EP001759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bohrmann B,
Loetscher H,
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuronal disorder; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dementia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003070760-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                    20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                           ADA90188;
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Kretzschmar

Rothe C; Huber W,

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (I) from the culture; (5) a composition comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) nor an antibody molecule produced by method (4); (6) a kit comprising (I), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody molecule, antibody, beta-A4 peptide, Abeta4; neuroprotective, nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
             Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with, amyloidosis Dutch type. Parkinson's disease, HIV-related dementa, amyloirophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huber W, Kretzschmar T;
Rothe C;
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Abeta antibody related amino acid sequence SEQ ID NO:125
                                                                                                                                                 Length 120
                                                                                                                                                                                     3; Indels
                                                                                                                                               Score 63; DB 6;
Pred. No. 0.0059;
1; Mismatches
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 191; 312pp; English.
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                                                                                                                                                                                                                                                                                                                                                            ADA90010 standard; peptide; 17
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                                                                                                                                                                                                                                                                64
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                                                                                                                                                 74.18;
76.58;
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                                                                                                                                                                                                                                                                48 VISETGKNIYYADSVKG
                                                                                                                                                                                                                          1 VISENGRIINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bohrmann B,
Loetscher H,
                                                                                                                                             Query Match
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuronal disorder; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-663848/62.
                                                                                                              Sequence 120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Loehning C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                  ADA90010;
                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                             ADA90010
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composition, comprising the resulting rand polarization initiary by painting district Abeta/Abeta4; (9) identifying optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a composition prepared by method (8). (1) has contropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule with a carrier acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a disease associated with anyloid-plaque formation. The antibody molecule anyloidogenesis and/or amyloid-plaque formation. The antibody molecule anyloidogenesis or for passive immunisation of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, creutzfeldt Jacob disease, motor neuropathy, Down's syndrome, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuropal disorders related to aging. The present sequence is used in the exemplification of the present invention.

Sequence 17 AA;

Gaps ö Score 62; DB 6; Length 17; Pred. No. 0.00084; 0; Mismatches 3; Indels 0; Mismatches 72.9%; 81.2%; Conservative Local Similarity 13; Query Match Matches

2 ISEOGRNIYYADSVKG 17 2 ISENGRTINYADSVKG

ઠે ద RESULT 13 ADA91195

ADA91195 standard; peptide; 17 AA. ADA91195;

20-NOV-2003 (first entry)

MS-R Fab/antibody related peptide #243.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creuzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(MORP-) MORPHOSYS AG.

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Loetscher H, œ, Bardroff M, Bohrmann Loehning C, Loetscher

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia) THE LICENSE BY SEX BY S

The present invention describes an antibody molecule (1) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Sar-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment, Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1); comprising the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) cucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Rab optimised clones; (10) expressing (1); (8) testing the resulting Rab optimised clones; (10) expressing of selected, optimised clones; (11) preparage of selected, optimised clones; (11) reader of (12); and formulating the composition, comprising optimised approach (12) a composition of (12) and composition of (13); and (12) and (12) and (12) and (13); a phramaceutical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be newed in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with anyloid pensating a disease associated with anyloid-plaque formation. The antibody molecule may also be used in preparing a disgnostic composition for the detection of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mention of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementa, Alzheimer's disease, motor neuropathy, Down's syndrome, amyloid plaque formation, derebral haemorrhage with amyloid disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis butch type, Parkinson's disease, HIV-related dementia, camyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. Example 13; Page 92; 312pp; English.

Sequence 17 AA;

ö Score 62; DB 6; Length 17; Pred. No. 0.00084; 1; Mismatches 3; Indels 1; 72.9%; Query Match
Best Local Similarity 76.5:

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Gaps

17 1 VISQTGRKIYYADSVKG 17 1 VISENGRTINYADSVKG ઠે 셤

RESULT 14

ADA91198 standard; peptide; 17 AA ADA91198

ADA91198;

20-NOV-2003 (first entry)

MS-R Fab/antibody related peptide #246.

nociropic, antiparkinsonian; gene therapy; anyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Jahlaniemer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary paral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Synthetic

Homo sapiens.

WO2003070760-A2.

28-AUG-2003

20-FEB-2003; 2003WO-EP001759.

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Val-Phe-Phe-Ala-Glu-Asp-Val-Cly-Tyr ADA89887 or its fragment, Also described: (I) a mucleic acid molecule coding (I); (2) a vector comprising the nucleic acid of (I); (3) a host call comprising the vector of (2); (4) preparing (I), comprising the vector of (2); (4) preparing (I), comprising (I) culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I), adainst AbetaAAbeta4; (9) identifying optimised clones; (II) esparing a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creuzzfeldt Jacob disease, hereditary cerebral haemorrhage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of selected, optimised clones, (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a
                                                                                                                                    Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                   Example 13; Page 92; 312pp; English.
                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · 1 VISENGRTINYADSVKG 17
                        20-FEB-2002; 2002EP-00003844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VISOTGRKIYYADSVKG
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                                                                                                                                      Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                           (MORP-) MORPHOSYS AG
                                                                                                                                                                                                       WPI; 2003-663848/62.
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                                                                                                                                                                                                                                                                                                                          (e.g. dementia).
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                                                                                                                                    Bardroff M,
Loehning C,
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ö Gaps ; 0 72.9%; Score 62; DB 6; Length 17; 76.5%; Pred. No. 0.00084; ive 1; Mismatches 3; Indels

17

antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; Anti-Abeta antibody related amino acid sequence SEQ ID NO:115.

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; altheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging

Synthetic.

Kretzschmar

Rothe C; Huber W,

Homo sapiens.

WO2003070760-A2.

28-AUG-2003

20-FEB-2003; 2003WO-EP001759

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Loehning C,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Disclosure; Page 188; 312pp; English

The present invention describes an antibody molecule (I) capable of appecifically recognising two regions of the beta-A4 peptide/Abbeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Appering the amino acid sequence Ala-Glu-Phe-Arg-His-Appering the Appendix of Ser-Gly-Tyx ADA8986 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-App-Val-Cdly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule conding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) collarising the host cell of (3) index conditions that allow synthesis of culturing the host cell of (3) index conditions that allow synthesis of culturing the host cell of (3) index conditions that allow synthesis of culturing the resulting Pab optimisation of (3); (7) optimising (I) or nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I) comprision (1) and formation of (1); and formulating the cell against AbetaA/Abeta4; (9) identifying optimisation of (1); and formulating the coptimisation of (I); and formulating the coptimisation of (I), and formulating the coptimisation of (I); and formulating a pharmaceutical composition for the disease mentioned and/or treatment of a disease as of disease is dementia, Alzheimer's disease, motor neuropathy, bown's syndrome, coffice the prevention and/or treatment of adeservation of the parawine of the disease, hereditary cerebral dementia, Alzheimer's disease, motor neuropathy, related dementia, any di

Sequence 17 AA;

Gaps ö Score 62; DB 6; Length 17; Pred. No. 0.00084; 3; Indels 1; Mismatches 72.9%; 13; Conservative Query Match Best Local Similarity Matches

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ADA91193; antibody

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17

1 VISQTGRKIYYADSVKG

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molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; MS-R Fab/antibody related peptide #241. ADA91193 standard; peptide; 17 (first entry) 20-NOV-2003 ADA91193
ADA

Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; nootropic, antiparkinsonian, gene therapy, amyloidogenesis, amyloid-plaque, formation, beta-amyloid plaque, immunisation, dementia, Alzhaimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage, amyloidosis, neuronal disorder; aging. Synthetic

Homo sapiens.

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(MORP-) MORPHOSYS AG

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Bohrmann Loehning

WPI; 2003-663848/62.

σţ New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia)

Example 13; Page 92; 312pp; English.

The present invention describes an antibody molecule (I) capable of grecifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (4) optimising (I), (8) testing the resulting Fab optimisation library by panning (I); (8) testing the resulting Fab optimised clones; (10) expressing of selected, optimised clones; (11) reparing a pharmaceutical composition, comprising optimisation of (I), and formulating the composition of (1), and carrier; and (12) a patimised antibody/Amistibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the disease mentioned above. The antibody is used for the detection of the disease mentioned above. The antibody is used for the

ö disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Ducch type, Parkinson's disease, HIV-related dementia, amyloicophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; althemismer; disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; Gaps ö Length 17; Score 62; DB 6; Length 17; Pred. No. 0.00084; .; Mismatches 3; Indels MS-Roche #3.4.H3 H-CDR2 amino acid sequence. ADA90430 standard; peptide; 17 AA. 1 VISENGRIINYADSVKG 17 1 VISOTGRKIYYADSVKG 17 72.9%; 76.5%; (first entry) 13; Conservative neuronal disorder; aging. Query Match Best Local Similarity Sequence 17 AA; 20-NOV-2003 Synthetic ADA90430; Matches ADA90430 ID ADA9 88888888 ò g

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Example 5; Page 64; 312pp; English. Loetscher H, WPI; 2003-663848/62. (e.g. dementia). Bardroff M, Loehning C,

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HOFFMANN LA ROCHE & CO AG

(MORP-) MORPHOSYS AG.

(HOFF)

Bohrmann B,

20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844.

WO2003070760-A2.

28-AUG-2003

Homo sapiens.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I)

optumizers anti-body microture with a callier and (12) a plarmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule amyloid-openesis and/or amyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the detection of the disease mentioned above. The antibody is used for the detection of the disease mayloid plaques or for passive immunisation. Compaints beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy. Down's syndrome, creuzfeldt Jacob disease, hereditary cerebral haemorthage with amyloidosis Dutch trype, Parkinson's disease, HIV-related dementia, amyloidosis Dutch trype, Parkinson's disease. HIV-related dementia, amyloidosis dutch trype, Parkinson's disease, related to aging. The present sequence is used in the exemplification of the present invention. comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (1) nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta/Abeta4, (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a 0

Sequence 17 AA;

ö Score 62; DB 6; Length 1/;
Pred. No. 0.00084;
3; Indels 17 1 VISQTGRKIYYADSVKG 17 72.9%; 76.5%; 1 VISENGRTINYADSVKG Conservative Local Similarity nes 13, Conserv Query Match Matches ઠે 셤

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Gaps

ADA91196 standard; peptide; 17 20-NOV-2003 (first entry) ADA91196; RESULT 18 ADA91196

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MS-R Fab/antibody related peptide #244.

Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, (HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. Bardroff M, Bohrmann B, Loehning C, Loetscher H,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Galu-Phe-Arg-His-Asp-Ser-Gay-Tyr ADA8986 or its fragment, and the second region comprises the amino acid sequence val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-App-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule cancoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host call comprising the vector of (2); (4) preparing (I), comprising the host cell of (3) under conditions that allow synthesis of call comprising the host cell of (3) under conditions that allow synthesis of call comprising the recentling Pab optimisation in the comprising (I), and recovering (I) from the culture; (5) a composition comprising (I), comprising the resulting Fab optimisation library by panning or selected, optimised clones; (1) preparing a pharmaceutical composition for (I), and formulating the optimised clones; (1) preparing a pharmaceutical composition prepared by method (8). (1) has composition for optimised antibody molecule with a carrier; and (12). a pharmaceutical composition prepared by method (8). (1) has composition for used in gene therapy. The antibody molecule (I), nucleic acid molecule. Weeter or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is capmined above. The antibody is used for the disease mentioned above. The antibody is used for the disease mention of beta-amyloid plaques or for passive immunisation. Companied the disease, hereditary cerebral hemorrhage with amyloid-sieses, hereditary cerebral hemorrhage with amyloid-sieses, hereditary cerebral hemorrhage or the prevention of beta-amylo ö Gaps diseases associated with amyloidogenesis or amyloid-plaque formation . 72.9%; Score 62; DB 6; Length 17; 76.5%; Pred. No. 0.00084; ive 1; Mismatches 3; Indels Example 13; Page 92; 312pp; English. 1 VISQTGRKIYYADSVKG 17 1 VISENGRIINYADSVKG 17 13; Conservative Best Local Similarity (e.g. dementia). Sequence 17 AA; Query Match Matches ò 셤

ADA90440 standard; peptide; 17 AA. 20-NOV-2003 (first entry) ADA90440; ADA90440

MS-Roche #3.4.H13 H-CDR2 amino acid sequence.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

neuronal disorder; aging

Homo sapiens. Synthetic

WO2003070760-A2.

28-AUG-2003.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; cretuzfeld Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; hereditary cerebral haemorrhage; amyloidosis; neuronal disorder; aging.

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Anti-Abeta antibody related amino acid sequence SEQ ID NO:301.
                                                                                                                                                                                                                                                                                                                                   ADA90186 standard; protein; 120 AA
     20-FEB-2003; 2003WO-EP001759
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                                                                                                                                                                                                                                                                                                          ISEQGRNIYYADSVKG 17
                                                                                                                                                                                                                                                                                                 ISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                       13; Conservative
                                       Bardroff M, Bohrmann
                                                     WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                               dementia).
                                                                                                                                                                                                                                                                    Sequence 17 AA;
                                             Loehning C,
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                                                                                                                                                                                                                                                                                                                                             ADA90186;
                                                                                                                                                                                                                                                                             Query Match
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Matches
                                                                                                                                                                                                                                                                                                                          RESULT 20
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TD ADA9
XX
AC ADA9
XX
DT 20-1
XX
DB ANT
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Bardroff M, Loehning C, The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Argg-His-Agp. Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a mucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) comprising the vector of (2); (4) preparing (I), comprising (I) comprising the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody antibody molecule (I), and formulating the composition, comprising pab optimised clones; (10) expressing deslected, optimised clones; (II) preparing a pharmaceutical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be used in ore herapy. The antibody molecule (I), nucleic acid molecule, and any least associated with Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. ŏ may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Example 5; Page 64; 312pp; English. (HOFF) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG. 20-FEB-2002; 2002EP-00003844. Bohrmann B, Loetscher H,

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation

Kretzschmar T;

Rothe C;

Brockhaus M, Nordstedt C,

Loetscher H,

WPI; 2003-663848/62.

Bohrmann B,

<u>ω</u>,

HOFFMANN LA ROCHE & CO AG MORPHOSYS AG.

(MORP-)

20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844.

WO2003070760-A2.

28-AUG-2003

Homo sapiens.

Synthetic

The present invention describes an antibody molecule (I) capable of first present invention describes an antibody molecule (I) capable of first region comprises the amino acid sequence Ala-Glu-Phe-Ala-Glu-Phe-Ala-Glu-Phe-Ala-Glu-Phe-Ala-Glu-Alap-Clu-Alaba9886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Aba98886 or its fragment, Alac described; (I) a uncleic acid molecule condoming (II); (2) a vector comprising the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or ala can be composition, comprising optimised clones; (II) preparing a pharmaceutical composition for (I); (8) testing the resulting Rab optimised clones; (II) preparing a pharmaceutical composition prepared by method (8); (I) has composition for the prevention and/or treatment of a disease associated with antibody molecule (C) cused in gene therapy. The antibody molecule (I), nucleic acid molecule, wector or host is useful in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule of also associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease in mantipody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease, motor neuropathy, Down's syndrome, controlle amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. Example 16; Page 270; 312pp; English. (e.g. dementia).

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Gaps

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Length 17;

Score 62; DB 6; Length 17; Pred. No. 0.00084; 0; Mismatches ' 3; Indels

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17

Gaps ö Score 62, DB 6; Length 120; Pred. No. 0.0088; 1; Mismatches 3; Indels 72.9%; 76.5%; Conservative Similarity Sequence 120 AA; Query Match Best Local Simil Matches 13; C

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nootropic; antiparkinsonian, gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: d disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                 antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                               Kretzschmar T;
                                                                                                                                           Anti-Abeta antibody related amino acid sequence SEQ ID NO:299.
                                                                                                                                                                                                                                                                                                                                                                                                               Huber W,
Rothe C;
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 16; Page 269; 312pp; English.
                                                                           ADA90184 standard; protein; 120 AA
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                    64
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                                                                                                                                                                                                                                                                                                                                                         20-FEB-2002; 2002EP-00003844.
                48 VISQTGRKIYYADSVKG
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                   neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                                             Bardroff M, Bohrmann
Loehning C, Loetscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-663848/62.
                                                                                                                                                                  molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. dementia).
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                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                 ADA90184;
                                                                                                                                                                  antibody
                                                      RESULT 21
                                                                  ADA90184
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The present invention describes an antibody molecule (I) capable of gpecifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host call comprising the vector of (2); (4) preparing (I), comprising of culturing the host cell of (3); (4) preparing (I), comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) culture; (6) a kit comprising (I) and recovering (I) from the culture; (5) a composition comprising (I); (8) testing the resulting Fab optimisation library by panning against Abeta4, (9) identifying optimised clones; (10) expressing composition, comprising optimisation of (I), and formulating the composition, comprising optimisation of (I), and formulating the composition of (I), and carrier; and (12) a composition composition of (I), and carrier; and (12) a pharmaceutical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule

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may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
atlaneimer g disease; mctor neuropathy; Down's syndrome;
Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
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the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Abeta antibody related amino acid sequence SEQ ID NO:136.
                                                                                                                                                                                                                                 Score 62; DB 6; Length 120;
Pred. No. 0.0088;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huber W,
Rothe C;
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 194; 312pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA90021 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                              1 VISENGRIINYADSVKG 17
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76.5%;
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Loetscher H,
                                                                                                                                                                                                                                     Query Match 72.9
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal disorder; aging
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                                                                                                                                                                                                 Sequence 120 AA;
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Loehning C,
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culturing the host cell of (3) under conditions that allow synthesis of

(1) and recovering (1) from the culture; (5) a composition comprising (1)

cor an antibody molecule produced by method (4); (6) a kit comprising (1),

conclusion antibody molecule produced by method (1); (7) optimising

(1); (8) testing the resulting Rab optimisation library by panning

conclusion (1); (8) identifying optimised clones; (10) expressing

composition, comprising optimisation of (11), and formulating the

composition, comprising optimisation of (11), and formulating the

composition, comprising optimisation of (11), and formulating the

pharmaceutical composition prepared by method (8). (1) has

controprotective, nootropic and antiparkinsonian activities, and can be

neuroprotective, nootropic and antiparkinsonian activities, and can be

controprotective, nootropic and antiparkinsonian activities, and conclusion of the antibody molecule (1), nucleic acid molecule,

concror or host is useful in preparing a pharmaceutical composition for

the prevention and/or amyloid-plaque formation. The antibody molecule

amyloidogenesis and/or amyloid-plaque formation. The antibody molecule

controprotection of beta-amyloid plaques or for passive immunisation

adainst bata-amyloid plaques or for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease; HIV-related demential amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                 8XGGGGGGGGGGGGGGGGGGGGG
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Sequence 17 AA;

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Gaps
                                 ;
0
Score 61; DB 6; Length 17;
Pred. No. 0.0013;
1; Mismatches 3; Indels
71.8%;
76.5%;
              Best_Local Similarity 76.5
Matches 13; Conservative
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1 · VISENGRTINYADSVKG 17 1 VISETGKFIYYADSVKG 17 8 셤

ADA90580 standard; peptide; 17 AA. 20-NOV-2003 (first entry) ADA90580; RESULT 23 ADA90580

MS-Roche #3.6.H3 H-CDR2 amino acid sequence.

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Synthetic

Homo sapiens.

28-AUG-2003.

WO2003070760-A2,

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Loehning C,

WPI; 2003-663848/62.

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The present invention describes an antibody molecule (I) capable of first present invention describes an antibody molecule (I) capable of first region comprises the amino acid sequence Ala-Glu-Phe-Ala-Glu-Abap-Ser-Gly-Tyr AbA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-App-Val-CG Jy AbA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid molecule conding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), nucleic acid of (I), vector of (2) or host in submission comprising optimised clones; (I) and recovering (I), and formulating the composition, comprising optimisation of (I), and formulating the optimised antibody molecule with a carrier; and (12) a plarmaceutical composition prepared by method (8). (I) has plarmaceutical composition prepared by method (8). (I) has plarmaceutical composition for the prevention and/or reatment of a disease associated with antibody molecule may also be used in preparing a pharmaceutical composition for the disease mentioned above. The antibody is used for the amy also be used in preparing a disease associated with any also be used in preparing a disease associated with antibody molecule may also be used in preparing a disease associated with any and can be admitted by a disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the dementa, Alzheimer's disease, metor neuropathy, Down's syndrome, admitted any old plateral solutions of present sequence is u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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        regions
New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plague formation
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Pred. No. 0.0013;
1; Mismatches 3; Indels
                                                                                                                                     Example 5; Page 65; 312pp; English.
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76.5%;
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Best Local Similarity
                                                                                   (e.g. dementia).
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AAG62968 standard; protein; 121 AA. 01-OCT-2001 (first entry) AAG62968; AAG62968

Amino acid sequence of variable heavy chain fragment of clone DH

Antibody; heavy chain; VH; amyloid protein; blood brain barrier; endothelial cell, brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; Alzheimer's disease; prion disease; Alzbeimer (a disease).

Homo sapiens,

WO200144300-A2

21-JUN-2001.

27-NOV-2000; 2000WO-GB004501.

Hilbert D;

Vaughan T,

Choi GH,

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                               Miller K;
                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 109; 109pp; English.
                                                                                                                                               Ward G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system
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75.0%;
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17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
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nes 12; Conservative
                                                                                                                                               Osbourn J,
                                                                                                                                                                                                       WPI; 2001-398131/42.
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                                                                                                                                               Webster C,
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (GVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2369-2370; 3148pp; English.
                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                   WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 248 AA;
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                                                                                                                                                                            Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an antibody variable heavy chain (VH) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the D5 VH and/or VL variable domain when bound to human service is useful for the selection of specific binding members with a desired property such as ability to cross BBB, ability to bind with a desired property such as ability to cross BBB, ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzheimer's disease, prion disease, AlDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.013;
2; Mismatches 2; Indels
                              99US-0170599P
                              13-DEC-1999;
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              71.8%; Score 61; DB 5; Length 248; 64.7%; Pred. No. 0.031; ive 3; Mismatches 3; Indels
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US-09-553-909A-130
US-09-553-909A-130
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US-08-478-039-95
US-08-311-394A-61
US-08-311-394A-61
US-08-311-394A-61
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US-08-311-304A-61
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Sequence 16,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Compugen Ltd.
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US-09-240-274-143

US-08-918-148-16

US-08-918-148-16

US-08-18-148-16

US-08-18-148-16

US-08-18-148-15

US-08-18-18-18-18

US-09-240-274-2

US-09-240-274-2

US-09-240-274-2

US-09-240-274-2

US-09-240-274-2

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US-08-652-816A-11

US-08-652-816A-11

US-08-652-816A-11

US-08-862-124-17

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              GenCore version (c) 1993 - 2004
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Listing first 150 summaries
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Gapop 10.0 , Gapext 0.5
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS(MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 1-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 14-JUN-1991
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wandy M.
REGISTRATION NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94080
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US-08-437-642B-4
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                                          Sequence 34, Appl Sequence 63, Appl Sequence 63, Appl Sequence 65, Appl Sequence 65, Appl Sequence 80, Appl Sequence 81, Appl Sequence 12, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 31, Appl Sequence 104, Appl Sequ
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) Sequence 4, Application US/07934373C
) Patent No. 5821337
) GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
ITILE OF INVENTION: Immunoglobulin Variants
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                          US-08-956-047-34
PCT-US94-14106-59
US-08-190-1914-65
US-08-190-1914-65
US-08-190-1914-65
US-08-190-1914-65
US-08-190-1914-65
US-09-56-047-25
US-09-56-1918-12
US-09-56-1918-12
US-09-56-1918-12
US-09-56-1918-12
US-09-56-1918-12
US-09-56-1918-12
US-09-56-1918-12
US-09-1914-658-48
US-09-1914-658-48
US-09-1914-658-48
US-09-1914-658-48
US-09-1914-658-48
US-09-1914-658-48
US-08-428-197-24
US-08-428-197-24
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US-08-428-197-24
US-08-428-197-24
US-08-428-197-24
US-08-428-197-24
US-08-428-197-24
US-08-428-197-28
US-08-428-197-28
US-08-428-197-38
US-08-438-104
US-08-476-349A-104
US-08-476-349A-104
US-08-276-852-74
US-08-276-852-74
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ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

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PCT-US93-07832-4
                                                US-09-705-686-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08146206C

Patent No. 6407213

GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION TOWNER:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB 4;
Pred. No. 0.0087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
         TOWNEY NAME TO WINDER TO 378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: P0709P2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
ATTORNEY/AGENT INFORMATION:
                                                           REFERENCE/DOCKET NUMBER: P070
TELECOMUNICATION INFORMATION:
TELEPAX: 650/252-1994
TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: POT
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VISENGSDTYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative C
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
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                                                                     APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.6%; Score 60; DB 4; Length 120; Best Local Similarity 76.5%; Pred. No. 0.0087; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER KEADABALE FURM:

WHOULUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINDBIN: (Genentech)
CURRENT APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UND-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 09/7049103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
HAPLICANT: Genentech, Inc.
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
GENERACH GENERACH INC.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Calsh San Francisco
STATE: Calsh San Francisco
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P0709P1D3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
Sequence 4, Application US/09705686 Patent No. 6639055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 VISENGSDTYÝADSVKG 66
                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
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Sequence 16, Application US/08918148A Patent No. 6342220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08665202 Patent No. 5977322 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ISSSGSTIYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: 5E5scFv VH CDR2
LOCATION: 1-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1-22; CTHER INFORMATION: US-08-918-148-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-665-202-31
         US-08-918-148-16
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 22
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TILLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

CURRENT FILING DATE: 1990-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,50

EARLIER PILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 143

LENGTH 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.6%; Score 60; DB 5; Length 120; Best Local Similarity 76.5%; Pred. No. 0.0087; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . OTHER INFORMATION: anti-Rh(D) antibody clone SH20 US-09-240-274-143
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/115272
FILING DATE: 14-JUN-1991
RICH APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 709P2PCT REFERENCE/DOCKET NUMBER: 709P2PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 VISENGGYTRYADSVKG 66
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-274-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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RESULT 7

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APPLICANT: Marks, James D.
APPLICANT: Schler, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 57; DB 4; Length 22; 75.0%; Pred. No. 0.0041; rive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPICE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
ATTOMEY/AGENT INFORMATION:
ANTERNEY/AGENT INFORMATION:
APPLICANT: Adame, Camellia
APPLICANT: W.
APPLICANT: Garter, Paul J.
APPLICANT: Carter, Paul J.
APPLICANT: Garter, Paul J.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT FILING DATE: 1997-08-25
CURRENT FILING DATE: 1997-08-25
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,498
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TELECOMMUNICATION INFORMATION:
TELEBEPAN: (415) 576-020
TELEBEAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
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SEQUENCE CHARACTERISTICS

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US-08-545-809A-99

Sequence 99, Application US/08545809A

Sequence 99, Application US/08545809A

Patent No. 6056878

Patent No. 6056878

Patent Honjo, Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1%; Score 57; DB 75.0%; Pred. No. 0.02 ive 1; Mismatches
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29,066
77 06501/004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 065(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
|| :| || |||||||
51 ISSSGSTIYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ISSSGSTIYYADSVKG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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02110-2804
                                                                                                                                                                                                                                                                                                                       ADDA...
STREET: 44...
-TW: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
CORRESPONDENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                               Gaps
                                                                                                                                                                     Length 98;
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Pred. No. 0.022;
1; Mismatches 3; Indels
                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Majestic, Parsons, Siebert & Haue P.C.
Pour Embarcadero Center, Suite 1100
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentln Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/315,574 FILING DATE: 20-MAY-99 CLASSIFICATION: 530
                                                                                                                                                                   Score 57; DB 2;
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION VUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
PRIOR APPLICATION NUMBER: US 60/65,202
FILING DATE: 13-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-4106
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              US-09-315-574-31
; Sequence 31, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                 Query Match 67.1%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                             51 ISSSGSTIYYADSVKG 66
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75.0%;
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Best Local Similarity 75.04
Matches 12; Conservative
                 LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-665-202-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-315-574-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCES. 141
CORRESPONDENCES. Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                       Gaps
                                       ö
DB 3; Length 117;
0.027;
                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
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Sequence 4, Application US/09240274

Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
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Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                           NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/240,274
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EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORWATION:
NAME: HURLEY, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-918-148-75; Sequence 75, Application US/08918148A; Patent No. 6342220
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75.08;
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                                                                                                                                                                                                                                                                            LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.1
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Adams, Camellia
                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-09-315-574-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: artificial US-08-918-148-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: W
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Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.1%; Score 57; DB 2; Length 123; 75.0%; Pred. No. 0.029;
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: A24
PRIOR APPLICATION NAMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 15-JUN-1995
ATPONDEY/AGENT INFORMATION:
NAME: NAME: 15-JUN-1995
ATPONDEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREESEE: Majestic, Parsons, Siebert & Hsue P.C. STREET: Four Embarcadero Center, Suite 1100 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC. Compatible
COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                  RECISTRATION NUMBER: 38,498
RECISTRATION NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPEAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ISSSGSTIYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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US-09-315-574-30
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                           US-09-240-274-7
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TILE REPERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: (0/091,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PACENTING PACE: 2.0
EARLIER PACENTING PACE: 2.0
EARLIER FILING DATE: 1996-10-11
SOFTWARE: PACENTING PACE: 2.0
EARLIER PACENTING PACE: 2.0
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TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4402
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 224
SOFTHARE: PALENTH VET: 2.0
SEQ ID NO 3
LENGTH: 124
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                                                                                                                                                                                                                             Length 124;
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                                                                                                                                                                                                                        Ouery Match 65.9%; Score 56; DB 3; Best Local Similarity 70.6%; Pred. No. 0.043; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 54; DB 3; 70.6%; Pred. No. 0.092;
                                                                                                                                                 ; OTHER INFORMATION: anti-Rh(D) chain C04
US-09-240-274-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain C01
US-09-240-274-2
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-240-274-2
; Sequence 2, Application US/09240274
; Patent No. 6255455
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; Sequence 3, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                         50 VISYDGHNKNYADSVKG 66
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50 VISYDGHHKNYADSVKG 66
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NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserve
                                                                                                                                   FEATURE:
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Sequence 7, Application US/09240274

Sequence No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPREBRUCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
MUMBER OF SEQ ID NOS: 224

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 7

ENRICH: 124
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US-08-545-809A-143
Sequence 143, Application US/08545809A
Patent No. 6056878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: Unihiko
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson, P.C.
STRET: 225 Franklin Street
CITY: Boston
STATE: MA
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                                                                                              Score 54; DB 3; Length 124; Pred. No. 0.092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.5%; Score 54; DB 3; Length 124; Best Local Similarity 70.6%; Pred. No. 0.092; Matches 12; Conservative 1; Mismatches 4; Indele
                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
PILING DATE: VS / 08 / 54 E 00000
                                                                                                                                              1; Mismatches
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain C03
US-09-240-274-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: anti-Rh(D) chain Cl0 US-09-240-274-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/545,809A
27-MAR-1996
                                                                                                                                                                                                                    50 VISYDGHHKNYADSVKG 66
                                                                                                                                                                                       1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 VISYDGHHKNYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VISENGRIINYADSVKG 17
                                                                                              Query Match 63.5%;
Best Local Similarity 70.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RY: US
02110-2804
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Gaps

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4; Indels

1; Mismatches

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11; Conservative
    Matches
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TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Ridout & Maybee
STREET: 2300 Kichmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 116; 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 1; Length 17; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECHONE: (416) 868-1482
TELEPHONE: (416) 868-1482
ITELEPHONE: (416) 868-1482
                                                                                                                                      06501/004001
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53;
Pred. No.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-264-093-22; Application US/08264093; Sequence 22, Application US/08264093; Patent No. 563963; GENERAL INFORMATION: APPLICANT: Michael D. Dan
                                                                                      NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not applicable
                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ 1D NO: 143:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VISTSGDTVLYTDSVKG 84
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                           LENGTH: 116 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-545-809A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-264-093-22
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STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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61.2%;

Query Match Best Local Similarity

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0
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APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 952504.9
FILING DATE: 3-MAY-1996
FILING DATE: 07-DEC-1992
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 20-DEC-1992
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 3-MAY-1996
PRIOR APPLICATION NUMBER: US 08/244,597
FILING DATE: 3-MAY-1996
PRIOR APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-UM-1994
ATTORNEY/AGENT INFORMATION:
NAME: DATA NUMBER: 36.107
REGISTRANTON NUMBER: 36.107
REGISTRANTON NUMBER: 36.107
REGISTRANTON NUMBER: 36.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 2;
Pred. No. 0.19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 28111/33308 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COMPUTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                 US-08-652-816A-11
; Sequence 11, Application US/08652816A
Patent No. 5872215
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.2%;
Best Local Similarity 68.8%;
Matches 11; Conservative
2 ISENGRIINYADSVKG 17
                                                      2 ISSNGGSTYYADSVKG 17
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APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLECTIDES ENCODING THE
TITLE OF INVENTION: PRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.2%; Score 52; DB 3; 70.6%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMULICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 28
CORRESSONDENCES:
ADDRESSEE: MOTTISON & FOERET LLP
STREET: 755 Page Mill Road
                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08862124
Patent No. 6207153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| :| | |||||||
111 VISYDGSTKYYADSVKG 127
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NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 179 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTIGEN BINDING FRAGMENTS H11, THAT
: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCO
: FRAGMENTO.
: FRAGMENTO.
: DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                 Sequence 14, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: ANTIGEN
INTER OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette - 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Morrison & Foerster LLP
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08862124
Patent No. 6207153
GENERAL INPORMATION:
APPLICANT: Dani, Michael D.
APPLICANT: Malti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: SPECIFICALLY D.
TITLE OF INVENTION: SPECIFICALLY D.
TITLE OF INVENTION: PRAGMENTS, AND TITLE OF INVENTION: DETECTION OF C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.2%;
68.8%;
                                          51 issnegstyrabsvke 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 ISSNGGSTYYADSVKG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (416) 868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 2J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                               US-08-264-093-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-264-093-14
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US-08-862-124-2
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                                        g
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Length 179; 4; Indels

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ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: G0606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: E10ppy disk
COMPUTER: E10ppy disk
COMPUTER: E10ppy disk
COMPUTER: E10ppy disk
COMPUTER: STEW FC COMPATIAL
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/211,202
FILING DATE: 23-SEP-1992
FILING DATE: 23-SEP-1991
FRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
FRIOR DATE: 15-MAY-1992
FRIOR DATE: 15-MAY-1992
FRIOR APPLICATION NUMBER: BCT/GB92/00883
FILING DATE: 15-MAY-1992
FRIOR DATE: 16-MAY-1992
ATORNEYAMON W. CIOUGH
NAME: DAVIG W. CIOUGH
REGISTRATION UNMBER: 36, 107
REGISTRATION UNMBER: 
                                                                                                                GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: BAIER, Michael
APPLICANT: BESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies -
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                             ; Sequence 116, Application US/08211202; Patent No. 5565332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ISSSSTIYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-211-202-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLECTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 0.52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lenhhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/POCKET UNBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.2%; Score 52; DB 3
Best Local Similarity 70.6%; Pred. No. 0.55;
Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Morrison & Foerster LLP
: 755 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08862124
Patent No. 6207153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: SPECIFICAL
TITLE OF INVENTION: PREGENEUS,
TITLE OF INVENTION: DETECTION
INTHER OF SQUENCES, 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOORTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| :| | |||||||
192 VISYDGSTKYYADSVKG 208
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VISENGRTINYADSVKG 17
                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              Query Match 61.2%;
Best Local Similarity 70.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 304 amino acids
amino acid
(650) 494-0792
                                                                                                                                     287 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-862-124-14
                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-862-124-17
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                                                                                                                                                             amino acid
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TELEFAX:
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Query Match 60.0%; Score 51; DB 1;
Best Local Similarity 68.8%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches '
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Sequence Sequence

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Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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US-10-032-423A-63
US-10-032-423A-79
US-10-032-423A-79
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US-10-033-423A-79
US-10-379-322-16
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US-10-293-418-2014
US-10-293-418-2014
US-10-293-418-2016
US-10-880-748-2016

Sequence

Sequence Sequence Sequence

3.5

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September 24, 2004, 01:54:43; Search time 98.4717 Seconds (without alignments) 55.513 Million cell updates/sec
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79,
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                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
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         5.1.6
Compugen Ltd.
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US-09-880-748-1648
US-09-880-748-1648
US-09-880-748-1503
US-10-293-448-1503
US-10-293-268-57
US-10-029-268-79
US-10-029-268-79
US-10-194-975-17
US-10-194-975-17
US-10-308-817-57
US-10-308-817-57
US-10-032-0378-63
US-10-032-0378-63
US-10-032-0378-63
US-10-032-0378-63
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 1349238 seqs, 321558718 residues
                                                                                                                   US-10-088-639A-2_COPY_177_193
85
1 VISENGRTINYADSVKG 17
         GenCore version (c) 1993 - 2004
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                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
                                                   protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
                                                                                                                                                                  Scoring table:
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Sequence:
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US-10-293-418-2041 US-10-293-418-2044 US-10-293-418-2045

US-09-880-748-2108 US-09-880-748-2113 US-09-880-748-2113 US-10-293-418-2007 US-10-293-418-2015 US-10-293-418-2025

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APPLICANT: DUBUC, GINETTE
APPLICANT: NARANG, SARAN
TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
FILE REFERENCE: 11054-1
CURRENT APPLICATION NUMBER: US/10/031,874A
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/207,234
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEC ID NOS: 212
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 172
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFOGRALION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-06-16

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PRECENTIN VEY: 2.0

SEQ ID NO 1648

LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                  76.5%; Score 65; DB 14; Length 17; 70.6%; Pred. No. 0.00043; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1648, Application US/09880748; Publication No. US20030059937A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LLSRSGRTTNYADSVKG 17
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Best Local Similarity 70.6
Matches 12; Conservative
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Best Local Similarity 64.7
Matches 11; Conservative
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CRGANISM: Homo sapiens
US-09-880-748-1648
                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-172
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US-09-880-748-1648
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    Sequence 2048, Ap Sequence 2105, Ap Sequence 2117, Ap Sequence 1117, Ap Sequence 1974, Ap Sequence 1974, Ap Sequence 1974, Ap Sequence 1974, Ap Sequence 1179, Ap Sequence 1179, Ap Sequence 106, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 1112, Ap Sequence 1112, Ap Sequence 210, Appl Sequence 210, Appl Sequence 210, Appl Sequence 230, Appl Sequence 24, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 27, Appl Sequence 28, Appl Sequence 27, 
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Sequence
Sequence
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  2 US-10-293-418-2048
2 US-10-293-418-2105
2 US-10-293-418-2110
2 US-10-293-418-2113
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7 US-10-309-77-39-6
7 US-10-309-77-39-6
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7 US-10-309-77-39-6
7 US-10-309-77-39-6
7 US-10-251-0858-151
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Gaps

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Sequence 1648, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPREBUCE: PF523P2
; CURRENT APPLICATION UNBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
RESULT 3
US-10-293-418-1648
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RESULT 1
US-10-031-874A-172
; Sequence 172, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID

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Gaps

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GENERAL INFORMATION:

APPLICANT: Ruben et al.

APPLICANT: Ruben et al.

TITILE OF INVENTION:

FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR PILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-10-19

PRIOR PILING DATE: 2001-10-19

PRIOR PILING DATE: 2001-01-09/880,748

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2000-01-17

PRIOR PELING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LEMERAL OF SEQ ID NOS: 3247
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Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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Pred. No. 0.15
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                     CURRENT APPLICATION NUMBER: US/09/880,748
                                                CURKENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER: 05-25
NUMBER: PATENTING DATE: 2001-05-25
SOFTWARE: PATENTING VOIS: 3239
SOFTWARE: PATENTING VOIS: 3239
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Publication No. US20030223996A1
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Best Local Similarity 76.5%;
Matches 13; Conservative 0
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Best Local Similarity 76.5%;
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-880-748-1503
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; ORGANISM: Homo sapiens
US-10-293-418-1503
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TITLE OF INVENTION: Rh(D) BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT PEDILORATION NUMBER: BARLIER APPLICATION NUMBER: 09/240,274
PRIOR PILING DATE: EARLIER PILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: BARLIER PILING DATE: 1996-10-11
LENGTHARE: DETERMINE VET: 2.0
LENGTH: 129
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 0.045;
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1 Similarity 76.5%; Pred. No. 0.046;
13; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: anti-Rh(D) antibody clone SH20
US-09-848-798-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR PELING DATE: 2001-2-19
PRIOR PELING DATE: 2001-66-15
PRIOR PELING DATE: 2001-66-15
PRIOR PELING DATE: 2001-66-15
PRIOR PELING DATE: 2001-67-25
PRIOR APPLICATION NUMBER: 60/293,49
PRIOR PILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-848-798-143
; Sequence 143, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1648
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ORGANISM: Homo sapiens
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US-09-880-748-1503
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Mismatches

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67.1%; Score 57; DB 12; Length 98; 75.0%; Pred. No. 0.073;
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Best Local Similarity 75.0
Matches 12; Conservative
                                                                                  Conservative
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                                                          Best Local Similarity
Matches 12; Conserv
US-10-029-926B-79
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US-10-194-975-17
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                                           Query Match
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Sequence 79, Application US/10029926B
Publication No. US20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY. et al.
TILLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 107935/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
FRIOR PILING DATE: 2002-2030
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAGAY, et al.
TITLE OF INVENTION: SPECIFIC.HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REPRENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT PILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR PLILING DATE: 12/29/2000
PRIOR FILING DATE: 12/29/2000
SOFTWARE: FASES TO NOS: 203
SOFTWARE: FASES OF ON WINDOWS VELSION 3.0
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                                                                              APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 02 CTP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                             Score 57;
Pred. No.
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                   Sequence 57, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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US-10-029-926B-63
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Best Local Similarity
                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: human
US-10-453-698-57
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LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/066,895
FILING DATE: 04-Feb-2002
CLASSIFICATION ATMORP.
APPLICATION NUMBER: 09/297,344
FILING DATE: 1999-UTM-09
APPLICATION NUMBER: 60/030,149
FILING DATE: 01-NOV-1997
                                                                                        Dillon, Susan B.
Porter, Terence C.
Sweet, Raymond A.
TITLE OF INVENTION: Human Monoclonal Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-066-895-4
Sequence 4, Application US/10066895
Publication No. US20020141990A1
GENERAL INFORMATION:
APPLICANT: Deen, Keith C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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                                                                                                                                                                                                                                                                                                                                                      ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-10-032-037B-79

US-10-032-037B-79

Sequence 79, Application US/10032037B

Sequence 79. Application US/20040001822A1

SEQUENCE 10 10 US 2004000182A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: WOISTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT PILING DATE: 2001-12-31

PRIOR PLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FeatsEQ for Windows Version 3.0

SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES, AND USES THEREOF FILE REPERBYCE: 10793/46

CURRENT APPLICATION NUMBER: US/10/029,988B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR PILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 53

LENGTH: 98
                                67.1%; Score 57; DB 15; Length 98; Conservative 1; Mismatrhes
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US-10-029-988B-63
US-10-029-988B-63
; Sequence 63, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
                                                                                                                                                                        51 ISSSGSTIYYADSVKG 66
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Best Local Similarity 75.09
Marches 12; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                           Query Match
Best Local Similarity
        US-10-032-037B-63
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US-10-029-988B-79
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Publication No. US20040001822A1
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: WOIFTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/44
CURRENT FILING DATE: 2001-12-31
PRIOR PILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
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Pred. No. 0.073;
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                                    TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3:1
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SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 98
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Publication No. US20030039649A1
GENERAL INFORMATION:
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75.08;
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Best Local Similarity 75.09
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Best Local Similarity 75.04
Matches 12; Conservative
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US-10-194-975-17
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ORGANISM: Homo sapiens
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LENGTH: 98
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APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Myer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Carvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILLE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/10/038,591
CURRENT FILING DATE: 2002-01-04
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
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75.0%; Pred. No. 0.073;
iive 1; Mismatches 3;
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51 ISSSGSTIYYADSVKG 66
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51 ISSSGSTIYYADSVKG
                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 12; Conservative
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Matches 12; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    US-10-032-423A-79
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US-10-379-392-16
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                   SEQ ID NO 79
LENGTH: 98
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Sequence 79, Application US/10029988B

Bublication No. US20040001839A1

GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-150LATED MOLECULES COMPRISING EPITOPES CONTAINING SULPATED TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
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Publication No. US20040002450A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: WUMBER: US/10/032,423A
CURRENT APPLICATION NUMBER: 60/258,948
PRIOR PILLING DATE: 12/29/2000
PRIOR FILLING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FRASESQ for Windows Version 3.0
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TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/45
CURRENT PRILING DATE: 201-12-31
PRIOR PILING DATE: 201-12-31
PRIOR PILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 98
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Pred. No. 0.073;
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. Sequence 63, Application US/10032423A
. Publication No. US20040002450A1
. GENERAL INFORMATION:
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51 ISSSGSTIYYADSVKG 66
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75.0%;
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Best Local Similarity 75.09
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US-10-032-423A-79
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-805-11
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         US-10-269-805-11
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APPLICANT: King, Chadwick T.
TITLE OF INVENTION: ANIT-CDR45RB ANTIBODIES FOR USE IN
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
FILE REPERENCE: ABGENIX.029A
CURRENT APPLICATION NUMBER: US/10/309,764
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200
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Fublication No. US20030124129A1
GENERAL INFORMATION
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT APLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
LENGTH: 122
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Query Match 67.1%; Score 57; DB 16; Length 98; Best Local Similarity 75.0%; Pred. No. 0.073; Matches 12; Conservative 1; Mismatches 3; Indels
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Sequence 23, Application US/10309764

Publication No. US20030232009A1

GENERAL INFORMATION:

APPLICANT: Babcook, John

APPLICANT: Palathumpat, Raju

APPLICANT: Yang, Xiao-dong

APPLICANT: Yang, Chadwick T.
                                                                                                               51 ISSSGSTIYYADSVKG 66
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Best Local Similarity 75.03
Matches 12; Conservative
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Matches 12: Conserv
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APPLICANT: Robl, James M.
APPLICANT: Goldaby, Richard A.
APPLICANT: Ferguson, Stacy E.
APPLICANT: Kurolwa, Yoshina
APPLICANT: Tomizuka, Kazuma
APPLICANT: Ishida, Isao
TITLE OF INVENTION: Expression of Xenogenous (Human)
TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates
FILE REFERENCE: 50195/008003
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; Sequence 11, Application US/10269805
; Publication No. US2003012412941
; GENERAL INFORMATION:
; APPLICANT OLINER, JONATHAN D.
; TITLE OF INVENTION ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF EGO ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11.
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS FILE REFERENCE: A-72-CURENT APPLICATION NUMBER: US/10/269,805
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 53, Application US/10269805; Publication No. US20030124129A1; GENERAL INFORMATION:
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Best Local Similarity 75.0%
Matches 12; Conservative
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; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,625
; PRIOR APPLICATION NUMBER: US 60/256,458
; PRIOR APPLICATION NUMBER: US 09/714,185
; PRIOR PILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-11-19
; PRIOR FILING DATE: 1990-11-1
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64.534 Million cell updates/sec
                                                                                                         September 24, 2004, 01:33:11 ; Search time 25.3396 Seconds
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(c) 1993 - 2004 Compugen Ltd.
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1 VISENGRTINYADSVKG 17
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Maximum Match 100%
Listing first 150 summaries
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Maximum DB seq length: 200000000
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CiSpecies: Homo sapiens (Man)
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CiSpecies: Action (man)
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Recession: S24252
Ristewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Scasso
R; Towninson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A; Reference number: S26885; MuID: 93021117; PMID: 1404388
A; Reference preliminary
A; Rocession: S26930
A; Return preliminary
A; Molecule type: DNA
A; Residues: 1-98 < TOM>
A; Cross-references: EMBL: Z12337; NID: 912892; PIDN: CAA78207.1; PID: 932893
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < INM>
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R;Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tonlinson, I.Z.; 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Score 58; DB 2; Length 115;
Pred. No. 0.038;
0; Mismatches 4; Indels
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67.1%; Score 57; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 12; Conservative 1; Mismatches 3; Indels
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75.0%; Pred. No. 0.046;
ive 1; Mismatches 3; Indels
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          68.2%;
76.5%;
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51 ISSSGSTIYYADSVKG
        Query Match 68.2
Best Local Similarity 76.5
Matches 13; Conservative
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nes 12; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-97 <STE>
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S26891
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S57445

Igheavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57445
R;Paterson, G; Willson, G; Willson, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropa A;Reference number: S57408
A;Accession: S57408
A;Acc
        ALIGNMENTS
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E69175
AF3591
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PH1658
A45953
A34964
S31121
M3HUPM
M3HULY
C36005
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$31118
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A; Reference number: S26885; MUID:93021117; PMID:1404388 A; Accession: S26891

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Cispecies: Homo sapiens (man)
Cibate: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change .23-Jul-1999
Cibate: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change .23-Jul-1999
Cibate: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change .23-Jul-1999
Rikaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-251, 1992
A;Tile: Restricted utilization of germ-line V(H) 3 genes and short diverse third compleme A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31105
A;Accession: S31105
A;Accession: Cibate acid sequence not shown; translation not shown A;Residues: 1-118 <RAA>
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Cibate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cibate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
Cibatesaion: S26796
RiMortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil A;Accession: S26790
A;Accession: S26790
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 137783; S25477
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. US.A. 91, 514-518, 1994
A;Fitle: Somatic diversification in the heavy Chain variable region genes expressed by ht.
A;Reference number: A36876; MUID:94119917; PMID:8290556
                                                                                                                                                                                                                                                                                                                                                                                                           A) Cross-references: EMBL:X63081; NID:g12648; PIDN:CAA44803.1; PID:g12649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                             Ig heavy chain (subclass IgM) - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-130 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1652
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyld
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S31120
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A; Title: Rmaunol. 22, 247-251, 1992
A; Title: Stricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633; PMID:1730252
A; Accession: S31120
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A;Note: the nucleoride sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                  A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross references: EMBL:Z12358; NID:g12935; PIDN:CAA78228.1; P.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                               67.1%; Score 57; DB 2; 75.0%; Pred. No. 0.046; iive 1; Mismatches
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Pred. No. 0.052;
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75.0%;
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Best Local Similarity 75.09
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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A; Residues: 1-110 < HIL>
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Best Local Similarity
Status: preliminary
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Rightiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; Raiffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; BYG, J. 1939 1. 725-734, 1993 1. 1914 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 1. 1918 
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Greetes: Homo sapiens (man)
Greetes: Homo sapiens (man)
Greetes: Homo sapiens (man)
Greete: Je-Pab-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Greete: Je-Pab-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Greete: Je-Pab-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Greete: Salate: Je-Pab-1994 #sequence_revision 10-Nov-1995 #text_change and expressed human B cell
Argenteence number: S2427
Argenteence number: S2427
Argenteence number: S2427
Argenteence number: S2427
Argenteence I-108 *STE>
Argenteence EMBL: K67072; NID:938401; PIDN:CAA47457.1; PID:938402
Greetences: EMBL: K67072; NID:938401; prom: mmunoglobulin homology
Greetences: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 336267
R; Graffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; RNBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S3626; MulD:93178448; PMID:7679990
A; Reference number: S3626; MulD:9317848; PMID:7679900
A; Reference number: S3626; MulD:9317848; PMID:7679900
A; Reference number: S3626; MulD:9317848; PMID:7679900
A; Reference number: S3626; MulD:9317848; PMID:76799000
A; Refere
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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Pred. No. 0.35;
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68.8%; Pred. No. 0.25;
ive 1; Mismatches
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62.5%;
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Best Local Similarity 68.8
Matches 11; Conservative
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Matches 11; Conservative
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Best Local Similarity
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A; Mesidues: 1-97 < MAN>
A; Residues: 1-97 < MAN>
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IVM>
F; 30-35/Region: complementarity-determining 1
F; 49-66/Region: complementarity-determining 2
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PH0875
Ig heavy chain V region (anti-DNA, H2F) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH0875
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J; Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A;Reference number: PH0862; MuID:92078875; PMID:1660528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: 147191
R;Sun, J; Kacskovics, I; Brown, W.R.; Butler, J.B.
Timunol. 153, 5618-5627, 1994
A;Title: Expressed swine VH genes belong to a small VH gene family homologous to human A;Reference number: 147177; MUID:95081609; PMID:7989761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain variable VDJ region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:U15450; NID:9571386; PIDN:AAA67016.1; PID:9571387; Superfamily: immunoglobulin V region; immunoglobulin homology 41-117/Domain: immunoglobulin homology < IMM>
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    A,Cross-references: EMBL:X67907; NID:g33584; PIDN:CAA48105.1; PID:g33585 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;22-105/Domain: immunoglobulin homology <IMM>
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836273
Ig heavy chain V region (clone alpha-THY-32) - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                   67.1%; Score 57; DB 2; Length 130; 68.8%; Pred. No. 0.062; 2; Indels sive 3; Mismatches 2; Indels
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Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.063;
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68.8%;
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                                                                                                                                                                                                                                                                                                                                                                      2 ISENGRTINYADSVKG 17
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58 MSSSGRTMYYADSVKG 73
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Best Local Similarity 68.8<sup>1</sup>
Matches 11; Conservative
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A; Residues: 1-132 <SUN>
A; Cross-references: RMBL:
C; Superfamily: immunoglob
F; 34-117/ Domain: immunoclob
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A;Molecule type: mRNA
A;Residues: 1-110 <GRI>
A;Cross-references: EMBL:218824; NID:g33111; PIDN:CAA79276.1; PID:g939891
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
       preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ISSSSTIYYADSVKG 66
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Best Local Similarity ***
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Matches 11; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-117 <KU2>
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R;GTiffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Embl. 12, 725-734, 193
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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C'Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S78694
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 277, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
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                                                                                                                                                                                                                                                     RESULT 15
$30532
$10532
Glavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30532
R;Mariette, X.
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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   Indels
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68.8%; Pred. No. 0.38;
iive 1; Mismatches
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68.8%; Pred. No. 0.43;
iive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1992 A;Reference number: $30520 A;Accession: $30532
Mismatches
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C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
   4
                                                                      ISENGRIINYADSVKG 17
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51 ISYDGRSVYYADSVQG 66
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51 ISSSSTIYYADSVKG
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Matches 11; Conservative
Conservative
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Best Local Similarity
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A;Residues: 1-123 <MAR>
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Residues: 1-98 <TOM>
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A; Status: prelimina:
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Matches
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S36282
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Ig heavy chain V-gene (clone WHG26) precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Date: 20-Sp51980 S60295; S21980
B;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm. A;Reference number: S60295; MUID:93122853; PMID:1282498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A;Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit
A;Reference number: A93964; MUID:83273707; PMID:6410398
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C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 31-Mar-2000
C;Accession: A02046
                                                                                      Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;17-98/Domain: immunoglobulin homology <IMM>
F;17/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96/Disulfide bonds: #status predicted
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
60.0%; Score 51; DB 2; Length 110;
68.8%; Pred. No. 0.49;
ive 1; Mismatches 4; Indels
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Indels

4;

Mismatches

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Conservative

11;

Matches

17

2 ISENGRTINYADSVKG

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70 issssriryAbsvkg 85

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C'Species: Howo sapiens (man)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C'Accession: S23624
R'Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; C J. Exp. Med. 175, 831-842, 1992
A'Fitle: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv A; Reference number: S23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: PH0874
R; Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
B. Exp. Med. 174, 1639-1652, 1991
A; Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype. A; Reference number: PH0862; MUID:92078875; PMID:1660528
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C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
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Pred. No. 0.55;
1; Mismatches
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                                                                       A;Cross-references: EMBL:218317
C;Superfamily: immunoglobulin V region; immunc
C;Keywords: hetroctetramer; immunoglobulin
F;I5-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
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Best Local Similarity 68.8%;
Matches 11; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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Matches 11; Conservative
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A; Residues: 1-143 <OLE>
A; Molecule type: mRNA
A; Residues: 1-125 < MAR>
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                                                                                                                                                                                                                                                                                                                                          igheavy chain V region (clone SJI) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1661
R;Hillson, J.L.; A3rr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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$30531
Ci beavy chain V region - human
Ci Species: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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    Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-98/Domain: immunoglobulin homology <IMM>

A;Molecule type: mRNA A;Residues: 1-123 <MOR> A;Cross-references: EMBL:X61011

A;Status: preliminary

Length 123; Indels

60.0%; Score 51; DB 2; 68.8%; Pred. No. 0.54;

C;Accession 330531
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number S30520
A;Accession: 830531
A;Status: preliminary

4.

Mismatches

à g

Conservative

Best Local Similarity Matches 11; Conser

Query Match

A; Residues: 1-121 attib.
A; Experimental source: B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology.
C; Keywords: heteroterramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

A; Molecule type: mRNA

A;Accession: PH1661

Score 51; DB 2; Length 121; Pred. No. 0.54; 2; Mismatches 4; Indels

60.0%; ilarity 64.7%; Conservative

Local Similarity nes 11; Conserv

Best Loc Matches

Query Match

à 셤

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RESULT 25
S26927
Ig heavy chain V region (DP-31) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26927
A;Tomlinson, 11.M; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G
J. Mol. Biol. 227, 776-798, 1992
A;Tomlinson, 11.M; Walter of human germline V(H) sequences reveals about fifty groups of A;Accession: S26927
A;Accession: S26927
A;Accession: S26927
A;Accession: S26927
A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Cossereferences: EMBL:212333; NID:912885; PIDN:CAA78203.1; PID:932886
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM*>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.8%; Score 50; DB 2; Length 98; Best Local Similarity 68.8%; Pred. No. 0.63; Matches 11; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ISWNSGSIGYADSVKG 66
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Gaps .. 0

Search completed: September 24, 2004, 01:54:34 Job time : 26.3396 secs

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Llama CDR
MS-R Fab/
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MS-R Fab/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VH chain
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                       (without alignments)
51.354 Million cell updates/sec
                                                          April 28, 2005, 17:57:45; Search time 128.031 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aau82607
Ada91299
Ada91290
Ada91201
Ada91319
Ada91319
Ad191350
Ad166612
Adp66612
Adp66612
Adp66610
Adp66606
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                         2105692 segs, 386760381 residues
                                                                                                US-10-088-639A-2_COPY_177_193
85
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                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
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ADP96609
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                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                     1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                   geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
                                                                                                                                                                                                                                                                                A Geneseq 16Dec04:*
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geneseqp2003as:*
geneseqp2003bs:*
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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9334 Anti-RAS	9336 Anti-RAS	9330 Anti-RAS		9333 Anti-RAS			0190 Anti-Abet	1188 Anti-Abet			_	1195 MS-R Fab/			1193 MS-R Fab/		1196 MS-R Fab/	1440 MS-Roche	6615 Anti-RAS
Ado79334	Ado79336	Ado79330	Ado79329	Ado79333	Ado79337	Ado79335	Ada90190	Ada90188	Adq75289	Adq75290	Ada 90010	Ada91195	Ada91198	Ada90000	Ada91193	Ada90430	Ada91196	Ada90440	Adp96615
AD079334	AD079336	ADO79330	AD079329	AD079333	AD079337	AD079335	ADA90190	ADA90188	ADQ75289	ADQ75290	ADA90010	ADA91195	ADA91198	ADA90000	ADA91193	ADA90430	ADA91196	ADA90440	ADP96615
Φ	æ	œ	æ	8	æ	80	9	9	œ	œ	9	9	9	ø	9	9	9	9	æ
115	115	115	115	115	115	115	120	120	242	244	17	17	17	17	17	17	17	17	35
Η.	Η.	۲.	۲.	۲.	٦.	٦.	٦.	٦.	٦.	٦.	6.	σ.	6.	ο.	6.	٥.		σ.	6.
74	74	74	74	74	74.1	74	74	74	74	74	72	72	72	72	72	72	72	72	72
63	63	63	63	63	63	63	63	63	63	63	62	62	62	62	62	62	62	62	62
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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    .33
    note= "Complementarity determining region (CDR) 1 of the .ight chain"

                                                                                                                                                                                                                                                  8. .98
note= "Complementarity determining region (CDR) 3 of the
ight chain"
                                                                                                                                                                                                                                                                                                                          177. .193
/note= "Complementarity determining region (CDR) 1 of the
heavy chain"
                                                                                                                                                                                                                                                                                                                                                                   226. .238
/note= "Complementarity determining region (CDR) 1 of the
heavy chain"
                                                                                                                                                                                                                                2 of
                                                                                                                                                                                                                                                                                                                note= "Complementarity determining region (CDR) 1 of
                                                                                 An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                    Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;
tumour-associated antigen; metastatic disease; malignant disease;
tumour typing; tumour screening; tumour.
                                                                                                                                                                                                                              = "Complementarity determining region (CDR) chain"
                                                                                                                                                                            Location/Qualifiers
                    AAB68087 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                  110. .127
/note= "linker"
158. .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-2000; 2000WO-SE002082
                                                                                                                                                                                                                                                                                                                         neavy chain"
                                                             (first entry)
                                                                                                                                                                                                                                           ight
                                                                                                                                              Synthetic.
Macaca fascicularis.
                                                                                                                                                                                                                                                                                                                                                                                                           WO200130854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-2001
                                        AAB68087;
                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                   Region
RESULT 1
AAB68087
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99SE-00003895.

28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB

The consensus variable domain sequences are derived from the most abundant sublasses in the sequence compilation of Kabat et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda MD (1987), namely, VL-Kappa subgroup I and VH group III. In such igG-gamma-1 human consensus sequences, the VI consensus domain has the AA sequence in AAR47041, and the VH consensus domain has the AA sequence in AAR47042. (Updared on 25-MAR-2003 to correct PN field.)

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Gaps

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Match 78.8%; Score 67; DB 2; Length 120; Local Similarity 82.4%; Pred. No. 0.0015; les 14; Conservative 0; Mismatches 3; Indels

Sequence 120 AA;

888888888888

Query Match Matches

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Sequence of the consensus antibody variable domain of the heavy chain.
                                                                                                                                                                                                                                                                 Monoclonal antibody; heavy chain; variable domain; consensus
                                                                                                                                                                                                                 AAR47042 standard; peptide; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 108; 126pp; English
                                                                                                                                                                                       177 VISENGRTINYADSVKG 193
                                                                                                                                                                             1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                           Carter PJ, Presta LG;
                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-083196/10.
                                                                                                                                                                                                                                                                                                            20-AUG-1993;
                                                                                                                                                                                                                                                                                       WO9404679-A1
                                                                                                                                                                                                                                                                                                                      21-AUG-1992;
                                                                                                                                                                                                                                                                                                 03-MAR-1994.
    Brodin TN,
Nilson BHK;
                                                                                                                                                                                                                                       25-MAR-2003
02-SEP-1994
                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                            AAR47042;
                                                                                                                                                                                                             RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cumour cells and transet structure especially comprises alphaébeta4 integrin. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premallignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                                                                                                                  Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Tordsson MJ, Kearney PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 55-56; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Bust Local Similarity luv...
These 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour deposits in humans
                                                                                                             WPI; 2001-308619/32.
N-PSDB; AAF84797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 249 AA;
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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama antidodies. The library is useful for in vitro selection against any fragments are isolated from the library using phage display technology fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it antigen-binding fragments having high affinity to almost any predetermined target (antiden of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. AAUG2435-AAUG2635 represent the lamma heavy chain domain fragments of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target.
                                                                                                                                                                                                 Llama; phage display library; variable heavy domain fragment; VHH; VH; sdAb fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDR1/H1; CDR2; CDR3; complementarity determining region.
                                                                                                                                                               Llama CDR2 region variable heavy chain fragment #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 19a; 46pp; English.
                     AAU82607 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2001; 2001WO-CA000763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207234P.
                                                                                                                        (first entry)
                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-083093/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dubuc G,
                                                                                                                                                                                                                                                                                                                                                      WO200190190-A2
                                                                                                   29-AUG-2003
23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001.
                                                                                                                                                                                                                                                                                                               Lama glama.
                                                            AAU82607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanha J,
AAU82607
                                        Preparation of improved humanised antibodies - by comparison of consensus and import complementarity determining regions and framework region sequences, e.g. to humanise murine.
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(revised)
(first entry)

93WO-US007832 92US-00934373

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence val-His-His-Glu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a mucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I), uncleic acid of (1), vector of (2) or host cell of (3); (7) optimising (I); (8) testing the resulting Fab optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (I), and formulating the composition of (I), and carrier, and (12) a
                                                                                                                                                                                                                                                                                                                                                                                                nootropic; antiparkinsonian, gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; mctor neuropathy; Down's syndrome; Crettzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                               antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kretzschmar T;
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                                     Length 17;
                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huber W,
Rothe C;
                                 Score 65; DB 5; 1
Pred. No. 0.00033;
                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                             MS-R Fab/antibody related peptide #347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 13; Page 93; 312pp; English.
                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                ADA91299 standard; peptide; 17
                                                                                                                            76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2002; 2002EP-00003844.
                                                                                                         1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuronal disorder; aging.
                                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bardroff M, Bohrmann
Loehning C, Loetscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MORP-) MORPHOSYS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-663848/62.
                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003070760-A2
Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (e.g. dementia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                       ADA91299;
                                                                       Matches
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neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is dementa, Alzheimer's disease, metor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, horeditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, and parkinson's disease, nor neuropathy. Down's syndrome, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, and parkinson's any or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Abeta antibody related amino acid sequence SEQ ID NO:119
                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                                               Score 63; DB 6; I Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 189-190; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA90004 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE & CO
                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                1 VISETGKNIYYADSVKG 17
                                                                                                                                                                                                                                                                                                                               74.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2002; 2002EP-00003844.
                                                                                                                                                                                                                                                                                                                                                                                                      1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuronal disorder, aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003070760-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e.g. dementia).
                                                                                                                                                                                                                                                                                          Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA90004;
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                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
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Kretzschmar T;

Huber W, Rothe C;

Brockhaus M, Nordstedt C,

Bohrmann B, Loetscher H,

Bardroff M, Loehning C,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation

Example 13; Page 92; 312pp; English.

(e.g. dementia).

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dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Abp-Val-Gly-AbB9887 or its fragment. Also described: (I) a mucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising the vector of (2); (4) preparing (I), comprising (I) culturing the host cell of (3) under conditions that allow synthesis of (I) an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), concepting the resulting Fab optimisation library by panning against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing (1); (1) testered, optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (I) has composition, comprising optimisation of (I), and formulating the composition prepared by method (8). (I) has controprotective, nootropic and antiparkinsonian activities, and can be consed in gene therapy. The antibody molecule (1), nucleic acid molecule, the prevention and/or treatment of a disease associated with antipody molecule of any formulation and constitution and companied and antiparkinsonian antipody molecule of a disease associated with antipody molecule of any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constituted any formulation and constitute

74.1%; Score 63; DB 6; I 76.5%; Pred. No. 0.00074; 1 VISENGRIINYADSVKG 13; Conservative Query Match Best Local Similarity Sequence 17 AA; Matches

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Gaps ô

Mismatches

Length 17; 3; Indels

> 1 VISETGKNIYYADSVKG 17 RESULT 6 g

MS-R Fab/antibody related peptide #249. ADA91201 standard; peptide; 17 AA. (first entry) 20-NOV-2003 ADA91201; 

antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; atlateimer's disease; mctor neuropathy; Down's syndrome; Creutzfeld Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.

Homo sapiens. Synthetic.

WO2003070760-A2

28-AUG-2003

20-FEB-2003; 2003WO-EP001759

20-FEB-2002; 2002EP-00003844.

(HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

neuronal disorder; aging.

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may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the distinceration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque for for passive immunisation dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody molecule, antibody; beta-A4 peptide, Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; Gisease; motor neuropathy; Down's syndrome; creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 6; Length 17; Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-Roche #3.4.H7 H-CDR2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA90434 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VISETGKNIYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA90434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
ADA90434
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Example 5; Page 64; 312pp; English.
       WO2003070760-A2.
                                            (e.g. dementia).
                                                                                                                   Sequence 17 AA;
   Homo sapiens.
           28-AUG-2003
                               Loehning C,
  Synthetic
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADAB9886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADAB9886 or its fragment. Also described: (1) a mucleic acid molecule cocding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of (2) under conditions that allow synthesis of (2) and recovering (I) from the culture; (5) a composition comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) and recovering (I) from the culture; (5) a composition comprising (I); (8) testing the resulting Fab optimisation library by panning (I); (8) testing the resulting Fab optimised clones; (10) expressing (I); (8) testing the resulting Fab optimised clones; (10) expressing (1); (8) testing the resulting potimised clones; (10) expressing (1); (8) testing optimisation of (1); (9) testing optimisation of the decreation of selected, optimised clones; (11) preparing a pharmaceutical composition for the prevention and/or antibody molecule with a carrier; and (12) a composition preparing a pharmaceutical composition for the detection cor host is useful in preparing a pharmaceutical composition for the dreamyloid degenesis and/or amyloid-plaque formation. The antibody molecule cor the prevention and/or treatment of a disease associated with amyloid ogenesis and/or amyloid plaques for passive immunisation cor the detection of beta-amyloid plaques or for passive immunisation cor dementian beta-amyloid plaques or for passive immunisation cor dementian beta-amyloid plaques or for passive immunisation cor dementian beta-amyloid plaques or proper the prevention of beta-amyloid plaques or post tor passive immun Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,

Gaps ö Length 17; Score 63; DB 6; Length 17; Pred. No. 0.00074; 1; Mismatches 3; Indels 74.1**%**; 76.5**%**; Local Similarity 76.5 nes 13; Conservative Query Match Matches

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RESULT 8 ADA91199

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, (HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. 20-FEB-2002; 2002EP-00003844. 20-FEB-2003; 2003WO-EP001759 Bohrmann B, Loetscher H, Bardroff M, Bohrmann WPI; 2003-663848/62.

antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Cretuzfeld Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; hereditary cerebral haemorrhage; neuronal disease; hereditary cerebral haemorrhage.

MS-R Fab/antibody related peptide #247.

(first entry)

20-NOV-2003

ADA91199;

ADA91199 standard; peptide; 17 AA

Rothe C; Huber W, Brockhaus M, Nordstedt C, œ, (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG. 20-FEB-2002; 2002EP-00003844. Loetscher H, Bohrmann B, Bardroff M, Loehning C, 

WPI; 2003-663848/62.

20-FEB-2003; 2003WO-EP001759.

WO2003070760-A2. Homo sapiens.

Synthetic

28-AUG-2003.

Kretzschmar T;

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Example 13; Page 92; 312pp; English.

The present invention describes an antibody molecule (I) capable of frequency comprises the amino acid sequence Ala-Glu-Phe-Aapper (1) and comprises the amino acid sequence Ala-Glu-Phe-Aapper (2) are region comprises the amino acid sequence or an antibody molecule caid molecule amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Aba89886 or its fragment, and the second region comprises the among (1); (2) a vector comprising the nucleic acid molecule caid molecule caid molecule fragment. Also described; (1) a nucleic acid molecule caid (1); (2) a vector comprising the nucleic acid of (1); (3) a host culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host coll of (3) under conditions that allow synthesis of culturing the host coll of (3) under coll of (3) a composition comprising (I), uncleic acid of (1), vector of (2) or host cell of (3) a kit comprising (I), uncleic acid of (1), vector of (2) or host cell of (3) a kit comprising (I), uncleic acid of (1), vector of (2) or host in an arbody molecule by method (4); (6) a kit comprising (I), against Abetea, (9) identifying optimised clones; (10) expressing of squimised antibody molecule with a carrier; and (12) a pharmaceutical composition of (1), and formulating the optimised antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has pharmaceutical composition prepared by method (8). (1) has a pharmaceutical composition preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any and con of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used any local places.

Creutzfeldt Jacob disease, motor

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), (1) and recovering (I) have method (4); (6) a kit comprising (I),
                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or an antibody molecule produced by method (4); (6) a kit comprising (1) nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4, (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plague formation
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                                                      Score 63; DB 6; Length 11, Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huber W,
Rothe C;
                                                                                                             1; Mismatches
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                              MS-R Fab/antibody related peptide #349.
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                                                                                                                                                                                                                                                                                   ADA91301 standard; peptide; 17
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                                                                                                                                                                       1 VISETGKNIYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2003; 2003WO-EP001759.
                                                                        74.1%;
76.5%;
                                                                                                                                                  1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuronal disorder; aging.
                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-663848/62.
present sequence is
                                                                      Query Match
Best Local Similarity
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                                     Sequence 17 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Loehning C,
                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                        ADA91301;
                                                                                                               Matches
                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                 ADA91301
SXS
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pharmaceutical composition prepared by method (B). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be cused in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule can also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the detection of the disease mentioned plaques or for passive immunisation of place amyloid plaques for previous, the disease is dementia, Alzheimer's disease, motor neuropathy. Down's syndrome, canyloidosis Dutch type, Parkinson's disease, INU'related dementia, anyloidosis Dutch type, Parkinson's disease, INU'related dementia, anyloidosis but seed in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel immunoglobulin molecules that comprise at least one antibody variable chain VH or VL framework region and are capable of binding to a specific antigens within an intracellular environment. Specifically, it refers to antibodies that can form an insoluble complex with a cognate antigen, such that it can then be target for degradation via the lysosome or proteosome systems. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of an intracellularly binding immunoglobulin comprising at least one antibody variable chain, in preparing a medicament for degrading one or more specific antigens, or for treating specific antigen positive cancer, e.g. leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VH chain clone J48 of an intracellularly binding immunoglobulin SeqID 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; variable chain; cytostatic; cytoplasmic degradation; intracellular relocation; specific antigen positive cancer; leukaemia; lymphoma; intracellularly binding immunoglobulin; ras.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 6; Length 17;
Pred. No. 0.00074;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; SEQ ID NO 41; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL91350 standard; protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lobato-Caballero MN, Rabbitts TH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VISETGKNIYYADSVKG 17
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15-NOV-2002; 2002GB-00026727.
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
74.1%;
Best Local Similarity 76.5%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003077945-A1
                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2002;
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Gaps

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74.1%; Score 63; DB 7; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels

17 99

2 ISENGRTINYADSVKG || :|||| ||||||| 51 ISSSGRTIYYADSVKG

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13; Conservative

Matches

Local Similarity

Query Match

Sequence 115 AA;

8833333

and reagent applications or in functional genomics. This polypeptide sequence is a variable heavy chain (VH) framework region of an intracellularly binding anti-ras antibody of the invention.

diagnostic applications both in vitro and in vivo, as well as for

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invention describes the specific target antigen as the oncogenic fusion protein BCR-ABL or the RAS antigen, such that this method can be used to prepare a cytostatic medicament for the cytoplasmic degradation or intracellular relocation of such an antigen or for the treatment of the specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore, the immunoglobulins may also be used for therapeutic, prophylactic or diagnostic applications both in vitro and in vivo, as well as for assay and reagent applications or in functional genomics. This polypeptide sequence is a variable heavy chain (VH) framework region of an intracellularly binding anti-ras antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               VH chain clone 33 of an intracellularly binding immunoglobulin SeqID 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; variable chain; cytostatic; cytoplasmic degradation; intracellular relocation; specific antigen positive cancer; leukaemia; lymphoma; intracellularly binding immunoglobulin; ras.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     ;
                                                                                                                                                                                      74.1%; Score 63; DB 7; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                ADL91351 standard; protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2002; 2002GB-00006043.
15-NOV-2002; 2002GB-00026723.
15-NOV-2002; 2002GB-00026727.
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51 ISSSGRTIYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004 (first entry)
                                                                                                                                                                                                     Local Similarity 81.2
nes 13; Conservative
                                                                                                                                                             Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003077945-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                            ADL91351;
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                                                                                                                                                                                                                    Matches
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Anti-RAS intracellular mutated scFV Con33 VH chain, SEQ ID

(first entry)

26-AUG-2004

ADP66612;

ADP66612 standard; protein; 115 AA.

RESULT 1: ADP66612

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RAS; immunoglobulin; anti-RAS antibody; scFV.

14-NOV-2003; 2003WO-GB004944.

WO2004046187-A2.

03-JUN-2004

Unidentified

15-NOV-2002; 2002GB-00026723

Rabbitts TH, Tanaka T; (MEDI-) MEDICAL RES

WPI; 2004-431948/40.

ö one VH framework region amino acid sequence showing at least 85 % identity with the framework region consensus sequence (1), and/or a molecule having at least one VH framework region amino acid sequence showing at least 85 % identity with (1), where one or more of amino acids 22 and 92 are not cysteine residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody variable domain type antibody is a heavy or light chain variable domain antibody. The antibody comprises at least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific of a ligand within an in vitro environment. Sequences ADP66604-represent variable domain heavy chain (VH) sequences of anti-RAS The invention relates to an immunoglobulin molecule comprising at least Gaps 74.1%; Score 63; DB 8; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels binding of a ligand within an in vitro environment 1; Mismatches Example 3; Fig 3; 67pp; English. 13; Conservative intracellular scFVs. Local Similarity Sequence 115 AA; Query Match Matches 

New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within

vitro environment

2 ISENGRTINYADSVKG 17

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This invention relates to novel immunoglobulin molecules that comprise at capable of binding to a specific antigens within an intracellular environment. Specifically, it refers to antibodies that can form an insoluble complex with a cognate antigen, such that it can then be target insoluble complex with a cognate antigen, such that it can then be target for degradation via the lysosome or proteosome systems. The present invention describes the specific target antigen as the oncognic fusion protein BCR-ABL or the RAS antigen, such that this method can be used to prepare a cytostatic medicament for the cytoplasmic degradation or intracellular relocation of such an antigen or for the treatment of the specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore, the immunoglobulins may also be used for therapeutic, prophylactic or

Use of an intracellularly binding immunoglobulin comprising at least one antibody variable chain, in preparing a medicament for degrading one or more specific antigens, or for treating specific antigen positive cancer, e.g. leukemia.

Rabbitts TH;

Lobato-Caballero MN, WPI; 2003-779088/73 Example 7; SEQ ID NO 42; 86pp; English.

Anti-RAS intracellular scFV 33 VH chain, SEQ ID 3.

RAS; immunoglobulin; anti-RAS antibody; scFV

14-NOV-2003; 2003WO-GB004944. L5-NOV-2002; 2002GB-00026723.

WO2004046187-A2.

3-JUN-2004.

Unidentified

(MEDI-) MEDICAL RES COUNCIL.

Rabbitts TH, Tanaka T; WPI; 2004-431948/40.

|| :|||| |||||| |SSSGRTIYYADSVKG 66

51

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one VH framework region amino acid sequence showing at least 85 $$$ identity with the framework region consensus sequence (I), and/or a molecule having at least one VH framework region amino acid sequence showing at least one VH framework region amino acid sequence showing at least one VH framework region amino acid sequence one or more of amino acids 22 and 92 are not cysteine residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody variable domain type antibody is a heavy or light chain variable domain antibody. The antibody sear least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences ADP66604-ADP66613 represent variable domain heavy chain (VH) sequences of anti-RAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an immunoglobulin molecule comprising at least
                                                                                                                                     Anti-RAS mutated scFV I21R33(VHC22S;C92S) VH chain, SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 8; Length 115;
Pred. No. 0.0073;
1; Mismatches 2; Indels
                                                                                                                                                                        RAS; immunoglobulin; anti-RAS antibody; scFV.
                                ADP66613 standard; protein; 115 AA
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81.2%;
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an in vitro environment.
                                                                                                                                                                                                                                                                                                                                                                                                                          Tanaka T;
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                                                                                                                                                                                                                                                WO2004046187-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbitts TH,
                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                               03-JUN-2004.
                                                                   ADP66613;
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RESULT 13
                  ADP66613
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The invention relates to an immunoglobulin molecule comprising at least to one VH framework region amino acid sequence showing at least BS $ identity with the framework region consensus sequence (1), and/or a molecule having at least one VH framework region amino acid sequence showing at least one VH framework region amino acid sequence can be or cysteine residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody variable domain type antibody is a heavy or light chain variable domain antibody. The single mantibody comprises at least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences ADP66604-ADP66611 represent variable domain heavy chain (VH) sequences of anti-RAS
                                                                                                                                                                                                                                                                                           New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.1%; Score 63; DB 8; Length 115; 81.2%; Pred. No. 0.0073; 2; Indels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAS; immunoglobulin; anti-RAS antibody; scFV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP66609 standard; protein; 115 AA
                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 3; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2003; 2003WO-GB004944.
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intracellular scFVs.
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Matches
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Gaps

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ADP66606 standard; protein; 115 AA.

(first entry)

26-AUG-2004

ADP66606

RESULT 14
ADP66606
ID ADP66
XX
AC ADP66
XX
DT 26-AU

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15-NOV-2002; 2002GB-00026723.

(MEDI-) MEDICAL RES COUNCIL.

Rabbitts TH, Tanaka T;

WPI; 2004-431948/40

New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.

Example 3; Fig 3; 67pp; English.

one VH framework region amino acid sequence showing at least 85 \$\frac{4}{8}\$ identity with the framework region consensus sequence (I), and/or a molecule having at least one VH framework region amino acid sequence showing at least 85 \$\frac{4}{8}\$ identity with (I), where one or more of amino acids sequence showing at least 85 \$\frac{4}{8}\$ identity with (I), where one or more of amino acids 22 and 92 are not cysteine residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody of the wire acids of the veriable domain type antibody is a heavy or light chain variable domain antibody. The antibody comprises at least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences ADF66604-ADF66613 represent variable domain heavy chain (VH) sequences of anti-RAS The invention relates to an immunoglobulin molecule comprising at least intracellular scFVs 

Sequence 115 AA;

Gaps ; Query Match 74.1%; Score 63; DB 8; Length 115; Best Local Similarity 81.2%; Pred. No. 0.0073; Matches 13; Conservative 1; Mismatches 2; Indels

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2 ISENGRIINYADSVKG 17

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51 ISSSGRTIYYADSVKG 66

Search completed: April 28, 2005, 18:17:28 Job time : 129.031 secs

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Sequence Sequence

US-09-424-840B-72 US-09-424-840B-88 US-08-211-202-116 US-08-211-202-134 US-08-511-202-134 US-08-552-558-52 US-08-553-949-7 US-09-533-949-7 US-09-533-949-7 US-09-424-840B-26 US-09-424-840B-26 US-08-983-607-48 US-08-983-607-48 US-08-983-607-48

Sequence

Sequence

Sequence Sequence Sequence

Sequence

ALIGNMENTS

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

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70.6%; Score 60; DB 2; Length 120; 76.5%; Pred. No. 0.012; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Daul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
PPLICATION DATA:
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1991
ATTONNEY, AGENT INFORMATION:
NAME: Lee, Wendy W.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/07934373C; Patent No. 5821337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match.

Best Local Similarity 76.5'
Matches 13; Conservative
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TOPOLOGY:
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Sequence 4, App...
Sequence 128, App
Sequence 2, Appli
".ence 3, Appli
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Sequence 2, Appli
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Sequence 4, Appl
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                                                                                                                      (without alignments)
36.750 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143,
Sequence 16,
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Sequence 73,
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Sequence 4,
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Sequence 31,
Sequence 31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 11
                                                                                                     April 28, 2005, 18:06:50; Search time 34.5312 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/jaa/SA_COMB.pep:*
/cgn2_6/ptodata/1/jaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/jaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/jaa/GB_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-146-206C-4
US-09-705-392A-4
US-09-705-392A-4
US-09-705-392-4
US-09-240-274-113
US-09-240-274-1143
US-09-240-274-1143
US-09-315-574-31
US-09-315-574-31
US-09-315-574-31
US-09-315-574-30
US-09-315-574-30
US-09-315-574-30
US-09-315-574-30
US-09-316-316-75
US-09-316-75-44
US-09-240-274-4
US-09-240-274-3
US-09-240-274-3
US-09-240-274-4
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64-093-22
                                                                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -652-816A-11
-264-093-14
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                                                                                                                                                                                                                                                                       513545 seqs, 74649064 residues
                                                                                                                                                              US-10-088-639A-2_COPY_177_193
85
1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                 Seguence:
                                                                                                     Run on:
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Gaps

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NAME: Lee, wendy M.
REGISTRATION NUMBER: 40,378
REBERENCE POCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 VISENGSDTYYADSVKG 66
                    ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 120 amino acids
Amino Acid
CORRESPONDENCE ADDRESS:
                                                                                              California
: USA
                                                                    CITY: SOUSTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-146-206C-4
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Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.6%; Score 60; DB 3; Length 120; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/437,642B FILING DATE: 09-May-1995
CLASSIFICATION NUMBER: US/08/437,642B FILING DATE: 21-AUG-1995
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 15-JUN-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: 15-JUN-1992
PRIOR APPLICATION NUMBER: 15-JUN-1992
PRIOR APPLICATION NUMBER: 17-NOW-1991
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 107/115272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 107/115272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 107/115272
                                                                                                                                         Sequence 4, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 477
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
50 VISENGSDTYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VISENGRTINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 120 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                              RESULT 2
US-08-437-642B-4
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US-08-146-206C-4
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Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: CETTET, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE General General Construction May
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITEBET: 1 DAM WAY
CITTES: 1 LOWA WAY
CITYS: South San Francisco
STATE: California
COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CIASSIFICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
ZUMPATER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEM PC compatible COMPUTER: IEM PC COMPATIBLE COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/146,206C FILING DATE: 17-No. 6407213-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.6%; Score 60; DB 4; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches
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APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/705, 398
FILING DATE: 02-NO. 6800738-2000
CLASSIETCATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P0709P1D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9307832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                 Sequence 4, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650/225-1994
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NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELEFAX: 650/952-9881
                       50 VISENGSDTYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                           STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-07832-4
                                                                                                                US-09-705-398-4
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                                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATIC CARLET, Paul J.
APPLICANT: CARLET, Paul J.
TILLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                       70.6%; Score 60; DB 4; Length 120; nilarity 76.5%; Pred. No. 0.012; Conservative 0; Mismatches 4: Indole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.6%; Score 60; DB.4; Length 120; 76.5%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705, 392A FILING DATE: 02-NO. 6719971-2002 CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-705-686-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-NOV-1993
APPLICATION UNDRER: 07/715272
FILING DATE: 14-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                REGISTRATION NUMBER: 40. REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                           LENGTH: 120 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 120 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650/225-1994
                                                                                         TELEPHONE: 650/225-199
                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             50 VISENGSDTYYADSVKG 66
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NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.6
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 13; Conserva
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US-09-705-392A-4
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                                     Gaps
Length 120;
                                     4; Indels
 Query Match 70.6%; Score 60; DB 4; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                             TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genemanoglobulin Variants
STRREM
                                                                                                                                                                                                                                                           STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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2 ISSSGSTIYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-138-091A-16
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-138-091A-16
                                                                 US-08-918-148-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-665-202-31
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                                              RESULT 9
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL:
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
SARLIER POS: 224
SOFTWARE: PRESIDENTIAL OFF: 2.0
SOFTWARE: 1996-10-11
SOFTWARE: PRESIDENTIAL OFF: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: anti-Rh(D) antibody clone SH20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 5;
Pred. No. 0.012;
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION NUMBER: PCT/US92/05126
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               709P2PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-274-143
; Sequence 143, Application US/09240274
; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 7C
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VISENGRIINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VISENGGYTRYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.6%;
nilarity 76.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                       FILING DATE: 19930820
                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
PCT-US93-07832-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-274-143
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51 VisybGSriyYAbSVKG 67

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| Sequence 16, Application US/08918148A
| Patent No. 243220
| GEREBAL INFORMATION CARE | 134
| Patent No. 243220
| GEREBAL INFORMATION CARE | 134
| Patent No. 242220
| GEREBAL INFORMATION CARE | 134
| Patent No. 242220
| Patent No. 242220
| Patent No. 242220
| Patent No. 242220
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| Patent No. 242220
| Patent No. 242220
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NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION NUMBER: US 60/000,238
RHIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
RHIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
RHIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-UN-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ISSSGSTIYYADSVKG 66
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 98 amino acids
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Matches 12; Conserva
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                     APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977122el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
TITLE OF INVENTION: Tumor Antigens
CORRESPONDENCE: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09315574

Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Emplacadero Center, Suite 1100
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATCOMEY/AGENT INPORMATION:
                                                                                                               STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hunter, Tom
REGISTATION NUMBER: 38,498
REGISTATION NUMBER: 02307E-061410
TELECOMMUNICATION INCORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ISENGRIINYADSVKG 17
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Marks, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-09-315-574-31
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APPLICANT:
                                                                                                                                                                                                                           COUNTRY:
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Sequence 99, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
BAPPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
67.1%; Score 57; DB 4; Length 98; 75.0%; Pred. No. 0.031; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
COUNTY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
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51 ISSSGSTIYYADSVKG
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-315-574-30
                                                                                               US-09-315-574-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 597732221 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
TUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                       Score 57; DB 3; Length 117;
Pred, No. 0.037;
                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: The PC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UNN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION 1714

APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOWN
REGISTRATION NUMBER: 02307E-061410
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION STG. 0200
TELEFONMUNICATION STG. 0200
TELEFONMUNICATION STG. 0200
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Best Local Similarity 75.0%; Pred. No. 0.04;
Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-665-202-30
; Sequence 30, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TYPE: 11 mino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           70 ISSSGSTIYYADSVKG 85
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
617-542-8906
                                                                                                                                                               ; MOLECULE TYPE: protein US-08-545-809A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-665-202-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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2 ISENGRTINYADSVKG 17

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| Wission: 15:-574-0
| Wission: 15:-574-0
| Wission: 15:-574-0
| Wission: 15:-574-0
| Bequence 30. Application US/09315574
| Patent No. 6410201
| CREMEAL INFORMATION: No. 6512097el High Affinity Human Antibodies to TITIE OF INVENTION: Nuo. 6512097el High Affinity Human Antibodies to TITIE OF INVENTION: Nuo. Theorem Titie OF INVENTION: Nuo. Theorem Titie OF INVENTION: Nuo. Theorem Titie OF INVENTION: Nuo. Theorem Titie OF INVENTION: Nuo. Theorem Titie OF INVENTION: Nuo. Theorem Titie OF Invention: A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A partical process. A pa
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Sequence 143, App
Sequence 105, App
Sequence 109, App
Sequence 1503, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
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Sequence 1648, Ap
Sequence 1648, Ap
                                                                                                                                                    April 28, 2005, 18:24:46; Search time 105.453 Seconds (without alignments) 53.700 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: \cgn2_6/ptodata/1/pubpaa/PGT_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PGT_BW_PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/BGG_NBW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-880-748-1648
US-10-823-418-1648
US-09-848-798-1648
US-10-492-668-105
US-10-492-668-109
US-10-293-418-1503
US-10-106-895-4
US-10-106-895-3
US-10-308-817-57
US-10-308-817-57
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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79, Appl
57, Appl
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30, Appl
16, Appl
601, App
639, App
23, Appl
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28, Appl
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11, Appl
53, Appl
5, Appli
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US-10-032-433A-63

US-10-032-433A-63

US-10-032-988B-79

US-10-032-926B-63

US-10-029-926B-79

US-10-029-926B-79

US-10-038-591-30

US-10-384-830-639

US-10-884-830-639

US-10-884-830-639

US-10-884-830-639

US-10-884-830-639

US-10-98-33-115

US-10-938-33-116

US-10-938-33-106

US-10-938-33-106

US-10-938-33-106

US-10-938-33-106

US-10-269-805-11

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Sequence 172, Application US/10031874A

Publication No. US20030190598A1

Fublication No. US20030190598A1

Fublication No. US2003019059BA1

APPLICANT: TANHA, AMERIED

APPLICANT: DUBUC, GINETE

APPLICANT: NARANG, SARAN

TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS

TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES

FILE REFERENCE: 11054-1

CURRENT FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/207,234

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1 glama ; TYPE: PRT ; ORGANISM: Lama US-10-031-874A-172

ö Score 65; DB 14; Length 17; Pred. No. 0.00067; 3; Mismatches 2; Indels 3; ::| :|| ||||||||| 1 LLSRSGRTTNYADSVKG 17 1 VISENGRTINYADSVKG 17 76.5%; 12, Conservative Query Match Best Local Similarity Matches 12; Conserv a

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Gaps

US-09-880-748-1648 ; Sequence 1648, Application US/09880748 ; Publication No. US20030059937A1

Sequence

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RESULT 4
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US-12/3-1989

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0
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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CURRENT PAPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239

SECTIAMENT OF 16-18
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 11; Conserv
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Matches 11; Conserv
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US-10-293-418-1648
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50 VISDDGNNVNYEDSVKG 66

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Sequence 105, Application US/10492668
Publication No. US20050054001A1
GENERAL INFORMATION:
APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
TITLE OF INVENTION: FUNCTIONAL HEAVY CHAIN ANTIBODIES, FRAGMENTS THEREOF, LIBRARY THEF
TITLE OF INVENTION: METHODS OF PRODUCTION THEREOF
     Sequence 143, Application US/09848798

Publication No. US20310040605A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 143

LENGTH 129
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Pred. No. 0.09;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.4%; Score 59; DB 10; Length 129; Best Local Similarity 76.5%; Pred. No. 0.067; Matches 13; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: anti-Rh(D) antibody clone SH20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: VIB-030-PCT
CURRENT APPLICATION NUMBER: US/10/492,668
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: EP01204037.4
PRIOR FILING DATE: 2001-10-24
PRIOR PILING DATE: 2002-01-11
PRIOR PILING DATE: 2002-01-11
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.1
SEQ ID NO 105
LENGTH: 120
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Best Local Similarity 70.6%;
Matches 12; Conservative
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), OTHER INFORMATION: C9-B
US-10-492-668-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-848-798-143
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Gaps
                                                               sequence 1503, Application US/10293418
publication No. US20030223996A1
GENERAL INFORMATION:
ITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
TILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
FRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-01-9
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR PRIOR DATE: 2001-05-25
PRIOR PRIOR DATE: 2001-05-26
PRIOR PRIOR DATE: 2001-05-26
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PRIOR PRIOR DATE: 2001-05-26
PRIOR PRIOR DATE: 2001-05-26
PRIOR PRIOR DATE: 2001-05-26
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIING DATE: 2001-01-17
PRIOR PRIING DATE: 2001-01-17
PRIOR PRIING DATE: 2001-01-17
PRIOR PRIING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
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ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/10/066,895
FILING DATE: 04-Feb-2002
CLASSIFTCATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon, Susan B.
Porter, Terence C.
Sweet, Raymond A.
TITLE OF INVENTION: Human Monoclonal Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Pred. No.
                                                   , Application US/10293418
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Publication No. US20020141990A1
GENERAL INFORMATION:
APPLICANT: Deen, Keith C.
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Best Local Similarity 76.5%;
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-1503
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  Sequence 109, Application US/10492668
Publication No. US2005034001A1
SERENAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FITLE OF INVENTION:
FETCH OF INVENTION:
FETCH OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: VIB-030-PCT
CURRENT APPLICATION NUMBER: US/10/492,668
FILE REFERENCE: 2004-04-15
FRIOR APPLICATION NUMBER: E901204037.4
FRIOR FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
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; Sequence 1503, Application US/09880748
; Publication No. US20030059337A1
; GENERAL INFORMATION:
    APPLICANT: Ruben et al.
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR APPLICATION NUMBER: 60/273,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; RIOR SEQ ID NOS: 3239
; SOFTWARE: PATENTIN VEY: 2.0
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.6
Matches 12; Conservative
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OTHER INFORMATION: C24-A
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ORGANISM: Homo sapiens
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Matches 13; Conserv
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JS-10-492-668-109
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; TYPE: PRT
; ORGANISM: human
US-10-308-817-57
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                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-194-975-17
Sequence 17, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/10308817
; Sequence 57, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Worther, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES;
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                    ATTORNEY AGENT INFORMATION:
NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-066-895-4
    APPLICATION NUMBER: 60/030,149
                                                                                                                                          TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                             LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                  TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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75.0%;
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Best Local Similarity 75.0%
Them 12; Conservative
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US-10-194-975-17
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US-10-308-817-57
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US-10-032-037B-63

Sequence 63, Application US/10032037B

Sequence 63, Application US/10032037B

Sequence 63, Application US/10032037B

Sequence 63, Application US/20040001822A1

PUBLICANT No. US20040001822A1

GENERAL INFORMATION:

TITLE OF INVENTION: WOLFIES, ANTIBODIES TO SUCH EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: WOLFIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION: WOMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SEQ ID NO 63

LENGTH: 98
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Sequence 79, Application US/10032037B

Sequence 79, Application US/10032037B

PUBLICATION NO. US20040001822A1

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: WOITIES, ANTIBODIES TO SUCH EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOITIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION NUMBER: US/10/032,037B

CURRENT APPLICATION NUMBER: 60/258,948

PRIOR PLILOR DATE: 2000-12-31

PRIOR FILING DATE: 2000-12-29
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Length 98;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
67.1%; Score 57; 75.0%; Pred. No.
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                                                                                            2 ISENGRIINYADSVKG 17
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Best Local Similarity 75.0°
Matches 12; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
                     Best Local Similarity 75.0
Matches 12; Conservative
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ORGANISM: Homo sapiens
US-10-032-037B-79
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ORGANISM: Homo sapiens
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US-10-029-988B-63
US-10-029-988B-63
US-10-029-988B-63
Sequence 63, Application US/10029988B
Sequence 63, Application US/0029988B
Sequence 63, Application No. US20040001839A1
SEQUENCE CONTAINTON:
TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-31
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOUTHARE: PRELSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 98
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US-10-029-988B-79
US-10-029-988B-79
| Sequence 79, Application US/10029988B
| Publication No. US20040001839A1
| GENERAL INFORMATION:
| APPLICANT BIO-Technology General Corp.
| TITLE OF INVENTION: WOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
| FILE REFERENCE: 10793/46
| CURRENT APPLICATION NUMBER: US/10/029,988B
| CURRENT APPLICATION NUMBER: 60/258,948
| PRIOR PILING DATE: 2000-12-31
| PRIOR FILING DATE: 2000-12-29
| NUMBER OF SEQ ID NOS: 204
| SOFTWARE: FastSEQ for Windows Version 3.0
| LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :| || |||||||
51 ISSSGSTIYYADSVKG 66
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ORGANISM: Homo sapiens
US-10-029-988B-79
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-029-988B-63
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GenCore version 5.1.6 (c) 1993 ~ 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

April 28, 2005, 18:05:55 ; Search time 23.375 Seconds (without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_177_193 85 1 VISENGRTINYADSVKG 17 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Iq heavy chain V-J	heavy	chain V		heavy chain V	heavy chain -	heavy chain				heavy chain	heavy chain	heavy chain		heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy chain	heavy	Ig heavy chain V r
SUMMARIES	ID	857445	10	S26891	93	PH1652	S31120	S31105	. 226790	137783	147191	PH0875	S36273	S24251	836267	S30532	S26894	S36282	M3HUWE	S21980	PH1661	S26794	S30531	\$23624	H08	269	S26927	574	S31104	ın
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	Length	115	97	98	98	110	114	118	128	130	132	97	120	108	115	123	98	110	114	117	121	123	125	143	98	98	98	113	121	128
	Query	68.2	67.1	67.1	67.1	67.1	67.1	67.1	67.1	67.1	7	65.9	•		61.2															
	Score	58	57	57	57	57	57	57	57	57	57	99	53	52	52	25	51	51	51	51	51	51	51	51	20	20	20	20	20	20
	Result No.	-	8	М	4	S	9	7	60	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain var	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	anti-SS-A/Ro 60K p	Ig heavy chain V r		Ig heavy chain V r		Ig heavy chain V r	-24	Ig heavy chain pre
147195	A60943	JL0048	S20777	G1HUDB	E49590	B34871	Alhutr	PC4281	D25913	S20781	S29545	S26928	800700	137778	G1MS21
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133	151	191	95	120	120	121	122	123	94	96	86	98	118	135	136
8.8	9.8	3.8	9.1	57.6	9.1	9.1	9.	9.7	ر. در	ر. در	٠. ت	5.5	5.5	3.	5.5
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20	20	20	49	49	49	49	49	49	48	48	48	48	48	48	48
30	31	32	33	34	35	36	37	38.	39	40	41	42	43	44	45

## ALIGNMENTS

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Signatory chain V-J region - human (fragment)
C.Species: Homo maplens (man)
C.Species: Homo maplens (man)
C.Species: Homo maplens (man)
C.Species: Homo maplens (man)
C.Species: Homo maplens (man)
C.Species: Homo maplens (man)
C.Species: Homo maplens
C.Species: Milson, G.; Kennedy, P.G.E.; Willison, H.J.
Submitted to the EMBL Data Library, June 1995
A.Pescription: Analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropat A.Pescription: S5744
A.Pescription: S5744
A.Scatus: preliminary
A.Scatus: preliminary
A.Scatus: preliminary
A.Scatus: preliminary
A.Scatus: preliminary
A.Scatus: mRNA
A.Scatus: MRB:X87891; NID:g871285; PIDN:CAA61142.1; PID:g871286
C.Genetics:
A.Status: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <IMM>
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68.2%; Score 58; DB 2; Length 115;
Best Local Similarity 76.5%; Pred. No. 0.04;
Matches 13; Conservative 0; Mismatches 4; Indels
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RESULT 2

Graces Homo sapiens (Ms4P3-D-JH6) - human
Graces: Homo sapiens (man)
Graces: Homo sapiens (man)
Graces: Homo sapiens (man)
Graces: Homo sapiens (man)
Graces: Peb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Graces: Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Ristewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A.Description: A single VH gene predominates in the rearranged and expressed human B cell
A.Reference number: S24247
A.Accession: S24252
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-97 <STE>
A.Molecule type: DNA
A.Residues: 1-97 <STE>
G.Superfamily: immunoglobulin V region; immunoglobulin homology
G.Superfamily: immunoglobulin

Gaps ö 67.1%; Score 57; DB 2; Length 97; 75.0%; Pred. No. 0.049; cive 1; Mismatches 3; Indels Query Match 67.1%; Best Local Similarity 75.0%; Matches 12; Conservative

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2 ISENGRIINYADSVKG 17

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Gaps

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Jurady Clark Homo sapiens (man)
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Accession: S31120
C; Maccession: S31120
A; Title: Restricted utilization of germ-line V(H) 3 genes and short diverse third compleme A; Residues: Dirac number: S31104; MUID:92111633; PMID:173052
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Rolecule Type: mRNA
A; Residues: 1-114 <RAA>
A; Residues: 1-114 <RAA>
A; Residues: 1-114 <RAA>
A; Coss-references: EMBL:X62972
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetraner; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens
C;Species: Homo sapiens
C;Species: Homo sapiens
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A;Ritle: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Reference number: sailos
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.1%; Score 57; DB 2; Length 118; 75.0%; Pred. No. 0.06; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.1%; Score 57; DB 2; Length 114; 75.0%; Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                         67.1%; Score 57; DB 2; 75.0%; Pred. No. 0.055; iive 1; Mismatches
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Best Local Similarity 75.0
Matches 12; Conservative
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Matches 12; Conservative
                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 12; Conservative
        A; Experimental source: B cell
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A; Residues: 1-118 <RAA>
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H1652
Ig heavy chain V region (clone 5D4) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: PH1652
R;Hillson, J.L; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                 Ig heavy chain V region (DP-58) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26891
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
$26930
Ig heavy chain V region (DP-35) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of NAccession: S26930
A;Accession: S26930
A;Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:Z12337; NID:g32892; PIDN:CAA78207.1; PID:g32893 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 2;
Pred. No. 0.049;
1; Mismatches
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28 ISSSGSTIYYADSVKG 43
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Best Local Similarity 75.0
Matches 12; Conservative
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A; Molecule type: mRNA
A; Residues: 1-110 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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CiAccession: PH0875
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Recession: PH0875
A;Rocession: PH0875
A;Rocession: PH0875
A;Rocession: PH0875
A;Rocession: PH0875
A;Rocession: PH0876
A;Rocession: PH0876
A;Rocession: PH0876
A;Rocession: PH0876
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A;Rocession: PH0876
A;Rocession: PH0876
A;Rocession: PH0876
A;Rocession: PH0876
A;Rocession: Complementarity-determining 2
F;49-66/Region: complementarity-determining 2
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Cispecies: Homo sapiens (man)
Cispecies: Most sapiens (man)
Cispecies: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
Ciscossion: 38673
Rightifiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J., EMBO J. 12, 725-734, 1993
A,Fitle: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36273
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                              Ig heavy chain V region (anti-DNA, H2F) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
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A;Cross-references: EMBL:Z18834; NID:g33116; PIDN:CAA79286.1; PID:g939896
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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68.8%; Pred. No. 0.27;
ive 1; Mismatches 4; Indels
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                                  Indels
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7
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                               Mismatches
68.8%; Pred. No.
                                                                                                                          70 ISDSGRRTDYADSVKG 85
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                                                                                        2 ISENGRTINYADSVKG
                               11; Conservative
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   Best Local Similarity
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                                        C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26790
C;Accession: S26790
B;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CiSpecies: Homo sapiens (man)
Cibate: 16-Feb-1996 #text_change 23-Jul-1999
Cibate: 16-Feb-1996 #text_change 23-Jul-1999
CiAccession: 137783; 825477
Ribemaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, S14-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene family homologous to human
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Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X61013; NID:g32798; PIDN:CAA43347.1; PID:g1335128 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
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J. Immunol. 153, 5618-5627, 1994
A; Title: Expersed awine VH genes belong to a small VH A; Reference number: 147177; MUID:95081609; PMID:7989761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 57; DB 2; 75.0%; Pred. No. 0.065; iive 1; Mismatches
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68.8%; Pred. No. 0.066;
ative 3; Mismatches
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Matches 12; Conservative
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A; Residues: 1-128 <MOR>
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C;Date: 21-Feb-1997
C;Accession: I47191
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Query Match

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51 ISWNSGTLGYADSVKG 66

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Search completed: April 28, 2005, 18:26:03 Job time : 30.375 secs
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submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel A;Reference number: $24247
A;Accession: $24251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <STE>
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C;Specis Homo sapiens (man)
C;Specis Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36267
C;Accession: S36267
Mulmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30532
R;Mariette, X.
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                                                                                                                                                                                                                A;Cross-references: EMBL:X67072; NID:g38401; PIDN:CAA47457.1; PID:g38402 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterchetramer; immunoglobulin P:11-94/Domain: immunoglobulin homology <IMM>
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A,Residues: 1-123 <MAR>
A,Crossereferences: UNIPROT:Q8WU38; EMBL:Z18318
C,Superfamily: immunoglobulin V region; immunoglobulin
C,Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                             Length 108;
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C;Species: Homo sapiens (man)
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A;Reference number: S30520
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2 ISENGRIINYADSVKG 17

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Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
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HV3U HUMAN

AC P01782,

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 1-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

E g heavy chain V-III region DOB.

S Homo sapiens (Human).

C Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
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"Amino acid sequence of the heavy-chain variable region of the crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
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Pred. No. 0.35;
3; Mismatches 3; Indels
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68.8%; Pred. No. 0.15;
ive 1; Mismatches 4; Indels
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PYRROLIDONE CARBOXYLIC ACID.
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HSSP, P01772; FPB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1.ike.
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                            HSSP, PO1772; 2FF4.

GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005823; F: antigen binding; NAS.
GO; GO: 0005952; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00596; Ig_v.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunglobulin V region; Pyrrolidone carboxylic acid.
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Immunoglobulin V region.
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"Amino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELIANBOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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10-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 01, Last annotation update)
11 heavy chain V-III region WEA.
11 heavy chain (Human).
12 heavy capiens (Human).
13 heavy capiens (Human).
14 home sapiens (Human).
15 heavy capiens (Human).
16 heavy capiens (Human).
17 home sapiens (Human).
18 heavy capiens (Human)
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MEDLINE=83273707; PubMed=6410398;
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ID _HV3B_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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Submitted (UNY-1975) to the PIR data bank.
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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D SEGMENT.
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                    [2]
SEQUENCE OF 17-136.
MEDLINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
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W -> H (IN REF. 2).
Y -> W (IN REF. 2).
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Pred. No. 0.58;
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InterPro, IPR007110, Ig-like.
InterPro, IPR003596; Ig-v.
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Cell 24:625-637(1981).
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136 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule.; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02045; AlHUTR.
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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MEDLINE-76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
Hilschmann N.;
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006595; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
PRAMT; SM004406; Ig-v;
PROSITE; SM004406; IG-v; I
PROSITE; PS50835; IG-LIKE; I.
Immunglobulin V region; Pyrrolidone carboxylic acid.
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10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
Mus musculus (Mouse).
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Last annotation update)
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10-OCT-2003 (Rel. 42, Last annot
11g heavy chain V-III region TRO.
Homo sapiens (Human).
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                                             51 ITWNGGSVLYADSVKG 66
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                    ISENGRTINYADSVKG
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Matches 10; Conservative
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OS Bukaryota, M.
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OX NCBI_TAXID=11
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P01762;
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Gaps

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117 AA; 13220 MW; 512B625003FA6ECB CRC64;
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MEDLINE=75046755; PubMed=4139708;
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Best Local Similarity 58.8
Matches 10; Conservative
                                             8; Conservative
                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                 Homo sapiens (Human).
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122 AA;
                       Query Match
Best Local Similarity
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P01774;
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HV3M_HUMAN
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                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-88144476; PubMed-312553; Wilden MEDINE Wilson M.R., Middleton D., Warr G.W.; Middleton D., Warr G.W.; Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 3.
                                                                                                                                                          116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988)
                                                                                                                                                                                Score 47; DB 1;
Pred. No. 0.72;
3; Mismatches
                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region 3 precursor.
Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                         117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-11ke.
                                                                                                                                       IG-LIKE.
                                                                                                                                                                                                                                                                                                          PRT;
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003596; Ig_v.
                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                   55.3%;
                                                                                                                                                                                                                              2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                              51 IKZBGSZZBYVDSVKG 66
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                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
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54
68
85
1117
1115
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NCBI_TaxID=7957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A28966; A28966.
HSSP; P01772; 2FB4.
            PIR; A02064; M3HUGL
HSSP; P01772; 2FB4.
                                                                                                                                                                                Query Match
Best Local Similarity
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HV03_CARAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH MACROGLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE=81013859; PubMed=6774332;
Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable region of a human mu chain:
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Pfam; PF00047; ig; 1.
SMART; SMO406; IGV; 1.
SMART; SMO4066; IGV; 1.
IMMUNICATION V PSGION; Pyrrolidone carboxylic acid.
Immunication V region; Pyrrolidone Carboxylic acid.
Infaminoglobulin V region; Pyrrolidone Carboxylic ACID.
PYRROLIDONE CARBOXYLIC ACID.
54.1%; Score 46; DB 1; Length 117; 50.0%; Pred. No. 1.1;
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Pred. No. 1.1;
2; Mismatches 5; Indels
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Conteans 1 immunoglobulin-like domain.
PIR; A02051; M3HUAM.
HSSP; P01772; PFB4.
GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005576; P: antigen binding; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR007110; IG-like.
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21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                      P01769;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                      5; Mismatches
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Ig heavy chain V-III region POM
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                                                                                                          2 ISENGRIINYADSVKG 17
                                                                                                                                        1 VISENGRTINYADSVKG
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52.9%;
                                     9; Conservative
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Best Local Similarity
Matches 9; Conserv
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105
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HV3K HUMAN
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 Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capra J.D., Kehoe J.M.; "Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M
                                                            Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036 (1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; P01772; 2FP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;
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                                                                                                                 -1- SIMIIARITY: Contains 1 immunoglobulin-like domain.
PIR; A02057; M3HUPM.
HSSP; P01772; 2FB4.
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, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v:
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21-JUL-1986 (Rel. 01, Last sequ.
10-OCT-2003 (Rel. 42, Last anno
1g heavy chain V-III region LAY
                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1. SMART; SMOAT; ig; 1. PROSITE; PS00406; IGV; 1. Immunoglobulin V region.
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Pfam; PP00047; Ig, 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 64.3%;
9; Conservative
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Best Local Similarity
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HV3N_HUMAN
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X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=81072295; PubMed=7441755;

Marquart M., Deisenhofer J., Huber R., Palm W.;

Marquart M., Deisenhofer J., Huber R., Palm W.;

To "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A and 1.0-A resolution.";

To Mol. Biol. 141:369-391(1980).

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A02055; GlHUNT.

PR A01055; GHHUNT.

PR A02055; GHUNT.

RO; GO:0003823; Frantigen binding; NAS.

GO; GO:0003823; Frantigen binding; NAS.

GO; GO:000595; P:immune response; NAS.

RO; GO:000495; P:immune response; NAS.

RO; GO:000495; Firmune response; NAS.

RO; GO:000495; Gl-1.

REFERO; IPR003596; Ig_V.

PEam; PPF0047; Ag; 1.

REFERO; PR00410; Ag; 1.

REFERO; PR00410; Ag; 1.

REFERO; PR00410; Ag; 1.

REFERO; PR00410; Ag; 1.

REFERO; PR00410; Ag; 1.

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REFERO; PR00410; Ag; 1.
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Score 45; DB 1; Length 119;
Pred. No. 1.6;
                                                                                         Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AA.
                                                                                    1; Mismatches
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SEQUENCE OF 1-135 FROM N.A.
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RA KUNBLINES-194044013; PURDMEGAS1843/17,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brussin C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Pabret C., Ferrariz E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rosport G., Rey M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Taragai T., Tarahashi H., Waltzenegger T.,
RA Takeuchi M., Tamakoshi A., Taragamata P., Topnoni A., Taramakoshi A., Taragamata P., Topnoni A., Taragai T., Tarahashi H., Waltzenegger T.,
RA Takeuchi M., Tamakoshi A., Taragamata P., Topnoni A., Taragamata P., Topnoni A., Tanamakoshi A., Taragamata P., Topnoni A., Taragai T., Tarahashi H., Waltzenegger T.,
RA Takeuchi M., Tamakoshi A., Tanamakoshi A., Wanbutte R., Wanbutte R., Wandler E., Wedler H., Waltzenegger T.,
RA Winters P., Wanbutt R., Wandler E., Wedler H., Watzenegger T.,
RA The complete genome sequence of the Gram-positive bacterium Bacillus
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                                                                                                            Gaps
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0
                                                                                 Length 126;
                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
109
116
124
13718 MW; E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                          P39753; P94582;
01-FEB-1995 (Rel. 31, Created)
15-7UL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Flagellar hook-basal body complex protein flhP.
FLHP OR BSU36390.
                                                                               Score 45; DB 1;
Pred. No. 1.7;
                                                                                                                                                                                                                                  268 AA
                                                                                                          4; Mismatches
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98015417; PubMed=9353933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:3313-3328(1997).
                                                                                                                                     1 VISENGRIINYADSVKG 17
                                                                                                                                                     52.9%;
                                                                                                          9; Conservative
                                                                                                                                                                                                                                  STANDARD;
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 109
113
120
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126
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                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 82:844-848(1985).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Caiman.
                                Abhayawardhane Y., Stewart G.C.; Bacillus subtilis possesses a second determinant with extensive sequence similarity to the Escherichia coli mreB morphogene."; J. Bacteriol. 177:765-773(1995).
                                                                                                                                                                      -!- SIMILARITY: Belongs to the flagella basal body rod proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.8%; Score 44; DB 1; Length 268; 50.0%; Pred. No. 5.7;
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MEDLINE=85140192; PubMed=2983316;
Litman G.W., Murphy K., Berger L., Litman R., Hinds K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 71 LAPL -> GLRLG (IN REP. 3).
268 AA; 29400 MW; 13C0CB83D0CB4AA3 CRC64;
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23-0cT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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EMBL, 299122; CAB15656.1; -.
EMBL, U12962, AAA67880.1; -.
PIR, G69623; G69623.
Subtilist; BG10918; Flhp.
InterPro; IPR001444; Flag_bb_rod.
Pfam; PP00460; flg_bb_rod; 1.
PROSITE, PS00588; FLAGELLA_BB_ROD; 1.
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MEDLINE=95138040; PubMed=7836311;
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Matches 8; Conserv
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the characterization of the protein, said the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymctryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ponstingl H., Hilschmann N.; "The rule of antibody structure of a
                                                                                                                                                  IG HEAVY CHAIN V REGION G4.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                 FRANCHIEMORR-Z.
COMPLEMENTARITY-DETERMINING-Z.
                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                    12994 MW; 6330D7469AAE55FC CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN I 112 IG-LIKE.
MOD_RES I PYRROLIDONE CARBOXYLIC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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1; Mismatches
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                                                                                                                                                                                                                                                               BY SIMILARITY
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HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0001823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                           FRAMEWORK-2
                                                                                                                                                                                                                                              FRAMEWORK-3
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MEDLINE=77070269; PubMed=826475;
                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                     InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                        50.68;
                                                                                                                                                                                                                                                                                                                                                        56.2%;
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Homo sapiens (Human)
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HSSP; P01810; 2FBJ
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AC P01770 H
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DT 21-JUL.
DT 21-JUL.
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W. Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate.
-!- PATHWAY: Galactose metabolism, first step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the GHMP kinase family. GalK subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
                                                                                                                                                                                      ö
                                                                                                                      Length 119;
                                                                                                                                                                                   Indels
22 96
119 119
119 AA; 13242 MW; C96935A6E55E165B CRC64;
                                                                                                                                                                                      ..
N
                                                                                                                      Score 43; DB 1;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Galactokinase (EC 2.7.1.6) (Galactose kinase) GALK ON YPOLI37 OR Y3045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AA
                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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HAMAP; MF_00246; -; 1.

InterPro; IPR000705; Galkinase.

InterPro; IPR000174; Galkinase.

InterPro; IPR006204; GHMP kinase.

InterPro; IPR006203; GHMP kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMPKnse ATP.
InterPro; IPR006206; Mev_galkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALI_YERPE
QBZG73;
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ414146; CAC89979.1; -. EMBL; AE013905; AAM86596.1; -.
                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                1 VISENGRTINYADSVKG 17
                                                                                                                   50.6%;
                                                                                                                                                                                                                                                                                   |:|:| :| :| |: | 50 VMSYBGBBKHYADSVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:523-527(2001).
                                                                                                                                                                                   9; Conservative
                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=632;
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Pyridine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: NAD blosynthesis; aspartate to NaMN; first step. SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE FAD-DEPENDENT OXIDOREDUCTASE FAMILY 2. NADB SUBFAMILY.
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
L-aspartate oxidase (EC 1.4.3.16) (LASPO) (Quinolinate synthetase B)
NADB OR NMA2092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919;
MEDLINE=2022556; PubMed=10761919;
MEDLINE=2022556; PubMed=10761919;
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Slmmonds M., Skelton J.,
Whitchead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iminoaspartate.
-!- CATALYTIC ACTIVITY: L-aspartate + H(2)O + O(2) = oxaloacetate
                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                 Length 383;
                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Catalyzes the oxidation of L-aspartate to
                                                                                     TIGRPAMS, TIGRO0131; gal kin; 1.
PROSITE; PS00106; GALACTÓKINASE; 1.
PROSITE; PS00627; GHMP KINASES ATP; 1.
Transferase; Kinase; Galactose metabolism; ATP-binding;
                                                                                                                                                                                                                        383 AA; 41865 MW; 548D19EB39D13281 CRC64;
                                                                                                                                                                                                                                                                 Score 43; DB 1;
Pred. No. 12;
                                                                                                                                                                                                   ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004112; Succ_DH_flav_C.
Pfam; PF00890; FAD_binding_2; 1.
TIGRPAMS; TIGR00551; nadB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Pfam; PF00288; GHMP kinases; 1.
PRINTS; PR00473; GALCTOKINASE.
PRINTS; PR00960; LMBPPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL162758; CAB85308.1; -. PIR; E81780; E81780.
                                                                PRINTS; PR00959; MEVGALKINASE.
TIGRFAMS; TIGR00131; gal_kin;
                                                                                                                                                                                                                                                                 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                  1 VISENGRTINYADSV 15
                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis Z2491.";
Nature 404:502-506(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NH(3) + H(2)O(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: FAD.
-!- PATHWAY: NAD bi
-!- SUBCELLULAR LOC
-!- SIMILARITY: BEL
                                                                                                                                                                              Complete proteome.
NP BIND 122
                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=65699;
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                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
NADB_NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSP;
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gamin M.L., DeBoy R., Petterson J.D., Hickey E.K., Nelson W.C., Garberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: NAD biosynthesis; aspartate to NaWN; first step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE FAD-DEPENDENT OXIDOREDUCTASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRPAMS; TIGR00551; nadB; 1. Pyridine nucleotide biosynthesis; Oxidoreductase; Flavoprotein; FAD; Complete protecome.
                                                                                                                                                                                                                                                                       Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
I-aspartate oxidase (EC 1.4.3.16) (LASPO) (Quinolinate synthetase B)
nucleotide biosynthesis; Oxidoreductase; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:1809-1815(2000).
-!- FUNCTION: Catalyzes the oxidation of L-aspartate to iminoaspartate.
-!- CATALYTIC ACTIVITY: L-aspartate + H(2)O + O(2) = oxaloacetate NH(3) + H(3)O(2).
-!- COPACTOR: FAD.
                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                  50.6%; Score 43; DB 1; Length 502; 53.3%; Pred. No. 16; 3; Indels iive 4; Mismatches 3; Indels
                                                        FAD (AMP PART) (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                039EC390B823BC34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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InterPro; IPR005288; NadB.
InterPro; IPR004112; Succ_DH_flav_C.
Pfam; PF00890; FAD binding_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
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                                                                                                                                                   54657 MW;
                                                                                                                                                                                                                                                                                                                                                                                           236 SENGRIFLISEAVRG 250
                                                                                                                                                                                                                                                                                                                                  3 SENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                           22
228
249
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                                                                                                                   249 2
502 AA;
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                                                                                                                                                                                                                                          Local Similarity
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                                  Complete proteome.
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                                                                                       228
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                                                                                       ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                 Query Match
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Q9K107;
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NADB NEIMB
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DOR WELL BERN THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouvani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kunh M., Kunst F., Kuraptar G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.";
Science 294:849-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRAC system protein B (UvrB protein) (Excinuclease ABC subunit B)
UVRB OR LIN2632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: The beta-hairpin motif is involved in DNA binding (By
                                                                                                                                                                                                              ;
                                                                                                                                                Score 43; DB 1; Length 502; Pred. No. 16; 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
FAD (AMP PART) (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
                                                                                         644152CC3753E294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the uvrB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
                                                                                      54562 MW;
                                                                                                                                                53.3%;
                                                                                                                                                                                                                                                                                                       236 SENGRTFLISEAVRG 250
                                                                                                                                                                                                                                                                  3 SENGRIINYADSVKG 17
                                                                                                                                                                            Local Similarity 53.3 les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                            UVRB LISIN
ID UVRB LISIN
NP_BIND
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q928Ã4;
                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subsequently bound by uvrc and the second uvrB is released. If no lesion is found, the DNA wraps around the other uvrB subunit that will check the other stand for damage (By similarity). SUBUNIT: Forms a heterotetramer with uvrA during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVABC system protein B (UvrB protein) (Excinuclease ABC subunit B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve B., de Daruvar A., Deboux P., Domanguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Feihi H., Garcia-Gel Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kunh M., Kunst F., Kurapkat G., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species.";
                                     R InterPro; IPR001410; DEAD.
R InterPro; IPR001410; DEAD.
R InterPro; IPR001943; UvrB/C.
R InterPro; IPR001943; UvrB/C.
R Pfam; PF00271; helicase_C; 1.
R Pfam; PF0271; helicase_C; 1.
R MART; SM00487; DEXC; 1.
R MART; SM00487; HELICC; 1.
R PROSITE; PS50151; UVR; 1.
R PROSITE; PS50151; UVR; 1.
W SOS response; Excision nuclease; DNA repair; DNA recombination; M DNA excision; ATP-binding; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1; Length 658;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                       7F15B338B0E3BB6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 AA
                                                                                                                                                                                                                                                                                                                                                           BETA-HAIRPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                         75616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||| | ||| :
544 NENGRVIMYADKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SENGRTINYADSV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
PIR; AC1761; AC1761.
SistiList; LIN02632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                       658 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UVRB OR LMO2489
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                    NP BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8Y4F5;
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
UVRB LISMO
ID _UVRB L:
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bisphosphate carboxylase, chlorophyll A/B binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.2
Local Similarity 6.2
Local Similarity 46.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ENGRIINYADSVK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||: ||:|::
59 ESGRSFNYSESIR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV02 CANFA
P01785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV02_CANFA
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION: Regulatory photoreceptor which exists in two forms that are reversibly interconvertible by light: the Pr form that absorbs maximally in the red region of the spectrum and the Pir form that absorbs maximally in the far-red region. Photoconversion of Pr in Pir induces an array of morphogenic responses, whereas reconversion of Fir to Pr cancels the induction of those responses. Pir controls the expression of a number of nuclear genes including those encoding the small subunit of ribulose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicoryledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae; Papilionoideae, Phaseoleae, Glycine. NCBI_TaxID=3847,
           similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: The beta-hairpin motif is involved in DNA binding (By
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50151; UVR; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
 lesions. Interacts with uvrC in an incision complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 658;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STARNE-ELiolated leaf; STRANTE-CV. Paldal; TISSUB-ELiolated leaf; Hahn T.R., WOO T.W., Seo H.S., Choi Y.D.; Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AA257263C2C71919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                similarity).
-!- SIMILARITY: Belongs to the uvrB family.
-!- SIMILARITY: Contains 1 UVR domain.
                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIA
BETA-HAIRPIN.
                                                                                                                                                                                              EMBL; AL591983; CAD00567.1; -
DIR; AI1385; AI1385.
Listilist; LM002489; -
InterPro; IPR001410; DEAD.
InterPro; IPR00140; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR001943; UVEB.
InterPro; IPR001943; UVEB.
Ffam; PF00271; helicase_C; 1.
Ffam; PF00271; helicase_C; 1.
SMART; SM00480; DEXDC; 1.
INGREAMS; TIGR0631; UVXb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            75562 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 61.55.
Best Local Similarity 61.55.
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544 NENGRVIMYADKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SENGRIINYADSV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                         39
92
622
658 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHYB SOYBN
P42499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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protochlorophyllide reductase, rkNA, etc. It also controls the expression of its own gene(s) in a negative feedback fashion. SUBUNIT: Homodimer.
                                                                                                                                    -!- SIMILARITY: Belongs to the phytochrome family.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                      -!- PTM: Contains one covalently linked tetrapyrrole chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
W; 76333AABDC42D297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wasserman R.L., Capra J.D., ^{\prime} "Primary structure of the variable regions of two canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1
Pred. No. 40;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; T07756; T07756.
InterPro; IPR001594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
InterPro; IPR003661; His_KinA_N.
InterPro; IPR005467; His_Kinase.
InterPro; IPR00014; PAS_domain.
InterPro; IPR001294; Phytochrome.
Pfan; PP01590; GAF; 1.
Pfan; PP02518; HATPase_C; 1.
Pfam; PP0512; HisKA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00229; sensory_box; 1. PROSITE; PS50109; HIS_KIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00245; PHYTOCHROME_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1156 AA; 129085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=77242268; PubMed=407924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASS C; 1.
SMART; SM00388; HisKA; I.
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PS50112; PAS; 1.
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54 GGTTYYADSVKG 65
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"Complete amino acid sequence of the alpha 2 heavy chain of a human igaz immunoglobulin of the AZM (2) allotype.";
Proc. Natl. Acad. Sci. US. A. 75.966-969(1978).
-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
--- HSSP: P01789; 1MCP.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.9;
0; Mismatches 3; Indels
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117 AA; 12703 MW; FCE07309E0A84B35 CRC64;
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Pred. No. 4.1;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region BUT.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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MEDLINE=78137069; PubMed=416441;
immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
                                                                                                                                                                   MEDLINE=80077682; PubMed=117299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; i. __
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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51 ISSSGQTY-YADAVKG 65
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tes 10; Conservative
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PROSITE; PS50835; IG I
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                                                                                                                        SEQUENCE OF 113-117
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P01767;
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SEQUENCE
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:55-56(1979):
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
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121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
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PIR; A02054; G1HUHL.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
      121 AA
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
      PRT;
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MEDLINE=98065943; PubMed=9403685;
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                                                                                                        Ig heavy chain V-III region HIL.
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Best Local Similarity 58.8
Matches 10; Conservative
    STANDARD;
                                                                                                                                Homo sapiens (Human).
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PROSITE; PS50835
HV3J HUMAN
P01771;
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9; Conservative

Best Local Similarity

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Gaps

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CHARACTERIZATION.
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ZN_FING
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HUMAN
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last Sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Muscleblind-like protein (Triplet-expansion RNA-binding protein)
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GO:0005737; C:cytoplasm; ISS.
GO:0005634; C:nucleus; ISS.
GO:0003725; F:double-stranded RNA binding; ISS.
GO:0001701; P:embryonic development (sensu Mammalia); IEP.
GO:00030326; P:limb morphogenesis; IEP.

    -!- FUNCTION: Binds to CUG triplet repeat expansion dsRNA (By

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 1; Length 201; Pred. No. 9;
                                    Smith H.O., Venter J.C.;
'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Complete proteome.
SEQUENCE 201 AA; 23138 MW; 199E43E0704B4575 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 4 C3H1-type zinc fingers.

    -!- SIMILARITY: Belongs to the HAM1 NTPase family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAWAP, MF 01405, -; 1.
InterPro, IPR002637; Hamlp_like.
Pfam; PF01725; Hamlp_like; 1.
TIGRFAMS; TIGR00042; TIGR00042; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF231110; AAF72159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001135; AAB91499.1; -. PIR; G70130; G70130.
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28-FEB-2003 (Rel. 41, Last seq
15-MAR-2004 (Rel. 43, Last ann
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126 ISKNGQILNFEGIIKG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 43.8 es 7; Conservative
                                                                                                                              Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q57679; 1B78.
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                                       Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBNL MOUSE
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MBNL_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9NR56-3; Sequence=VSP 006429, VSP 006430;
-!- DISEASE: Muscular dystrophy may be caused by aberrant recruitment of MBNL to the DMPK transcript (CUG)(n) expansion.
-!- SIMILARITY: Contains 4 C3H1-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NR56; 043311; 043797;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Muscleblind-like protein (Triplet-expansion RNA-binding protein).
MBNL1 OR MBNL OR EXP OR KIAA0428.
                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING, AND
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borsani G., Barbieri A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                8E008DB5C7EF8AB9 CRC64;
GO, GO:0007517; P:muscle development; IEP.
GO; GO:0045445; P:myoblast differentiation; IDA.
GO; GO:007399; P:neurogenesis; IEP.
InterPro; IPRO0571; Znf CCCH.
Pfam; PF00642; zf-CCCH; 4.
Zinc.finger; Repeat; Nuclear protein; RNA-binding.
Zn_FING
14
40
C3H1-TYPE 1.
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                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                C3H1-TYPE 1.
C3H1-TYPE 2.
C3H1-TYPE 3.
C3H1-TYPE 4.
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                                                                                                                                                                                                                                                                                                                                                      Pred. No.
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                                                                                                                                                                                                                                                                                                                                                           64.38;
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                                                                                                                                                                                                                               205
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341 AA;
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Search completed: September 24, 2004, 01:55:23 Job time: 16.1132 secs

중 음 Colosus Michaela esco sitt

Searched:

Database

Result No.

Sequence:

Run on:

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Q8fw49 brucella su Q9iv97 human immun Q9a430 caulobacter Q9zqx5 arabidopsis Q9ul91 homo sapien Q9il94 homo sapien Q9il96 mus musculu Q7vj23 helicobacte Q8lz05 mus musculu Q7vj23 helicobacte Q8lx47 bacillus an Q8lsi3 bacillus ac Q8lx47 bacillus ce Q9iwgy3 homo sapien Q45948 caenoxhabdi
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Q8BUD8
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Q8CHF5
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Q43152
Q9M4Z1
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P94448
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Q84PF4
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Q84J86
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Q84UT1
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Q947B9
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Q8SZ70
Q9VW14
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Q95205
Q96RE3
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Q9u187 homo sapien
Q9u187 homo sapien
Q9u29 homo sapien
Q9u193 homo sapien
Q8uk1 homo sapien
Q8uk1 homo sapien
Q9u171 homo sapien
Q9aRh8 caulobacter
Q9ebb9 methanobact
Q9bb9 homo sapien
Q9b1h9 samia cynth
Q9b1h9 samia cynth
Q9b1h9 samia cynth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
                                                                                               September 24, 2004, 01:47:17; Search time 81.4717 Seconds (without alignments) 65.836 Million cell updates/sec
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                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                      protein search, using sw model
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08N5K4
09UU37
08UU38
09HCC1
09HCC1
09UL93
08KW71
09UL71
09UL71
09UL71
09UL71
09GE78
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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Maximum Match 100%
Listing first 150 s
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                               Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Poustka A., Lundeberg J., "The European IMAGE consortium for integrated Molecular analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Immunoglobulin heavy chain variant (Fragment).
Mono sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC03249; AAH32249.1; -.
InterPro; IPR003599; IG.
R InterPro; IPR003599; IG.-I.Ke.
R InterPro; IPR003599; IG.-I.Ke.
R InterPro; IPR003596; IG.-V.
R InterPro; IPR003596; IG.-V.
R EMBL; SM00409; IG; 4.
SWART; SM00409; IG; 4.
SWART; SM00406; IG; 4.
R SWART; SM00406; IG; 4.
R SWART; SM00406; IG; 4.
R PROSITE; PS00390; IG. ILKE; 4.
R PROSITE; PS00290; IG.-MHC; 1.
                                                                                                                                                                                                                                                       Numan gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALSA9978; CAB97534.1; --.
HSSP; P01789; JUNP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003006; Ig_WC.
InterPro; IPR003009; Ig_WC.
InterPro; IPR003096; Ig_W.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
RNOSITE; PS00290; IG_MHC; 2.
NON TER 1 1 1
SEQÜENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%; Score 58; DB 4; Length 416; 68.8%; Pred. No. 0.34; ive 3; Mismatches 2; Indels ...
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                                                                                                            SEQUENCE FROM N.A. Planting M., Sumoy L.; Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein.
499 AA; 53376 MW; 93A5C89582054F32 CRC64;
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|| :| ||::||||||
11 ISSSGDTVDYADSVKG 26
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Best Local Similarity 68.8%
Matches 11; Conservative
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Best Local Similarity 68.9
Matches 11; Conservative
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                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Blood;
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SEQUENCE 45
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QBN5K4;
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QBN5K4

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Q8xkg6 clostridium
Q8xkg6 clostridium
Q8xt92 influenza a
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Q9r7y7 streptococc
Q9r7y5 streptococc
Q9r6x6 streptococc
Q9r6x1 streptococc
Q9r7y4 streptococc
Q9r7y4 streptococc
Q9r7y6 streptococc
Q9r26 streptococc
Q9r26 streptococc
Q9r26 streptococc
Q9r39 streptococc
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Q7x5g5 streptococc
Q7x5g1 streptococc
Q7x5f7 streptococc
Q7x5f5 streptococc
Q7x5f6 streptococc
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Q7x5g7
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Q9RK53
Q94B77
Q9FIU0
Q8ZA73
Q94JM6
Q9UL72
   002657
009642
098XKG
08XKG
08QT92
08QT92
08UYC0
08UYC0
08QT93
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08QT93
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Q8B2T6
Q809F7
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Q9IIJ8
Q9IIJ4
Q8QT87
Q8V032
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Q9IBX8
Q67164
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09R7Y6
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Q9ZEF1
Q8RJ49
Q9R7Y4
Q9R321
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Q9ZEF0
Q9R394
Q9R3E8
Q9RCP5
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Q9R7Y8
Q7X5G9
Q7X5G6
Q7X5G6
Q7X5G5
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Q7X5F5
Q7X5F4
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     PRELIMINARY;
     OSNOPE

ID OSNOPE

AC QONPPE;

AC QONPPE;

DT 01-OCT-2000 (CDT OF CONPPE)
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Gaps

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Created) Last sequence update) Last annotation update)

(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 25,

RESULT 1

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RESULT 3

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Kikuchi M., Takeda C., TBujimoto Y., Asada S., Nagata K.;
Kikuchi M., Takeda C., TBujimoto Y., Asada S., Nagata K.;
"An antibody fragment2A3 specific for native lysozyme :Isolaion from thuman synthetic phage display library and characterization.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049915; BAB16829.1; -.
HSSP; P0172; 2FB4.
InterPro; IPR003196; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                          Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.5%; Score 48; DB 4; Length 112; 62.5%; Pred. No. 3.7; ive 2; Mismatches 4; Indels
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                 Indels
           573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                              Query Match 58.8%; Score 50; DB 4; Best Local Similarity 68.8%; Pred. No. 11; Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, APO35021, AAD56257.1; -.
PIR; PL0120, PL0120.
HSSP, P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 1. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                   70 ISWNSGSIGYADSVKG 85
                                                                                                                                                                                                                                   2 ISENGRTINYADSVKG 17
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Homo sapiens (Human).
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nes 10; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Last annotation update)
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                                           |: || : |||||||||||| 70 INWNGGSTNYADSVKG 85
2 ISENGRIINYADSVKG 17
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Homo sapiens (Human).
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Zhong Z., Toukdarian A., Helinski D.R.;
Zhong Z., Toukdarian A., Helinski D.R.;
"Nuclectide sequence-based characterization of two cryptic plasmids
from the marine bacterium Ruegeria isolate PRID.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF416331; AAN05192.1;
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Elwacyaga, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Rhodobacteraceae; Ruegeria.
NCBI_TaxID=185588;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC02040; AAH20240.1; -.
PIR; PL0120; PL0120.
PIR; S15590; S15590.
InterPro; IPR007110; Ig-like.
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                                                                                                                                            116 AA; 12434 MW; 0DA0348154DD6061 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OTT-2003 (TrEMBLrel. 24, Last annotation update)
RC119.
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  InterPro; IPR007110; Ig-like.
                                    Pfam; PP00047; 1g; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
                         InterPro; IPR003596; Ig_v.
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Best Local Similarity 66.7
Matches 8; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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55.3%; Score 47; DB 4; Length 613;
Best Local Similarity 64.7%; Pred. No. 37;
Matches 11; Conservative 1; Mismatches 5; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMAR; PF00046; IGv. 1.
PROSITE; PS00290; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypochetical protein.
SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CC1375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 58.89
Matches 10, Conservative
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Gaps

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54.1%; Score 46; DB 16; L 47.1%; Pred. No. 1.1e+02; ive 6; Mismatches 3;

Length 1187;

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1187 AA; 127874 MW; A237F711DB6CE4E5 CRC64;
                                   PRINTS; PRO0605; CYTCHROMECIC.
PROSITE; PS00190; CYTOCHROME_C; 3.
PROSITE; PS00030; RRM_RNP_1; 1.
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152 VIASNGSTLSFAELVQG 168
                                                                                                                                                                                                                                                                                                1 VISENGRIINYADSVKG 17
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Matches 8; Conser
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SEQUENCE 1187 AA
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        Pfam; PF00034;
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01-JAN-1998
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026670
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Matches
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SEQUENCE FROM N.A.

STATIN-ATCC 19089 / CEB15;

A MEDLINE-21173699; PubMed=11259647;

A MEDLINE-21173699; PubMed=11259647;

A MEDLINE-21173699; PubMed=11259647;

A MEDLINE-21173699; PubMed=11259647;

A Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

B Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A DeBoy R.T., Dourkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ernolaeva M., White O.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

B PIR, H87419; H87419.
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Nelson K.E., weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Chris Lee T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Elsen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Aldehyde dehydrogenase family protein, putative/cytochrome c family protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO: 000548; C: mitochondrial electron transport chain; IEA.

R GO; GO: 000548; F: electron transporter activity; IEA.

R GO; GO: 0003676; F: nucleic acid binding; IEA.

R GO; GO: 0006118; F: caid binding; IEA.

R GO; GO: 0006118; P: electron transport; IEA.

R InterPro; IPR008274; Aldxan_dh_hamm.

R InterPro; IPR009345; CytC, heme_BS.

R InterPro; IPR009345; CytC, heme_BS.

R InterPro; IPR0093168; CytC_TC.

R InterPro; IRR009504; RNA rec_mot.

R Pfam; PF01315; Ald Xan_dh_C; 1.

R Pfam; PF01315; Ald Xan_dh_C; 1.
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Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.1%; Score 46; DB 16; Length 466; 53.3%; Pred. No. 40; ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008557; DUF839.
Pfam; PF05787; DUF839; 1.
Hypothetical protein; Complete proteome;
SEQUENCE 466 AA; 49864 MW; 141B7137A7CB1511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1187 AA.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         TIGR; CC1375;
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08 FX8
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MEDLINE=98037514; PubMed=9371463;

Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Banhirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougail S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol 179:7135-7155(1997).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
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Pred. No. 37;
2; Mismatches 4; Indels
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PIR; E69175; E69175. E69176.
Hypothetical protein; Complete proteome.
SEQUENCE 310 AA; 35223 MW; 70F30E12BA6110A6 CRC64;
                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update) Hypothetical protein WTH570.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
  310 AA.
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                                                                                                                                                                                                 Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                               Methanobacterium thermoautotrophicum.
  PRT;
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                                           (TrEMBLrel. 05, (TrEMBLrel. 05,
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PRELIMINARY;
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TISSUE=B-cell;
Strausberg R.;
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Excinuclease ABC, B subunit.
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                                                                                                                                                                                                                                                                                                                              Samia cynthia (Cynthia moth) (Ailanthus silkmoth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Saturniidae; Saturniinae; Attacini; Samia.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-1219196; PubMed=11319268;
MEDLINE-1219196; PubMed=14 Analysis of TRAS, Telomeric Repeat-Specific Non-LTR Retrotransposon Families in Lepidopteran Insects.";
MOL. Biol. Bvol. 18:848-857(2001).

EMBL; AB046674; BA821517.1; ---
GO; GO:0003743; F:RNA directed DNA polymerase activity; IEA.
GO; GO:000364; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0006278; P:RNA-directed DNA replication; IEA.
InterPro; IPR000473; RVTse.
InterPro; IPR000477; RVTse.
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                                                                                                                                  52.9%; Score 45; DB 4; Length 597; 62.5%; Pred. No. 77; ive 2; Mismatches 4; Indels
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 (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                           PROSITE; PS50815; IC_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
HYPOCHELICAL DYCLEIN_
SEQUENCE 597 AA; 65039 MW; 4FCAJADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73783 MW; 3ADAB436AE58060C CRC64;
                                                                                                                                                                                                                                                                               01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-directed DNA polymerase; Transferase.
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PF00078; rvt; 1.
         EMBL; BC015760; AAH15760.1; -...
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PP00047; Ig; 5.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                2 ISENGRIINYADSVKG 17
                                                                                                                                                                                            70 ISGSGGSTYYADSVKG 85
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                                                                                                                                                                                                                                                                                                                  TRASSC4 protein (Fragment)
                                                                                                                                  Query Match 52.9
Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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Q8BLF9;
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01-JUN-2003 (
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SEQUENCE
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Q88LF9
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DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; "The genome sequence of the facultative intracellular pathogen Brucella melitensis."
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-2243060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Foute D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjeppandic D., Hoheisel J., Straetz M., Heim S.,
Fraser C.M.;
                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0065524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004519; F:DNA binding; IEA.
GO; GO:0006289; P:nuclease activity; IEA.
GO; GO:0006289; P:nucleotide-excision repair; IEA.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Alkaline phosphatase (EC 3.1.3.1)
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EMBL, AE009700; AAL53897.1; -.
PIR; AF3591; AF3591.
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1; Mismatches
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MEDLINE=20020109; PubMed=11756688;
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UVRB OR PP1974.
Pseudomonas putida (strain_KT2440)
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InterProj IPR001943; UVRB/C.
Pfam; PF00271; helicase C; 1.
Pfam; PF02151; UVR; 1.
PR0SITE; PS50151; UVR; 1.
Complete proteome.
SEQUENCE 671 AA; 76034 MW; 517
                                                                                             Pseudomonadaceae; Pseudomonas.
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Best Local Similarity 69.2
Matches 9; Conservative
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Gaps

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Length 853;

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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 853 AA; 95995 MW; 85E4A320F516B1B2 CRC64;
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50.0%; Pred. No. 1.1e+02;
ive 3; Mismatches 5; Indels
                                                                    AIDS Res. Hum. Retroviruses 16:1183-1189(2000).
            CRF02.AG subtype G recombinants.";
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les 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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MEDLINE=20418941; PubMed=10954895;
Janssens W., Salminen M.O., Laukkanen T., Heyndrickx L.,
Janssens W., Solminen M.O., Laukkanen T., Heyndrickx L.,
Van der Auwera G., Colebunders R., McCutchan F.E., Van der Groen G.;
"Near full-length genome analysis of HIV type I CRF02.AG subtype C and
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MEDLINE-22247741; PubMed=12271122;
MEDLINE-22247741; PubMed=12271122;
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraull M., Shetty J., Malek J., Van Aken S.E.,
Hoover D.L., Lindler L.E., Halling S.M., Mbite O., Salzberg S.L.,
The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. US.A., 99:13148-13153(2002).
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                                                                                                                                                        Query Match 52.9%; Score 45; DB 16; Length 729; Best Local Similarity 50.0%; Pred. No. 96; Matches 8; Conservative 5; Mismatches 3; Indels
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Brucellaceae; Brucella.
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                                                          Hydrolase; Complete proteome.
SEQUENCE 729 AA; 78103 MW; 21F7888632E30CDE CRC64;
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SEQUENCE 729 AA; 78147 MW; 964E74BAF188B292 CRC64;
GO; GO:0004035; F:alkaline phosphatase activity; IEA. GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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57 VSEDGKTLIYSDSPYG 72
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nes 8; Conservative
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08FW49
AC 08FW41
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X MEDLINE=21173698; PubMed=11259647;

MEDLINE=21173698; PubMed=11259647;

A Bisen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potcoka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Folonay J.F., Smit J., Darkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

R. Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R. EMBL, AR02954; AAKZ4975.1;

R. FIR, CG3013;
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                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
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                                                                                           Last sequence update)
Last annotation update)
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PRT; 1105 AA.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                Created)
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Pfam; PF00593; TonB_dep_Rec; 1.
                                                                                                                                                                                                                                                                                        Caulobacteraceae; Caulobacter
NCBI_TaxID=155892;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                foung D.C.; Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ULB4,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                              51.8%; Score 44; DB 4; Length 118; 68.8%; Pred. No. 18; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 122;
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122 AA; 13579 MW; 36054D41366545B8 CRC64;
                                                                                                                                                                                                                                  118 AA; 12843 MW; D0633949F2AC149D CRC64;
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Last sequence update)
                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035030; AAD56266.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AA.
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MEDLINE=98277139; PubMed=9614934;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                      HEARP, POLITZ; ZFB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                              2 ISENGRIINYADSVKG 17
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                                                                              EMBL; AF035023; AAD56259.1;
PIR; S21205; S21205.
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                                                                                                                                                                                                                                                                              Local Similarity 68.8
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Matches
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Q9UL84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
Kaplan N., Johnson D., Schutz K., Gnoj L., Hoffman J., Till S.,
de la Bastide M., Granat S., Hameed A., Gottesman T., Hasegawa A.,
Shohdy N., Parnell L., Dedhia N., Johnson A.F., Lodhi M.,
Martfenseen R., Chen E.Y., Wilson R., McCombie W.R.,
"Sequence of A. thaliana BAC T10P11 from chromosome IV.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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PROSITE; PS00678; WD REPEATS 1; 1.
PROSITE; PS50082; WD REPEATS 2; 1.
PROSITE; PS50934; WD REPEATS REGION; 1.
Hypochetical protein; Repeat; WD repeat.
SEQUENCE 3449 AA; 385006 MW; 6BB0DBA778690184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AC002330, AAC78268.1;
EMBL; AL161495; CAB77751.1; -.
                                   01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                Putative transport protein.
T10P11.5 OR AT4G02660.
Arabidopsis thaliana (Mouse-ear cress).
                        Created)
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SMART; SM00320; WD40; 2.
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InterPro; IPR008938; ARM.
InterPro; IPR000409; Beige BEACH.
InterPro; IPR001680; WD40.
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185 VASEGEKTVNYEEKVEG 201
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Pfam; PF00400; WD40; 2.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                        A Obtoko K., Obkuma M., Moriya S., Kudo T.;

Torotists in the hindgut of termite Reticulitermes speratus.";

Torotists in the hindgut of termite Reticulitermes speratus.";

Embi: AB045165; BAA98035.1;

R HSSP; P43316; ZENG.

R O; GO:0008810; F:callulase activity; IEA.

GO; GO:0008810; F:callulase activity; IEA.

R O; GO:0008975; P:carbohydrate metabolism; IEA.

R InterPro; IPR000309; Barwin like.

InterPro; IPR000309; Barwin like.

InterPro; IPR000314; Glyco_Indro_45.

PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.

PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strauberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1;
RGD; GC10005489; F:electron transporter activity; IEA.
GO; GC10006118; F:electron transport; IEA.
RO; GC10000345; CYCC hame—BS.
RINterPro; IPR007110; Ig-1Ïke.
R InterPro; IPR007110; Ig-1Ïke.
R InterPro; IPR007110; Ig-1Ïke.
R InterPro; IPR007156; Ig-V.
R Ffam; PF00047; ig; 3.
R SWART; SM00466; Ig-V.
R PROSITE; PS00190; CYTOCHROME C; 1.
R PROSITE; PS00190; CYTOCHROME C; 1.
R PROSITE; PS00290; IG-MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Family 45 cellulase homologue.
unclassified eukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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nes 9; Conservative
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les 9; Conserv
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                                                                                                          NCBI_TaxID=42452;
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Q91205;
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AC 091200
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Helicobacteraceae; Helicobacter.
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MEDLINE-22709201; PubMed=12810954;
Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.
Schauer D.B., Shen Z., Weber J., Prosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
Helicobacter hepaticus.";
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Pred. No. 94;
1; Mismatches 4; Indels
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EMBL, AE017145; AAP77024.1; -
Hydrolase; Complete proteoners
SEQUENCE 504 AA; 55287 MW; 88BB31A9CSFF2469 CRC64;
                                                                                      Last sequence update)
Last annotation update)
Q7VJ23 PRELIMINARY; PRT;
Q7VJ23;
01-0CT-2003 (TERMELFE]. 25, Last seq
01-0CT-2003 (TERMELFE]. 25, Last seq
01-0CT-2003 (TERMELFE]. 25, Last ann
POF1-type ATP synthase (EC 3.6.3.14)
ATPA OR HH0427.
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27 ISETGKVIAYADGV 40
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                       Helicobacter hepaticus.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=32025;
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Search completed: September 24, 2004, 02:18:47 Job time : 88.4717 secs

2 ISENGRIINYADSVKG 17 |: || |||: ||| |INSGSTTIYYADTVKG 85

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70

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homo sapien influenza a homo sapien

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pseudomonas brucella me

brucella su human immun

samia cynth

Q9a430 caulobacter

ALIGNMENTS

methanobact homo sapien

sapien

P01774

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Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC27165 protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pluvinet R., Estivill X., Escarceller M., Sumoy L., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, Ala89978, CAB97534.1; -. EMBL, POL876; LOWO. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_cl. InterPro; IPR003597; Ig_cl. InterPro; IPR003596; Ig_w. Effect; IPR003596; Ig_w. PP07654; Cl-set; Z.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain variant (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 2;
Pred. No. 0.54;
3; Mismatches
                HV3N HUMAN
HV3K HUMAN
O26670
HV3M HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
                                                                     Q6MZQ6
Q6ZW64
Q6WG02
Q96BB9
                                                                                                                                           Q9BLH9
Q88LF9
Q8YC77
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Q9IV97
Q9A430
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68.8%;
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11 ISSSGDTVDYADSVKG 26
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Best Local Similarity 68.8
Matches 11; Conservative
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494
566
597
640
729
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105
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                                                                                                              April 28, 2005, 17:57:45 ; Search time 109.969 Seconds (Without alignments) 79.162 Million cell updates/sec
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P01763
Q6ddq7
Q9u187
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P01782
P01762
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Q6gmx2
P01781
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Q68cn4 |
Q6ink3 :
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P01768
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Q65zc9
Q8kw71
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Q6n093
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       1612378 segs, 512079187 residues
                                                                                                                                                                                  US-10-088-639A-2_COPY_177_193
85
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09UL53

065ZC9

065ZC9

068ZV7

068ZV7

068ZV7

061W3

061W3

06GWY2

06WUX1

HV03 CARAU

HV03 CARAU

09UL71

HV3G HUWAN
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HV3U_HUMAN
HV3A_HUMAN
Q9HCC1
HV16_MOUSE
Q6N089
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HV3B HUMAN
Q6DDQ7
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Q6MZV6
Q6PDB8
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Gapop 10.0 , Gapext 0.5
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Q88FX8
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Gaps

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499

Length 416; Indels

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HSSP; P01772; 2PB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                 11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=MGC69066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Hopkins R.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bahat N.K.,
A Hopkins R.F., More T., Max S.I., Wang J., Heich F.,
B pietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B monstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nichards S., Worley D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated galactose
in Klebsiella polysaccharides K730 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 54; DB 2; Length 499; 68.8%; Pred. No. 3; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93A5C89582054F32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig heavy chain V-III region WEA.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCEPPO; IPRO07110; IG-like.
INCEPPO; IPRO03597; IG_C1.
INCEPPO; IPR003597; IG_C1.
INCEPPO; IPR003596; IG_WHC.
INCEPPO; IPR003596; IG_V.
Pfam; PF07654; C1-set; Z.
Pfam; PF07654; C1-set; Z.
Pfam; PF07654; IG; 1.
PROSITE; P550835; IG_LIKE; 4.
PROSITE; P550835; IG_LIKE; 4.
PROSITE; P550835; IG_MHC; UNKNOWN 1.
SEQUENCE 499 AA; 53376 MW; 93A5C89
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Best Local Similarity
                          SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Blood;
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P01763;
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against 3,4-pyruvylated galactose and isolated from a patient with Waldenstrom's macroglobulinemia.
--- Instructive Contains 1 immunoglobulin-like domain.
PIR, A02046; WHUWE.
HSSP, P01772; 2FB4.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Pyrrolidone carboxylic acid.
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SMART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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NCBI_TaxID=9606;
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05-JUL-2004
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P01782;
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                            Q8WU38
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           RESULT 6
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'Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                               60.0%; Score 51; DB 2; Length 614; 64.7%; Pred. No. 12; ive 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                             TISSUB-Spleen;
Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC07477; AAH77477.1; -.
                                                                                                                                                        104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;
          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035027; AAD56263.1; -.
HSSP; P01810; 2FBJ.
InterPro; IFR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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                                                                                   Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR003596; Ig MHC.
Interpro; IPR003596; Ig WHC.
Interpro; IPR003596; Ig v.
                                                                                                                                                                                                                                                                                       1 VISENGRIINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ISENGRIINYADSVKG 17
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                                                                                                                                                                                                                                                                   11; Conservative
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les 11; Conservative
                                                                                                                                           Pfam; PF07654; Cl-set; 4.
Pfam; PF00047; ig; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
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                                       SEQUENCE FROM N.A.
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XI TISSUB=Primary B-Cells;

XI Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XI Strausherg R.L., Zeeberg B.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B.B., Barder C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Brocherton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton E., Ketteman M., Madan A., Xoung A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marra M.A.,

Y Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1; -.
PIR; S21205; S31205.
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                                                     20, Created)
20, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
573 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.8%; Score 50; 68.8%; Pred. No.
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Pfam; PF07654; C1-set; 2.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; P550835; IG_LIKE; 4.
PROSITE; P500290; IG_MHC; UNKNOWN_2.
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573 AA; 62967 MW;
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les 11; Conservative
PRELIMINARY;
                                                                                                        01-MAR-2004 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human).
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TISSUE=Primary B-Cells;
                                                                                   (TrEMBLrel.
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51 INWNGGSTGYADSVKG 66
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InterPro; IPR003596; Ig_v.
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nes 10; Conservative
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nes 10; Conserv
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01-MAR-2001 (
01-OCT-2003 (
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P01783;
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0
                                                                                                                                                                                                                                                                                         deletion.";
Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: This gamma-1 myeloma protein has a deletion in the hinge region. There are no light-heavy or inter-heavy chain disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The antho acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-!- MISCELLANEOUS. The sequence of the C region is also given.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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05-JUL-2004 (Rel. 44, Last annotation update)
1g heavy chain V-III region TRO.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  Steiner L.A., Lopes A.D.; "The crystallizable human myeloma protein Dob has a hinge-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                       Steiner L.A., Garcia Pardo A., Margolies M.N.; Margolies of the leavy-chain variable region of the crystallizable human myeloma protein Dob."; Biochemistry 18:4068-4080(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE-76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
Hilschmann N.;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AA; 13440 MW; 880DDE307C4B2627 CRC64;
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PIR; A90431; G1HUDB.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                         CRYSTALLIZATION.
MEDLINE=80020920; Pubmed=114208;
                                                                                   MEDLINE=80020921; PubMed=114209;
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21-JUL-1986 (Rel. 01, Last seq
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51 ITWNGGSVLYADSVKG 66
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                       NCBI_TaxID=9606;
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P01762;
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MEDLINE-81234548; PubMed-6788376; DOI=10.1016/0092-8674(81)90089-1;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%; Score 48; DB 2; Length 112; 62.5%; Pred. No. 5.9; .tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                               57.6%; Score 49; DB 1; Length 122; 62.5%; Pred. No. 4.4;
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; --

HSSP; P01783; 11GC.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

SMART; SM00406; IGV; 1.-

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                       Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                              122 122
122 AA; 13472 MW; 2E21A11DA04DB0F9 CRC64;
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112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
19 heavy chain V region MOPC 21 precursor (Fragment).
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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TISSUE-Spleen;

MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hang L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlywik S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nichards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Riczywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                          11 SEQUENCE FROM N.A.

12 TISSUE=Human rectum tumor;
13 THe German Human cDNA Consortium;
14 Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
15 Submitted (Aug_-2003) to the EMBL/GenBank/DDBJ databases.
16 Submitted (Aug_-2003) to the EMBL/GenBank/DDBJ databases.
17 Style (Aug_-2003) to the EMBL/GenBank/DDBJ databases.
18 FASP; PO1861; 1ADQ.
18 RASP; PO1861; 1ADQ.
19 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
10 RICEPPO; IPR003599; Ig_-1.
11 SWART; SW00409; IG_-1.
12 SWART; SW00409; IG_-1.
13 SWART; SW00406; IG_-1.
14 RESIDER PROSITE; PSC03599; IG_-MHC; UNKNOWN_2.
                                                                                                               Bukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotherical protein DKFZp686F15220.
Name=DKFZp686F15220;
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70 ISWNSGSIAYADSVKG 85
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                                                                                                       Homo sapiens (Human)
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Matches 11; Conserv
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
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D segment.
JH4 segment.
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                                                                      MEDLINE=77100366; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
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-> H (in Ref. 2).
-> W (in Ref. 2).
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56.2%; Pred. No. 7.3;
iive 3; Mismatches
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PDB; 11GC; X-ray; H=-.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.
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Matches 9; Conservative
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136
136 AA;
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PRELIMINARY;

Q6N089 Q6N089;

RESULT 11 Q6N089 ID Q6N08 AC Q6N08

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Length 472; Indels

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  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hilschmann N.;
Submitted (JUN-1975) to the PIR data bank.
-!- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 30;
4; Mismatches 3; Indels
                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073771; AAH73771.1; -
                                                                                                                                                                                                                                                                              52865 MW; 55B999305B286203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macroglobulin.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02064; M3HUGL.
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PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 112 IG-like.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
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                                                                                                                     InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF07654; C1-set; Z.
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INSDGSSTSYADSVKG 85
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Best Local Similarity 50.4.
Best Occupantive
9; Conservative
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SMART; SM00407; IGC1; 3
SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 493 AA;
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                                                             SEQUENCE FROM N.A.
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                                                                           rissum=spleen;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
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                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 116;
                                                       DB 1; Length 116;
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116
12730 MW; 2C67CA9AAAA1282 CRC64;
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Last annotation update)
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EMBL, AF035021, AAD56257.1; -.

PIR, PH1644; PH1644.

PIR, PL0120; PL0120.

HSSP, P01772; 2FB4.

InterPro; DF007110; Ig-like.

InterPro; IPR001710; Ig-like.

InterPro; IPR001710; Ig-like.

InterPro; IPR001596; Ig-v.

SMART; SM00406; IGV; I.

NON TER 116 116
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                                                       55.3%; Score 47; 50.0%; Pred. No.
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                                                                                                                                            2 ISENGRIINYADSVKG 17
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51 IKZBGSZZBYVDSVKG 66
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                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL, Y13056; CAA73499.1; -.

DR InterPro; IPR003599; Ig.,

DR InterPro; IPR00710; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SW00409; IG; 2.

DR SMART; SW00406; IGv; 2.

DR PROSITE; PS50835; IG_LIKE; 2.

FT NON_TER 240 240

SQ SEQÜENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
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 Query Match
 55.3%;
 Score 47;
 DB 2;
 Length 240;

 Best Local Similarity 64.7%;
 Pred: No. 20;
 No. 20;
 Indels

 Matches 11;
 Conservative 1;
 Mismatches 5;
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N. gonorr Peptide # Peptide #

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                                           6; Search time 83.6415 Seconds (without alignments)
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      GenCore version 5.1.6
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                                                                  US-10-088-639A-2_COPY_226_238
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                                           September 24, 2004, 01:32:26
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Maximum Match 100%
Listing first 150 summaries
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Rat skin

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Energen-r Human ZAD

"note= "Complementarity determining region (CDR) 1 of the light chain" 'note= "Complementarity determining region (CDR) 2 of the

ocation/Qualifiers

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Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                       26-OCT-2000; 2000WO-SE002082.
                                                                                                                                         (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                              WPI; 2001-308619/32.
N-PSDB; AAF84797.
                                                                                                     WO200130854-A2
                                                                                                                                28-OCT-1999;
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Nilson BHK;
                                                                                                              03-MAY-2001
                                               Peptide
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/note= "Complementarity determining region (CDR) 1 of the heavy chain" 226. .238

'note= "Complementarity determining region (CDR) 1 of the

"linker"

12 'note=

.162

neavy chain"

note= "Complementarity determining region (CDR) 3 of light chain"

ight chain"

/note= "Complementarity determining region (CDR) 1 of the heavy chain"

Kearney PP;

Tordsson MJ,

Ohlsson LG,

Karlstroem PJ,

99SE-00003895

## ALIGNMENTS

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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;
tumour-associated antigen; metastatic disease; malignant disease;
tumour typing; tumour screening; tumour.
                                                                                                      An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                         AAB68087 standard; protein; 249 AA
                                                     AAB68087;
RESULT 1
               AAB68087
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Synthetic. Macaca fascicularis.

RESULT 2 AAU64492 ID AAU64492 standard; protein; 527 AA. |||||||||||||||||||||| EGGPGTTSNRLDA 238 EGGPGTTSNRLDA 13 226 Q ò

ö The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, in vito, in vivo diagnosis and prognosis of human malignant disease, compressing tumour tryping, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to tumour deposits in humans Gaps ö 4; Length 249; 100.0%; Score 69; DB 4; Length 24 clarity 100.0%; Pred. No. 0.0031; Conservative 0; Mismatches 0; Indels Claim 1; Page 55-56; 75pp; English. Query Match Best Local Similarity Matches 13; Conserv Sequence 249 AA;

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

immunostimulant; immune response; vaccine; immunogenic

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

Propionibacterium acnes immunogenic polypeptide #29377.

(first entry)

20-OCT-2003

ABM64701;

```
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                          Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                  Propionibacterium acnes immunogenic protein #25388
                                                                                                      dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 25687; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                      02-JUN-2000; 2000US-0208841P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.8%;
80.0%;
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                                                                                                                                                                                                             21-APR-2000; 2000US-0199047P.
                              (first entry)
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les 8; Conservative
                                                                                                                           Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                             treating acne vulgaris.
                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                         2001-616774/71.
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS59645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 527 AA;
                                                                                                                                              WO200181581-A2
                              27-FEB-2002
                                                                                                                                                                                                                     02-JUN-2000;
                                                                                                                                                                   01-NOV-2001
          AAU64492;
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Best Local S
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New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Claim 7; SEQ ID NO 29377; 1481pp; English

Maisonneuve JL; Jones R, Carter D;

Bhatia A, Benson DR,

Persing DH, Lodes MJ,

Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36.

Skeiky YAW,

Mitcham JL,

(CORI-) CORIXA CORP

11-OCT-2002; 2002WO-US032727. 15-OCT-2001; 2001US-00978825.

```
The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polymeptides encoded by the polymucleotides (BBM35624-ABM64536) and to immunogenic fragments of P. acnes polymeptides. The invention additionally encompasses expression vectors and host cells comprising a comprising a polymeptide cells comprising a polymeptide of the invention; antibodies against polymeptides of the invention; and the invention; and the invention; and the invention; and the invention; and the invention; and polymeptide and an isolated T cell population comprising T cells prepared polymeptide and an isolated T cell population comprising T cells prepared to the invention; and method; usion proteins, T cell populations, or antigen-presenting cells that express the polymeptide); a method and kit conditions the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; The P. acnes polymeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymeptides are useful for inhibiting the development of P. acnes in a patient; The polymucleotides can also be used as probes or primers for uncleic acid hybridisation. The vaccine composition is useful for the vocatine composition is useful for the vaccine composition is useful for the printed preception of an immune response against P. acnes polymeptide which is thought to contain an immunogenic region. Note: The sequence data for this patent did not form part of the printed specification, but was the contained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Length 527;
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80.0%; Pred. No. 92;
ive 1; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne by acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting the sample with a canes infections. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as call agains and the protein and activity of P. acnes polypeptides and chagnostic agents for determining P. acnes presence, for example, by canzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was considered and activities of the printed specification, but was considered and activities of the printed specification, but was considered and activities.
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Gaps

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GGPGTASHRL

ABM64701 standard; protein; 527 AA.

RESULT 3 ABM64701

|||||| |:|| GGPGTASHRL 16 2 GGPGTTSNRL 11

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The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides. ABMA3562-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; antibodies polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide of the invention; a comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide, autient polymetrial or comprising P. acnes polypeptides, polymetrials, and method an autient express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; The P. acnes polypeptides, polymelectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes polymetrials, or for stimulating an immune response specific for a P. acnes for unclair acid hybridisation. The polymuclectides can also be used as probes or priners for nucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The preating account the kit is useful for performing a diagnostic assay. The preasent cand the kit is useful for performing a diagnostic assay. The preasent cand the kit is useful for performing a diagnostic assay. The preasent cand the kit is useful for performing a diagnostic assay. The preasent cand the printed specification, but was obtained in electronic format directly from Wipo at ftp.vubo.int/published_pot_esquance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #25687.
                                                                                                                                                                                                                               Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes MJ,
                                      ABM61011 standard; protein; 527 AA.
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Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001; 2001US-00978825.
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7hang Y. Wang S, Jen S,
                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                    WO2003033515-A1.
                                                                                                                                     20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2003
                                                                                         ABM61011;
RESULT 4
                        4BM6101
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Carter D;

Maisonneuve JL; Jones R, Carte

Bhatia A, Benson DR,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 4; Lengtn 77.)
Pred, No. 1.9e+02;
                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 8199
                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP76682 standard; protein; 19938 AA.
                                                                                     ABB60469 standard; protein; 749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%;
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                              Drosophila melanogaster.
Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
N-PSDB; ABL04572.
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                                                                                                                                                                                                                    pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions.
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                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                     Drosophila;
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                                                                                                                 ABB60469;
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63.8%; Score 44; DB 6; Length 527; 80.0%; Pred. No. 92; iive 1; Mismatches 1; Indels

Gaps

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Length 224; 1; Indels

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acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAV7814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis.
                           New human nucleic acid sequences from pancreatic tumors, and related
                                                                                     This invention describes novel polypeptides and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen SEQ ID NO:13317.
                                                                                                                                                                                                        Score 40; DB 2; I
Pred. No. 1.7e+02;
I; Mismatches 1;
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                                                             Claim 23; Page 422; 502pp; German
                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                         58.0%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                          AAM85724 standard; protein;
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   N-PSDB; AAZ52948
                                                                                                                                                                                    Sequence 224 AA;
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                                                                                                                                                                                                                                                                                                                 virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
                                                                                                                                                                                                                                                                                                     The invention relates to avilamycin derivatives (I) with antibacterial,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
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Pred. No. 1.2e+04;
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                                                                                                                                                                                  Bechthold A;
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                                                                                                                                                                                  Muehlenweg A, Trefzer A,
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                                                                                                                                                                                                                                                                               Example 1; Page 68-301; 319pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY74086 standard; protein; 224 AA
                                                                                                                                                          (COMB-) COMBINATURE BIOPHARM AG
                                     Streptomyces viridochromogenes
                                                                                                           24-AUG-2001; 2001WO-EP009815.
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nes 8; Conserv
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                                                          WO200268436-A1
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2000US-0232399P.
2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
2000US-0233064P.
2000US-0233065P.
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2000US-0237040P.
2000US-0239935P.
                                                                             2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
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2000US-0229287P.
2000US-0229343P.
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2000US-0241221P.
2000US-0241785P.
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2000US-0241808P.
2000US-0241809P.
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2000US-0244617P.
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                      2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
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                                                                                                                                         2000US-0227182P
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14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
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01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
30-AUG-2000; 2
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02-0CT-2000;
02-0CT-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
creatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
creatment of diseases to treat disorders associated with decreased
creatment of diseases used to treat disorders associated with decreased
creatment they may be used to treat disorders in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting the
creation of the nest into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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2000US-0246532P.
2000US-0246609P.
2000US-0246611P.
2000US-0246613P.
2000US-024920P.
2000US-0249209P.
2000US-0249210P.
2000US-0249211P.
2000US-0249213P.
2000US-0249213P.
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2000US-0250391P.
2000US-0251030P.
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2000US-0249216P.
2000US-0249217P.
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2000US-0256719P.
2000US-0251479P.
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2001US-0259678P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251856P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483426/52.
N-PSDB; AAK58505.
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05-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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0; Gaps

56.5%; Score 39; DB 4; Length 77; 63.6%; Pred. No. 84; 1; Mismatches 3; Indels tive

Query Match 56.5 Best Local Similarity 63.6 Matches 7; Conservative

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody scapable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a containing an antibiotic; (10) profiling a containing a containing an antibiotic; (10) profiling a containing a containing an antibiotic; (10) profiling a containing a containing an antibiotic; (10) profiling a containing a containing and antibiotic; (10) profiling a containing a containing and antibiotic; (10) profiling and antibiotic; (10) profiling and antibiotic; (10) profiling and antibiotic; (10) profiling and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and antibiotic; (10) and ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #27084.
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                                                                                                                                                                                                            ABU41557 standard; protein; 130 AA.
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-01942921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                  (first entry)
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                           EGGPGTTSNRL 11
                                                                       EGGPGRASRRV 57
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas syringae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2.
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Wall D,
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The invention describes an isolated mammalian secreted polypeptide (MSP) (I). (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide, to screen for cell metabolism effecting receptors, for identifying new target receptors and drug design, for identifying for protein purification, for determining the weight of expressed MSP polypeptides as ratio to total protein expressed, for identifying peptide cleavage sites, for monitoring biological activities of the protein in vitro and in vivo, and to teach analytical skills and as reagents for the study of cells, receptors, and other binding molecules. The polymucleotide is useful for radiation hybrid mapping, and somatic cell genetic technique developed for constructing high-resolution, contiguous maps of mammalian chromosomes. Reagents disclosed in the contiguous maps of mammalian chromosomes. Reagents disclosed in the method of the mammalian secreted polypeptide, described in the method of the
                                                                                                                                                                           ö
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits.
                                                                                                                                                                             Gaps
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                                                                                                                                       Length 130;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein secretion; mammalian secreted polypeptide; MSP
                                                                                                                                                       1.4e+02;
                                                                                                                                     56.5%; Score 39; DB 6;
61.5%; Pred. No. 1.4e+02
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 194-195; 397pp; English
                                                                                                                                                                                                                                                                                                                                                      AAU83139 standard; protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted protein Z838027G3P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2001; 2001WO-US020638
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                               Conservative
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N-PSDB; ABK33054.
                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                   Sequence 130 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          AAU83139;
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

pharmaceutical

23-MAR-2001; 2001WO-US009231.

Drosophila melanogaster polypeptide SEQ ID NO 32385.

26-MAR-2002 (first entry)

ABB68531;

ABB68531 standard; protein; 302 AA.

QGGPGSTNSKRQA 122

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The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynuclectides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                              Neuroprotective; immunomodulator; cancer; chromosome 15; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J, Zhao QA, Ren F;
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     Score 39; DB 5; Length 219;
Pred. No. 2.5e+02;
5; Mismatches 2; Indels
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T, Drmanac I
                                                                                                                                                                                  ABP43778 standard; protein; 296 AA.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001; 2001WO-US027760.
      56.5%;
46.2%;
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                                                                                                                                                                                                                                                (first entry)
                                                                    1 EGGPGTTSNRLDA 13
                                      6; Conservative
                                                                                         GGGPGSTNSKRQA
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABQ61022
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200231111-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                  ABP43778;
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                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL01840-ABL16175) and the encoded proteins (ABB0181737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 3.5e+02;
5; Mismatches 0; Indels
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                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                   2001-656860/75
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Best Local Similarity
Matches 6; Conserv
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N-PSDB; ABL12634.
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Gaps

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56.5%; Score 39; DB 5; Length 296; 46.2%; Pred. No. 3.4e+02; ive 5; Mismatches 2; Indels

Ota T,

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The present sequence is encoded by a liver-associated gene. The expression level of this gene changes in liver (hepatic) cancer. Liver-associated gene can be used as markers in blood tests for screening for the early stages of the liver cancer. The encoded proteins and peptides can also be used as targets for screening for compounds to treat the disease. They can also be used for predicting the progress of the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
T, Hippo Y, Taniguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genes and their proteins found in hepatic cancer, vectors, antibodies, and screening method for compounds with binding activity, useful as diagnostics and targets for treatment agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Liver-associated gene; hepatic cancer; liver cancer; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%; Score 39; DB 4; Length 396; 46.2%; Pred. No. 4.6e+02; ive 5; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis cellular proliferation protein #394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 79-80; 99pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU35107 standard; protein; 454 AA.
                                                                                                                                                                        28-JUL-2000; 2000WO-JP005064.
                                                                                                                                                                                                                       99JP-00248036
                                                                                                                                                                                                                                            99JP-00300253
                                                                                                                                                                                                                                                              99US-0159590P.
                                                                                                                                                                                                                                                                                                          17-FEB-2000; 2000US-0183322P.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                                                                                                                                                                                                                        09-JUN-2000; 2000JP-00241899
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210 QGGPGSTNSKRQA 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii S, Sugiyama T
Kodama T, Hippo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-541221/60.
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Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH77810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200170955-A2
                                                                                     WO200109318-A1
                                           Homo sapiens.
                                                                                                                                                                                                                                                                                     11-JAN-2000;
                                                                                                                                                                                                                                            27-AUG-1999;
18-OCT-1999;
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                                                                                                                                 08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T,
Ishii S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an Oilgo-dr primer and an Oilgoncoleotide comprisent to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the collsonucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end comprises a 1'-end sequence complementary to a polynucleotide comprises a 1'-end sequence complementary to a polynucleotide comprises a 1'-end sequence, where the combination of the 5'-end sequence 3'-end sequence in an oilgonucleotide comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the specification The primer sets can be used in antisense therapy and in specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent complexities, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 15405; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 4; Length 396; Pred. No. 4.6e+02; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                           Saito K, Ya
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human liver-associated gene.
                                                                                                                                                                                                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG67257 standard; protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                         ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
99-JUN-2000; 2000JP-00241899.
                                                                                                                                                 28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.5%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                           Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
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                    Homo sapiens.
                                                            EP1074617-A2
                                                                                                                                                                                           29-JUL-1999;
                                                                                                     07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG67257;
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RESULT 14 AAG6725

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Gaps

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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                              υŗ
                                                              Wang |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
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  임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia chamselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalls. The invention is also useful for the identification of potential new targets for antibiotic conceptule used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for nomologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                            Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%; Score 39; DB 4; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 5.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #14736.
                                                                                                                                                                                                                            Example 3; SEQ ID NO 10700; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU29209 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                   27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
           2000US-0207727P.
                                                             16-FEB-2001; 2001US-0269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.08;
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                                                                                                              Ohlsen KL,
                                                                                      ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 GRPGTFSNRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis.
                                                                                                                           Xu HH;
                                                                                                                                                  2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                              N-PSDB; AAS52966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 454 AA;
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                                                                                                              Haselbeck R,
Yamamoto RT,
                        23-OCT-2000;
             26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU29209;
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The invention relates to an isolated in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid conditions are polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular consideration or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway considered for proliferation, (7) identifying a compound that inhibits proliferation of an equired for proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture or collection of an organism. The antisense mucleic acids required identifying proteins or screening for homologous nucleic acids required in organism. The antisense mucleic acids required in organism. The antisense mucleic acids required in the collection of an organism. The antisense mucleic acids required in the collection of an organism. The antisense mucleic acids required in a cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human; antiparkinsonian; virucide; antibacterial; antifungal; antimigraine; analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
                                                                               Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                               Ohlsen KL,
Forsyth RA,
                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 57133; 1766pp; English.
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                                                                                    Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein kinase SGK146.
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(ELIT-) ELITRA PHARM INC.
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                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 GRPGTFSNRL
                                                                                                                                                                                                           WPI; 2003-029926/02.
N-PSDB; ACA33079.
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c interingue polynotections are useful for treating a disease or disorder such as cancer, immune-related diseases, cardiovascular disease, polypeptides and their modulators are useful for treating a disease or disorder such as cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, and disorders, attention disorders, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, dyskinesias, metabolic disorders, and organ transplant rejection. They are also useful to retarting thinitis, autoimmunity, atherosclerosis, psoriasis, concearthritis, asthma, chronic inflammatory pelvic disorders neumatoid arthritis, metabolic disorders of inflammatory bowel disease, rheumatoid arthritis, metabolic disorders of cortarions diseases such as glaucoma, retinopathy and macular degeneration, injury, coronary thrombosis, clotting disorders and atherosclerosis, cullar diseases such as glaucoma, retinopathy and macular degeneration, dementia, manic depression, etc. The polymucleotides are useful in gene therapy techniques to treat the above mentioned disorders. Sequences therapy techniques to treat the human protein kinases of the invention
antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropic; antidiabetic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides human protein kinases and protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manning G, Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 215; 218pp; English.
                                                                                                                                                                                                                                                               25-JAN-2000; 2000US-0178078P.
31-JAN-2000; 2000US-0179364P.
17-FEB-2000; 2000US-018173P.
17-MAR-2000; 2000US-0190162P.
29-MAR-2000; 2000US-0193404P.
13-NOV-2000; 2000US-0247013P.
                                                                                                                                                                                                                        25-JAN-2001; 2001WO-US002337
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N-PSDB; AAH46903.
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                                                                                                                                    WO200155356-A2
                                                                                            Homo sapiens
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                        56.5%; Score 39; DB 4; Length 600; 87.5%; Pred. No. 7.1e+02; ive 0; Mismatches 1; Indels
                                      Local Similarity 87.9
                                                                                1 EGGPGTTS 8
Sequence 600 AA;
                         Query Match
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AAE24147 standard; protein; 600 AA. EGGPGATS 194 187 RESULT 18 AAE24147 셤

AAE24147;

23-SEP-2002 (first entry)

Human kinase (PKIN)-18 protein.

Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hlv; neuroprotective; hepatotropic; hypetensive; cardiant; nephrotropic; hyperlipidaemia; enzyme.

Homo sapiens

278. .535 /note= "Eukaryotic protein kinase domain" 280. .525 /note= "Protein kinase domain" 'note= "Protein kinase domain" Location/Qualifiers . 526 Domain Domain Domain

WO200233099-A2

25-APR-2002

20-OCT-2001; 2001WO-US047728

20-OCT-2000; 2000US-0242410B. 27-OCT-2000; 2000US-0244068B. 03-NOV-2000; 2000US-024508P. 09-NOV-2000; 2000US-02476722. 16-NOV-2000; 2000US-0249565P.

22-NOV-2000; 2000US-0252730P. 01-DEC-2000; 2000US-0250807P.

(INCY-) INCYTE GENOMICS INC.

Lal PG; Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, L Recipon SA, Lu DAM, Borwaky ML, Thornton M, Swarnaker A; Thangavelu K, Khan FA, Ison CH;

WPI; 2002-454603/48. N-PSDB; AAD38861. New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.

Claim 1; Page 171-172; 210pp; English.

The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, charled and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (ALDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting, cardiovascular disorder (e.g., hypertension, myocardial infarction, cardiovascular disorder (e.g., hypertension), myocardial infarction, cardiovascular disorder (e.g., hypertension), myocardial infarction, cancher's disease, hypercholasterolaemia, hyperlipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a biological sample. A composition comprising PKIN or an agonist of principle of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN bNA is useful for creating knockin humanised animals or transgenic animals to model human diseases,

Gaps

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Length 609

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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Score 39; DB 3; Lengtn vv. Pred. No. 7.2e+02;
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                                                                                           1; Mismatches
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11-JUL-2000; 2000US-00614150.
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Delymoleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardioactive; immunomodulatory; muscular active; vulnerary; asstrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
and in somatic or germline gene therapy. The present sequence is human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer associated polypeptide sequence SEQ ID 797.
                                                                                                                                                           Score 39; DB 5; I
Pred. No. 7.1e+02;
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(ROSE/) ROSEN
                              PKIN protein
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Disclosure; SEQ ID NO 16845; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%; Score 39; DB 4; Le. llarity 77.8%; Pred. No. 1.4e+03; Conservative 0; Mismatches 2;
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ID ABB6
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Sequence 609

08-MAR-2000; 2000WO-US005881.

WO200055173-A1

21-SEP-2000.

Homo sapiens.

(HUMA-) HUMAN GENOME SCI INC.

12-MAR-1999;

Rosen CA, Ruben SM; WPI; 2000-611515/58.

N-PSDB; AAF21981

ABB60494;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breast and ovarian cancer associated antigen protein sequence SEQ ID 786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 4; Length 125
Pred. No. 1.5e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                  Drosophila melanogaster polypeptide SEQ ID NO 8274.
                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB59078 standard; protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.5%;
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1233 ESGQPTTSNQLD 124
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                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75
                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL04597
                                                                                                                                                                                          WO200171042-A2.
                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001
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Best Local S
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proteins AAP21614 - AAP22031 represent DNA sequences encoding human proteins AAB59711 - AAB59128. The DNA and protein sequences are proteins AAB59711 - AAB59128. The DNA and protein sequences are sesociated with breast and ovarian cancer. Included in the invention are sequences AAP22032 - AAP22040 and AAB59129 which are used in the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; noctropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidabetic; antifungal; antiple are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                    New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NOVX; cardiomyopathy; atherosclerosis; cell signal processing; breast cancer; Alzheimer's disease, epilepsy; Huntington's disease; anxiety; behavioural disorder; multiple sclerosis; myathenia gravis; neurodegeneration; Parkinson's disease; pain; stroke; endometriosis; autoimmune disease; allergy; addiction; asthma; transplantation; graft versus host disease; systemic lupus erythematosus; scleroderma; psoriasis; Crohn's disease; HIV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fatty-acid binding protein-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1249-1250; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG76902 standard; protein; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infectious diseases
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 102 AA;
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disease, pancreatitis, renal tubular acidosis, skin disorders,

kidney

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(CURA-) CURAGEN CORP.
                                                                                                WPI; 2002-590434/63.
                                                                                                  N-PSDB; ABS59331.
                                  WO200233087-A2
                                                                                        Padigaru M,
Zerhusen BD,
                              Homo sapiens,
                                              17-OCT-2000;
                                      25-APR-2002.
                                                                                    Edinger S,
                                                                                            Gorman L;
                                                                                                             diabetes.
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atherosclerosis; cirrhosis; rheumatoid arthritis; diabetes; pancreatitis; thrombocytopenia; bleeding disorder; metabolic disorder; obesity; glucose transport defect; glomerulonephritis; hypercalcaemia; polycystic kidney disease; renal tubular acidosis; skin disorder; congenital diarrhoea; respiratory disease; gastro-intestinal disease; muscle disorder; bone disorder; joint disorder; skeletal disorder; haematopoietic disorder; urinary system disorder; septemoresis; dental infection; growth disorder; reproductive disorder; hypogonadism; fertility disorder; viral infection; gene therapy; zinc metalloprocease; ADAM-TS 7; alpha-2-macroglobulin precursor; ileal sodium/bile acid corransporter; prohibitin; MT; CIP4; spinesin; macrophage stimulating protein precursor; fatty acid-binding protein; gap junction beta-5 protein; hepsin/plasma transmembrane serine protease. e.g. Shimkets RA; Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating cancer, Alzheimer's disease, cardiomyopathy, metabolic disease and Macdougall JR, Malyankar UM, Smithson G; Burgess CE; Fernandes ER; Peyman JA, Stone DJ, Gunther E, Ellerman K, S. Guo X, Patturajan M, Taupier RJ, Burgess CE; J. Kekuda R, Spytek KA, Gangolli EA, Pernandes 17-OCT - 2000; 2000US - 0241058P. 17-OCT - 2000; 2000US - 0241058P. 17-OCT - 2000; 2000US - 0241152P. 23-OCT - 2000; 2000US - 0242482P. 23-OCT - 2000; 2000US - 0242482P. 23-OCT - 2000; 2000US - 0242611P. 23-OCT - 2000; 2000US - 0242611P. 24-OCT - 2000; 2000US - 0242880P. 24-OCT - 2000; 2000US - 0242881P. 29-DEC - 2000; 2000US - 0259028P. 20-FEB - 2001; 2001US - 0269813P. 25-APR-2001; 2001US-0286324P. 29-MAY-2001; 2001US-0294108P. 17-OCT-2001; 2001WO-US032496 09-JUL-2001; 2001US-0303698P 16-OCT-2001; 2001US-00981151 Gerlach V,

Claim 1; Page 78; 305pp; English.

24-MAY-1999; The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a NOVX-sesociated disorder, such as cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway could in humans. NOVX polypeptides, nucleic acids and antibodies are modulation in humans. NOVX polypeptides, nucleic acids and antibodies are useful for treating or preventing disorders or syndromes including breast cancer, Alzheimer's disease, epilepy, Huntington's disease, autoimmune disease, behavioural disorders, multiple sclerosis, myasthenia gravis, allergies, addiction, asthma, endometricosis, graft versus host disease, systemic lupus erythematosus, scleroderma, transplantation, psoriasis, crohn's disease, HIV (human immunodeficiency virus) infection, atherosclerosis, cirrhosis, rheumatoid arthritis, diabetes, carbonemia, bleeding disorders, metabolic disorders, obesity, thrombocycopenia, bleeding disorders, metabolic disorders, obesity, glucose transport defect, glomerulonephritis, hypercalcaemia, polycystic

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      congenital diarrhoea, respiratory disease, gastro-intestinal diseases, muscle, bone, joint and skeletal disorders, haematopoietic disorders, urinary system disorders, osteoporosis, dental disease and infection, growth and reproductive disorders, hypogonadism, fertility, and/or other pathologies and disorders, viral, bacterial, or parasitic infections. The present amino acid sequence represents a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                              Gaps
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                                                                                                       Score 38; DB 5; Length 134; Pred. No. 2.2e+02;
                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 28250.
                                                                                                                            2; Mismatches
                                                                                                                                                                                                                           AAG24538 standard; protein; 174 AA.
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99US-01308510P.
99US-01318991P.
99US-0131449P.
99US-013240PP.
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99US-0126785P.
99US-0127462P.
99US-0128234P.
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99US-0135353P.
99US-0135629P.
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                                                                                                      55.1%;
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                                                                                                      Query Match
Best Local Similarity 53.8%
Matches 7; Conservative
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                  1 EGGPGTTSNRLDA 13
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25 EGGVGTALRKMDA 37
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                   Sequence 134 AA;
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99US-0147038P. 99US-0147204P. 99US-0147302P.	99US-014/192F. 99US-0147260P.	99US-0147303P.	99US-0147493P.	99US-0147935P.	99US-0148319P.	99US-0148341P.	99US-0148684P.	99US-0149368P.	99US-0149175P.	99US-0149426P.	990S-0149722F.	99US-0149929P.	99US-0149902P.	99US-0149930P.	99US-0150884P.	99US-0151065P.	99US-0151066P.	99US-0151080P.	990S-0151303F.	99US-0151930P.	99US-0152363P.	99US-0153070P.	99US-0153758P.	99US-0154018P.	99US-0154059F.	99US-0155139P.	99US-0155486P.	99US-0155659P.	99US-0156596P.	99US-0157117P.	99US-0157753P.	99US-0157865F.	99US-0158232P.	99US-0158369P.	99US-U159293F.	99US-0159295P.	99US-0159329P.	99US-0159330P.	99US-0159551F.	99US-0159638P.	99US-0159584P.	99US-0160741P.	9903-0160/6/2.	99US-0160770P.	99US-0160814P.	99US-0160815P.	99US-0160981P.	99US-0160989P.	99US-0161404P.	99US-0161405P.	99US-0161359P.	99US-0161360P.	99US-0161361P.	99US-0161992P.
03-AUG-1999; 04-AUG-1999; 04-AUG-1999;																																																						
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25-MAY-1999; 27-MAY-1999; 28-MAY-1999;	1-00N-199 3-JUN-199	4-JUN-199	8-JUN-199	0-1000-0	4-JUN-199	6-JUN-199	661-NDC-2	8-JUN-199	8-JUN-199	8-JUN-199	9-1-NUL-8	8-JUN-199	8-JUN-199	8-JUN-199	8-JUN-199	8-JUN-199	8-JUN-199	1-JUN-199	991-NIII-E	3-JUN-199	4-JUN-199	8-JUN-199	9-NUL-6	0-JUN-199	1-00E-199 1-JUL-199	2-JUL-199	6-JUL-199	8-JUL-199	2-JUL-199 2-JUL-199	3-JUL-199	4-JUL-199	5-JUL-199	6-JUL-199	9-JUL-199	9-700-199 9-707-199	9-JUL-199	9-JUL-199	9-JUL-199	0-JUL-199	0-JUL-199	1-JUL-199	1-JUL-199	1-000-199 1-111-0	2-JUL-199	2-JUL-199	2-JUL-199	3-JUL-199	3-JUL-199	6-JUL-199	7-JUL-199 IIII7	7-JUL-199	8-JUL-199	2-AUG-199	2-AUG-199 2-AUG-199
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99US-0138540P.
99US-013119P.
99US-0139452P.
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990S-0139463P.
990S-0139763P.
990S-0139817P.
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990S-01440605P-
990S-0144066P-
990S-0144325P-
990S-0144334P-
990S-0144334P-
990S-0144334P-
990S-0144334P-
990S-0144334P-
990S-0144632P-
990S-0144632P-
990S-0144632P-
990S-014632P-
990S-014508PP-
990S-014508PP-
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9903-0145218P.
9903-0145224P.
9903-0145213P.
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99US-0147260P.
99US-0147303P.
99US-0147416P.
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99US-0139455P.
99US-0139456P.
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is Sequence 17299, Application US/09252991A

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is APPLICANT: Marc J. Rubenfield et al.

is TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

is TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND.THERAPEUTICS

is TITLE OF INVENTION: AUGUST 1920-02-18

is PRIOR TAPLICATION NUMBER: US/09/252,991A

is PRIOR FILING DATE: 1998-02-18

is PRIOR FILING DATE: 1998-02-18

is PRIOR FILING DATE: 1998-07-27

is SEQ ID NOS: 33142

is LENGTH: 351
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Sequence 5551, Application US/09134000C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 5551

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Best Local Similarity
Matches 8; Conserv
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Fatent No. 6551795
GENERAL INFORMATION:
FATELE NEF INVENTION:
FITLE OF INVENTION:
FILE REFERENCE:
FILE REFERENCE:
FILE NEFERENCE:
FILE NOT SERVICE AND THERAPEUTICS
FILE NEFERENCE:
FILE NOT SERVICE TO NUMBER:
FILE NOT SERVICE TO NUMBER:
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Sequence 411, App
Sequence 15, Appl
Sequence 34, Appl
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Sequence 29810, A
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Sequence 6158, Ap
          Sequence 32240,
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Sequence 6, Al
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Sequence 2768
Sequence 2, A
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Sequence 6
Sequence 3
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US-08-804-227C-6
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US-09-91-609-2
US-09-91-609-2
US-09-91-609-2
US-09-621-976-633
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US-08-621-976-633
US-08-552-991A-36542
US-09-252-991A-36542
US-09-252-991A-36742
US-09-252-991A-36742
US-09-252-991A-26715
US-09-367-891A-26715
US-09-367-891A-2678
US-09-352-991A-2678
US-09-394-455-38
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: 195/09/312,283C
CURRENT PILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 818;
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Pred. No. 98;
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 4;
Pred. No. 3.2e+02;
1; Mismatches 4
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                         PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 818
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                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
1999-02-18
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Best Local Similarity 61.5%;
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US-09-25-991A-20299

Sequence 20299, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION: Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TILLE APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

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                                                                            Sequence 27594, Application US/09252991A

Sequence 27594, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27594
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Patent No. 5551795
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Patent No. Through No. 1000 Patent No. 500 Patent No. 500 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 700 Patent No. 
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Pred. No. 2.3e+02;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27594
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US-09-252-991A-20299
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Best Local Similarity
7; Conserv?
                                                                            US-09-252-991A-27594
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US-09-252-991A-16691
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                                                                                                                                      Sequence 234, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ontust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILES REPRENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348

SOFTWARE: PESESEQ for Windows Version 3.0

SEQ ID NO 294
LENTH: 294
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Fatent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steaman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 294
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Patent No. 5514544
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Best Local Similarity 70.0
Matches 7; Conservative
81 EGPPGRTGNR 90
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                                                                                                                               US-09-188-930-294
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; ORGANISM: Rat
US-09-188-930-294
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US-07-736-178C-2
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| Sequence 2. Application US/09552204A
| Patent No. 662090
| GENERAL INFORMATION:
| APPLICANT: Biddington, Christopher S.
| APPLICANT: Bishop, Paul D.
| TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRPZ FILE REFERENCE: 99-08 NUMBER: US/09/552,204A
| CURRENT FILING DATE: 2000-04-19
| PRIOR PAPLICATION NUMBER: 60/130,207
| PRIOR FILING DATE: 1999-04-20
| SOGTWARE OF SEQ ID NOS: 20
| SOGTWARE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE FRESE F
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Patent No. 6573095

GENERAL INPORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Concust, Rene
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions Isolated
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425

SOFTWARRE: FRESEQ for Windows Version 4.0
                                                                                                                         53.6%; Score 37; DB 4; Length 198; 70.0%; Pred. No. 98;
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Pred. No. 1.5e+02;
0; Mismatches 3; Indels
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70.0%;
                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
                             ORGANISM: Mouse
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US-09-312-283C-382
                                                          US-09-312-283C-138
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US-09-552-204A-2
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LENGTH: 285
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1 EGGPGTTSNR 10

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Sequence 29606, Application US/09252991A
Sequence 29606, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR PELING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29606
LENGTH: 1287
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APPLICANT: Lee, Mong-hong
TITLE OF INVENTION: 1 SOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
SIREET: 1185 Avenue of the Americas
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
CLASSIFICATION: 435
ATCASSIFICATION: 435
ATCASSIFICATION: 1NFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 1747/47418
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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TELECOMMULCATION INFORMATION:
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Pred. No. 7.7e+02;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: not releve
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Best Local Similarity 63.0.
Local 7; Conservative
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  306 PGTTANRM 313
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                                                                                               US-09-252-991A-29606
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US-08-415-655-7
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                   ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/736,178C
FILING DATE: 19910726
CLASSIFICATION: 435
                         APPLICANT: Turner, Jan R
TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
TITLE OF INVENTION: BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.6%; Score 37; DB 4; I Best Local Similarity 75.0%; Pred. No. 5.9e+02; Matches 6; Conservative 2; Mismatches 0.
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Pred. No. 3.7e+02;
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                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly And Company
STREET: Lilly corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INPORMATION:
NAME: CONTEAL ROBERT A
REGISTRATION NUMBER: 32089
REFERENCE/DOCKET NUMBER: X814
TELECPHONE: 317-276-3334
TELEPHONE: 317-276-1294
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APPLICANT: Rao, Ramachandra N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 655 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.7
Matches 8; Conservative
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MOLECULE TYPE: protein
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US-09-252-991A-24069
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LENGTH: 1003
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                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                     STATE:
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US-09-252-991A-29227
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
NUCLEIC ACID ANNO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-08-15
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                                                                                                                      52.2%; Score 36; DB 3; Length 159; 66.7%; Pred. No. 1.1e+02;
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Pred. No. 1.7e+02; ° °
0; Mismatches 3; Indels
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                 1; Mismatches
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NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 266
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CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
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US-09-134-000C-4443
Sequence 4443, Application US/09134000C
; Patent No. 6617156
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Patent No. 6355411
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Mahajan-Miklos, Shalina
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4443
LENGTH: 229
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Goodman, Howard M.
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not relevant
                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPGTTSNRLD 12
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                                                            ANTI-SENSE: NO
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US-09-199-637A-157
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                                                                               US-08-415-655-7
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQ ID NOS: 33142
SEQ ID NO 29227
LENGTH: 275
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APPLICANT: Craik, Charles S.
APPLICANT: Unal, Apoce B.
APPLICANT: Ganem, Donald E.
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Protease and Assembly Protein Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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Score 36; DB 4; Length 266; Pred. No. 2e+02; 2; Indels 3; Mismatches 2; Indels
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2.1e+02;
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SOFTWARE: FastSEQ for Windows Version 2.0
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STREET: P.O. Box 60850
CITY: Palo Alto
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APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09064703 Patent No. 6033894
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FILING DATE: 22-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42,995
       52.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
       Query Match 52.2
Best Local Similarity 54.5
Matches 6; Conservative
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158 GEPDTTNNRME 168
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246 KGGPGTAEARI 256
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Score 36; DB 3; I
Pred. No. 3.3e+02;
1; Mismatches 1;
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CURRENT FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 417
TYPE: PRT
TYPE: PRT
TYPE: PRT
US-08-640-906-4
                                                                                                                                                  Sequence 23098, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 4, Application US/08640906B
Patent No. 6140100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23098
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75.0%;
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Matches 6; Conservative
                                                       273 PNPTSNRLEA 282
                    PGTTSNRLDA 13
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Best Local Similarity
Matches 6; Conserv
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US-08-640-906-4
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APPLICANT: Crait, Charles S.
APPLICANT: Unal, Ayce
APPLICANT: Unal, Ayce
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Reposi's Syndrome Herpesvirus
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                           52.2%; Score 36; DB 3; Length 300; 70.0%; Pred. No. 2.3e+02;
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Pred. No. 2.3e+02;
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MEDIUM TYRE: Disketter
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSRQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA: 40/04,152
FILING DATE: 22-APR-1997
ATTONISY/AGENT INFORMATION:
NAME: PETILINGY, JOANNE RESISTATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: KSHV AP encoded by SEQ ID NO:8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: KSHV AP encoded by SEQ ID NO:9
REFERENCE/DOCKET NUMBER: 2002-0002.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09064703
Patent No. 6033894
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                     TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.2%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 70.0
Matches 7; Conservative
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XY: linear
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US-09-064-703-11
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GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: 05 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23098
LENGTH: 325
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APPLICANT: Smith, Gary K
APPLICANT: Blumenkopf, Todd A.
APPLICANT: Blumenkopf, Todd A.
APPLICANT: Cory, Michael
TITLE OF INVENTION: Cell-Targeting Molecule Comprising a Mutant Human
TITLE OF INVENTION: Carboxypeptidase A
FILE REFERENCE: PBISOUSW
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Sequence 4, Application US/09395936

Sequence 4, Application US/09395936

Patent No. 6319702

GENERAL INFORMATION:

APPLICANT: Smith, Gary

APPLICANT: Cory, Michael

APPLICANT: Cory, Michael

TITLE OF INVENTION: Nucleic Acids Encoding Mutant Human Carboxypeptidase A

TITLE OF INVENTION: Nucleic Acids Encoding Mutant Human Carboxypeptidase A

TITLE OF INVENTION: Nucleic Acids Encoding Mutant Human Carboxypeptidase A

FILE REFERENCE: PB1500US3

CURRENT FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

IENGTH: 417

TYPE: PRT

ORANISM: homo sapiens

US-09-395-936-4
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## APPLICANT: Blumenkopf, Todd A.

### APPLICANT: Cory, Michael

### TITLE OF INVENTION: Call-Targeting Molecule Comprising a Mutant Human

### TITLE OF INVENTION: Calboxypeptidase A.

### TITLE OF INVENTION: Calboxypeptidase A.

### CURRENT APPLICATION NUMBER: US/08/640,906B.

### CURRENT FILING DATE: 1996-05-09

### NUMBER OF SEQ ID NOS: 22

### SEQ ID NO 18

### SEQ ID NO 18

### TYPE: PRT

### TYPE: PRT

### ORGANISM: Homo sapiens

US-08-640-906-18
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                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 3; Length 417; Pred. No. 3.3e+02; 1; Mismatches 1; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Matches 6; Conservative
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US-09-395-936-4
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Search completed: September 24, 2004, 02:20:06 Job time: 25.0755 secs

Sequence 797, App Sequence 797, App Sequence 141326, Sequence 786, App Sequence 18, App Sequence 18, App Sequence 248992, Sequence 195589,

Sequence 18,

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Sequence 38825, A Sequence 65647, A

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Sequence 166000,
Sequence 4888, Ap
Sequence 7646, Ap
Sequence 163360,
Sequence 206460,
Sequence 39568, A
Sequence 190792,
Sequence 130, App
Sequence 12542, A
Sequence 10700, A
Sequence 57133, A
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                                                                                        September 24, 2004, 01:54:43; Search time 75.3019 Seconds (without alignments) 55.513 Million cell updates/sec
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US-10-424-599-166000
US-10-369-493-7646
US-10-084-84A-8
US-10-084-84A-8
US-10-424-599-163360
US-10-424-599-206460
US-10-282-122A-69481
US-10-767-701-39568
US-10-437-963-190792
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US-10-156-761-12542
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US-10-182-243-45
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Maximum Match 100%
Listing first 150 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Sequence 150859, Sequence 122878, Sequence 11132, Sequence 2611, App Sequence 138, App Sequence 38, App Sequence 2, Applisequence 2, Applisequence 35, App Sequence 359, App Sequence 359, App Sequence 359, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App Sequence 351, App S

3903, Ap 4, Appli 2, Appli 26, Appli 4, Appli 11, Appl 112022, 219730,

Sequence Sequence Sequence

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Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence 1198, Ap

Sequence Sequence 1

Sequence

Sequence 101;

Sequence

Sequence

Sequence

Sequence 17, Sequence 18, Sequence 21,

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US-10-424-599-166000

i Sequence 166000

i Sequence 166000

i Requence 166000

i Reduction No. US20040031072A1

i GENERAL INFORMATION:

i APPLICANT: La Rosa Thomas J

i APPLICANT: A Coa Yongwe K

APPLICANT: A Coa Yongwe K

i APPLICANT: A Coa Yongwe K

i TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

I TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: 1632231

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

i SEQ ID NO 166000

LENGTH: 566
                APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Seven W.
APPLICANT: Taylor, Sary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DIBENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICANTION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 2326
LENGTH: 3149
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Pred. No. 3e+02;
0; Mismatches 3; Indels
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Pred. No. 8.5e+02;
1; Mismatches 1; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_120914C.1.pep
US-10-424-599-166000
                                                                                                                                                                                                                                                                                                                                                                             63.8%;
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Best Local Similarity 72.7%;
Matches 8; Conservative
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  Fahy, Eoin D.
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                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-408-765A-2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Glycine max
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Sequence 242, App
Sequence 244, App
Sequence 244, App
Sequence 150, App
Sequence 228, App
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Sequence 576, App
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Sequence 121, Appli
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Sequence 64386, A
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Sequence 19226,
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Sequence 390, App
Sequence 1672, Ap
Sequence 1916, Ap
                                       65, Appl
2770, Ap
2763, Ap
157, App
246, App
181524,
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2 US-10-424-599-133291

2 US-10-424-599-133291

2 US-10-282-122A-60329

6 US-10-437-963-154817

6 US-10-437-963-154817

6 US-10-282-122A-48557

4 US-10-282-122A-48557

6 US-10-372-095-5

6 US-10-437-963-169783

0 US-09-931-009A-1

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0 US-10-437-963-132807

5 US-10-437-963-132807

6 US-10-437-963-120040

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US-10-437-963-199907
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US-10-199-485-8
US-10-380-727-2
US-10-156-761-8812
US-09-764-891-3390
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Length 3149;

## ALIGNMENTS

US-10-408-765A-2326 Sequence 2326, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S.

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NEGRO 10-369-493-4888

Sequence 4888, Application US/10369493

Sequence 4888, Application US/10369493

FUDILICATION NO. US20030233675A1

FUDILICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B
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Sequence 163360, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exceleration and Uses John Applicant:
APPLICANT: Exceleration Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163360
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Show Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)322) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206460
                          TYPE: PRT ORGANISM: Streptomyces viridochromogenes PEATURE: PEATURE: OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1. OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3. US-10-084-846A-8
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US-10-424-599-163360
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US-10-424-599-206460
                                                                                                                                                                                        Score 41; DB 15;
Pred. No. 1.7e+04;
0; Mismatches 4;
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63.6%; Pred. No. 99;
iive 2; Mismatches 2
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-163360
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       LENGTH: 19608
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7646
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Pred. No. 3e+02;
1; Mismatches 2; Indels
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Pred. No. 3e+02;
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Publication No. US2004006026A1
GENERAL INFORMATION:
APPLICANT: WEITHAUER, GABRIELE
APPLICANT: WHILENWEG, AGNES
APPLICANT: WHILENWEG, AGNES
APPLICANT: TERFERE, ARXEL
APPLICANT: RECHTHOLD, ANDERAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFRENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR APPLICATION NUMBER: DE 101 09 166.4
SEQ ID NO 8
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4888
LENGTH: 398
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia cepacia
                                                                                                                                                                                                                                                            Query Match 59.4%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72...
8; Conservative
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ORGANISM:
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US-10-437-963-190792
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ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                        Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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                        1; Indels
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  Pred. No. 1.2e+02;
0; Mismatches 1
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Pred. No. 1.9e+02;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                 Sequence 69481, Application US/10282122A
Publication No. US20040029123A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR PLING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20, 335
PRIOR PLING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25, 625
PRIOR APPLICATION NUMBER: 60/25, 625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: KOVALIC, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.5%;
61.5%;
87.5%;
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Forsyth, R.
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Matches 7; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
Trawick, John
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                                                                                                                     52 GGPGTTIN 59
                                                                       2 GGPGTTSN 9
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US-10-282-122A-69481
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J. Sequence 190792, Application US/10437963

J. Sequence 190792, Application No. US20040123343A1

GENERAL INFORMATION:
J. Publication No. US20040123343A1

GENERAL INFORMATION:
J. APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Branzuk, Brad

APPLICANT: Branzuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 190792

LENGTH: 203
Page 4

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE OF INVENTION: 19133518

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

WUMBER OF SEQ ID NOS: 63128

EDENGTH: 188
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Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C20858_1.pep
US-10-767-701-39568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

COTHER INFORMATION: Clone ID: PAT_MRT4530_87172C.1.pep
US-10-437-963-190792
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Retent No. US20020110855A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presentl, Scott R.
TITLE OF INVENTION: MAMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 16;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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70.0%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 70.0
Matches 7; Conservative
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109 GPSTTDEKLDA 119
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71 GPGTSSHRSD 80
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ORGANISM: Oryza sativa
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 9; Length 454; Pred. No. 7e+02;
                                                            PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASSEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: PASSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57133, Application US/10282122A Publication No. US20040029129A1
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OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR PILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
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OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
                                           60/206,848
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PRIOR FILING DATE: 2000-03-21
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APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecalis
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                            Score 39; DB 9; Length 219; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                               2; Indels
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IITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9e+02;
                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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| CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL | CONTROL
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; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SCHWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 219
; TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-737-130
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Sequence 10700, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
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Zyskind, Judith W.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 77.8
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APPLICANT:
APPLICANT:
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| Sequence 797, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies |
| FILE REFERENCE: PA104 |
| CURRENT APPLICATION NUMBER: US/09/925,302 |
| CURRENT FILING DATE: 2001-08-10 |
| PRIOR APPLICATION NUMBER: PCT/US00/05918 |
| PRIOR FILING DATE: 1999-03-12 |
| NUMBER OF SEQ ID NOS: 896 |
| SEQ ID NO 797 |
| LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%; Score 39; DB 12; Length 600; 87.5%; Pred. No. 9.4e+02; tive 0; Mismatches 1; Indels
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; OTHER INFORMATION: Incyte ID No. US20040053394A1 7474648CD1
US-10-415-011-18
                                                                                                                                                                                                 APPLICANT: SWARMARK Anica
APPLICANT: THANGAVELU, Kavitha
PAPLICANT: THANGAVELU, Kavitha
APPLICANT: KHAN, Farrah A.
TITLE REPERBYCE: PI-0262 USN
CURRENT FILING DATE: 2003-04-18
PRIOR PILING DATE: 2003-04-18
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-20
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PRIOR PILING DATE
                                    LAL, Preeti G.
RECIPON, Shirley A.
LU, Dyung Aina M.
BOROWSKY, Mark L.
THORNYON, Michael B.
SWARNAKER Anita
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Best Local Similarity 87.5.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-925-302-797
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                                                                                                                                                                                                                 Score 39; DB 12; Length 454;
Pred. No. 7e+02;
0; Mismatches 2; Indels
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Publication No. US20040053394A1
GENERAL INFORMATION:
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: GTRWLA, Nariah R.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: ARVIZU, Chandra S.
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YO, Yuming
APPLICANT: YAO, Monique G.
APPLICANT: RAMKUMAR, Jayalaxmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/10182243
Publication No. US20040048310A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
                                                                                                                         ORGANISM: Enterococcus faecalis US-10-282-122A-57133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANG, Y. Tom
HAFALIA, April J.A.
NGUYEN, Danniel B.
GANDHI, Ameena R.
SOFTWARE: Patentin version 3.1
SEQ ID NO 57133
LENGTH: 454
                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative.
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BANDMAN, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                152 GRPGTFSNRL 161
                                                                                                                                                                                                                                                                                                                                                     2 GGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEO ID NO 45
LENGTH: 600
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-182-243-45
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Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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78 QGGPQSRQNRKDA 90
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                               586 GGPGSGGNRL 595
                                                                                                                                                                                                                                                                     2 GGPGTTSNRL 11
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ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
FEATURE:
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     LOCATION: (599)
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US-09-925-298-786
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                                                                                                                   LOCATION: (506)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                         LOCATION: (577)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                      LOCATION: (584)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-797
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                             LOCATION: (446)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                      INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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JTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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JTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-035-302-797
i Sequence 797, Application US/09925302
j Publication No. US20030064072A9
i GENERAL INFORMATION:
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: NUMBER: US/09/925,302
CURRENT APPLICATION NUMBER: PCT/US00/05918
j PRIOR APPLICATION NUMBER: PCT/US00/05918
j PRIOR APPLICATION NUMBER: 60/124,270
j PRIOR APPLICATION NUMBER: 60/124,270
j PRIOR APPLICATION NUMBER: 60/124,270
j PRIOR PILING DATE: 1999-03-12
j NUMBER OF SEQ ID NOS: 896
j SEQ ID NOS: 896
j SEQ ID NO 797
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Pred. No. 9.5e+02;
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Best Local Similarity 70.0.0
Laga 7; Conservative
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ORGANISM: Homo sapiens
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US-10-49/3-14126
US-1-41326, Application US/10437963
; Sequence 141326, Application US/10437963
; Publication No. US2040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Shou, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brad
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (608)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-797
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APPLICANT: ROSen et al.; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PALO3; CURRENT FILING DATE: 2001-08-10; PRIOR PAPLICATION NUMBER: PCT/US00/05881; PRIOR PILING DATE: 2000-03-08; PRIOR FILING DATE: 2000-03-08; PRIOR FILING DATE: 1999-03-12; NUMBER: OF SEQ ID NOS: 846; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 786
                                                                                                                                                                                                                                                                                                      Length 609
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US-10-437-963-141326
                                                                                                                                                                                                                                                                                                 Score 39; DB 12;
Pred. No. 9.5e+02;
1; Mismatches 2
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CURRENT FILING DATE: 2001-10-16
PRIOR PULICATION NUMBER: 60/241,040
PRIOR PLILNG DATE: 2000-10-17
PRIOR PLILNG DATE: 2000-10-17
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PRIOR PLILNG DATE: 2000-10-27
PRIOR PLILNG DATE: 2000-10-20
PRIOR PLILNG DATE: 2000-10-20
PRIOR PLILNG DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/242,482
PRIOR PPLICATION NUMBER: 60/242,613
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
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APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
Pred. No. 2.1e+02;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09981151A Publication No. US20030212256A1 GENERAL INFORMATION: APPLICANT: Edinger, Shlomit R
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Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
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Shimkets, Richard A
Padigaru, Muralidhara
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MacDougall, John R
Malyankar, Muriel M
Smithson, Glennda
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Spytek, Kimberly A
Best Local Similarity 53.8%;
Matches 7; Conservative :
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Peyman, John A
Stone, David J
                                                                                              1 EGGPGTTSNRLDA 13
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SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunther, Erik
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CRGANISM: Homo sapiens
US-09-981-151A-18
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-102-806-786
                                                                                       NAME/KEY: SITE
LOCATION: (33)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                             LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                      LOCATION: (64)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-298-786
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Fublication No. US20030054421A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAL03PICI.
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 12; Length 102;
Pred. No. 2.1e+02;
2; Mismatches 4; Indels
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Best Local Similarity 53.8%;
Matches 7; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 786
LENGTH: 102
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LOCATION: (84)
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 Length 134;
                      4; Indels
Score 38; DB 11;
Pred. No. 2.8e+02;
2; Mismatches 4;
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Query Match

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4; Indels
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US-10-767-701-38825
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Best Local Similarity 58.3
Matches 7; Conservative
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ORGANISM: Sorghum bicolor
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      13 GSSGNTSNRVD 23
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US-10-767-701-38825
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEG ID NOS: 204966
SEQ ID NO 195589
LENGTH: 152
                                                                                                               Sequence 24892, Application US/10424599
Publication No. US20040031072A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599.
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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US-10-424-599-248992
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US-10-437-963-195589
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Pred. No. 3.2e+02;
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 63.6%;
Matches 7; Conservative
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25 EGGVGTALRKMDA 37
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ORGANISM: Oryza sativa
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ORGANISM: Glycine max
                                                                                                   US-10-424-599-248992
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LENGTH: 151
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                                                                   September 24, 2004, 01:33:11; Search time 19.3774 Seconds (without alignments) 64.534 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                   283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 150 summaries
                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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H95964
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AG2884
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Maximum DB seq length: 200000000
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Match Length DB
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probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Note: this species has also been called Salmonella typhi C;Nove-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0618 R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
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R. Mitternan, W. C. Feldblyum, T. V. Paulsen, I. T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M. T.; Dodson, R. J.; Durkin, A.S.; Gwinn, M.L.; Heit, D.H.; Kolon

N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U. S.A. 98, 413-64441, 2001

A.; Title: Complete Genome Sequence of Caulobacter crescentus.

A; Reference number: A87249; MUID:21173698; PMID:11259647

A; Acatus: preliminary

A; Molecule type: DNA

A; Residues: 1-149 <STO>

A; Cross-references: GB:AE005673; NID:g13425071; PIDN:AAK25327.1; GSPDB:GN00148

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R;Ghersevich, S.; Nokelainen, P.; Poutanen, M.; Orava, M.; Autio-Harmainen, H.; Rajaniem Endocrinology 135, 1477-1487, 1994
A;Title: Rat 17-beta-hydroxysteroid dehydrogenase type 1: primary structure and regulati A;Reference number: S57901; MUID:95009707; PMID:7925110
A;Accession: S57901
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SCC22.20 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Dacc-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T36010 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A;Reference number: Z21574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL096839; PIDN:CABS0763.1; GSPDB:GN00070; SCOEDB:SCC22.20
A;Experimental source: strain A3(2)
C;Genetics:
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A,Residues: 1-1073 <PAU>
A;Cross-references: EMBL:AF101304; PIDN:AAC69200.1; GSPDB:GN00023; CESP:C02E11.1
A;Experimental source: strain Bristol N2; clone C02E11
                                                                                                                                                                              A;Residues: 1-344 «GHE»
A;Cross-references: EMBL:X78811; NID:g561532; PIDN:CAA55389.1; PID:g561533
C;Superfamily: 17beta-dehydrogenase; short-chain alcohol dehydrogenase homology C;Keywords: oxidoreductase
F;4-189/Domain: short-chain alcohol dehydrogenase homology <SADH>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33764
R;Pauley, A.; Harper, M.
submitted to the EmBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid CO2E11.
A;Reference number: Z21403
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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Pred. No. 30;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 40; DB 2; Length 344; 61.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
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A;Molecule type: DNA
A;Residues: 1-351 <SEE>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A:Introns: 37/1; 174/3; 248/3; 511/3; 702/2; 1043/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Matches 8; Conservative
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A;Gene: CESP:C02E11.1
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- Sinorhizobium meliloti (£
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A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Retence number: A95842; MUID:21396508; PMID:11481431

A; Retence number: A95842; MUID:21396508; PMID:11481431

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1.9398 CDIE>
A;Cross-references: EMBL:Y16563; NID:93413503; PIDN:CAA76287.1; PID:93413504
A;Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                          probable outer membrane secretion protein SMb21543 [imported] - Sinorhizobio
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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70.0%; Pred. No. 5.6e+02;
tive 1; Mismatches 2; Indels
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Best Local Similarity 77.8
Matches 7; Conservative
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3 GPGTTSNRLD 12
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Gordon-Kamm,

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Gaps

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Indels

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hypothetical protein AGR C 4553 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: D9766 G. R; Cattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: F70134
A;Accession preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                              A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordonster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; WUID:21608550; PMID:11743193
                                                                                                                                                                                                                            A; Accession: AG2884
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-312 < KUNS
A; Cross-references: GB: AbC008688; PIDN: AAL43493.1; PID: G17741000; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
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Pred. No. 59;
3; Mismatches
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Pred. No. 59;
3; Mismatches
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A,Map position: circular chromosome
C,Superfamily: inner membrane protein ugpA
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C,Superfamily: inner membrane protein ugpA
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50.0%;
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50.0%;
                                     ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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252 QGGPGTASETIN 263
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Matches 6; Conservative
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      G.; Gillet, W.; Grant,
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-312 <KUR>
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                                                                                                                                                                                                                                  C,Accession: E69174
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D., Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: succinate-CoA ligase (ADP-forming) alpha chain
C;Keywords: acid-thiol ligase; ATP; coenzyme A; phosphohistidine; phosphoprotein; tricar
F;249/Active site: His (phosphohistidine intermediate) #status predicted
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A;Residues: 1-293 <STO>
A;Cross-references: GB:AE004459; GB:AE004091; NID:g9946043; PIDN:AAG03598.1; GSPDB:GN001
A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-293 <MTH>
A;Cross-references: GB:AE000839; GB:AE000666; NID:g2621637; PIDN:AAB85069.1; PID:g262164
A;Experimental source: strain Delta H
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A,Accession: F83618
A,Stacus: preliminary
                                                                                                                                       succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain - Methanobacterium thermoaut
C,Species: Methanobacterium thermoautotrophicum
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dupont
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AG2884

Hypothetical protein Atu2506 [imported] - Agrobacterium tumefaciens (strain C58, Dupont C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG2884
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
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55;
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1; Mismatches
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Pred. No.
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Best Local Similarity 61.5%;
Matches 8; Conservative
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255 EGGTGTASSKREA 267
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Best Local Similarity 53.8
Matches 7; Conservative
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A,Gene: PA0209
C,Superfamily: citG protein
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Vugt, B.

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Length 312 Indels

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Cjaccession: E75346

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; P. Mahhte, O.; Eisen, J.A.; Heidelberg, D.F.; McDonald, L.; Utterback, T.; Zalewski, C.; Mah S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Residues: 1-139 <WHI>
A,Cross-references: GB:AE002025; GB:AE000513; NID:g6459627; PIDN:AAF11408.1; PID:g6459634
A,Experimental source: strain R1
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C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Accession-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession-157523
R;Shaknovich, R.; Shue, G.; Kohtz, D.S.
Mol. Cell. Biol. 12, 5059-5068, 1992
A;Title: Conformational activation of a basic helix-loop-helix protein (MyoDl) by the C-t A;Reference number: 157523; MUID:93024452; PMID:1406681
A;Reference number: Is7523
A;Status: preliminary; translated from GB/SMBL/DDBJ
A;Introns: 58/3; 330/3; 366/3; 498/3; 544/3; 605/3; 896/3; 924/1; 1023/1; 1139/2; 1217/3,
                                                                                                                                                                                                                                                                                                                                                                             organic hydroperoxide resistance protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C;Superfamily: heat shock protein 90
                                                         Length 1872;
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                              Score 38; DB 2; Length 18/, Pred. No. 3.88+02; 3; Indel8
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Pred. No. 38;
2; Mismatches 4
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                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
C;Superfamily: hypothetical protein yklA
                                                         55.1%;
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                              Ouery Match
Best Local Similarity 50.04
The Grand Conservative
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338 KGAPGLITNRID 349
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Best Local Similarity 53.8
Matches 7; Conservative
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C;Species: Aeropyrum pernix
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-194 <RES>
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                        A,Cross-references: GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC66670.1; PID:g268818
A,Experimental source: strain B31
C,Superfamily: flagellar motor switch protein flim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, & Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Sahandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :Residues: 1-667 <COL>
:Cross-references: GB:Z81368; GB:AL123456; NID:g3261656; PIDN:CAB03731.1; PID:g1655665
:Experimental source: strain H37Rv
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Cross-references: EMBL:AL021180; PIDN:CAA15982.1; GSPDB:GN00021; CESP:T08A11.1
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Molecule type: DNA
;Residues: 1-1872 «MIL»
Cross-references: EMBL:250875; PIDN:CAA90776.1; GSPDB:GN00021; CESP:T08A11.1
;Experimental source: clone T08A11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T08All.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T24683; T26904
R;Chut, C; Sulston, J.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19922
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 667;
                                                                                                                                          Score 38; DB 2; Length 352;
Pred. No. 67;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.1%; Score 38; DB 2; I ilarity 53.8%; Pred. No. 1.3e+02; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, January 1998
A;Reference number: 220284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: clone Y44F5A
                                                                                                                                          Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                              250 GVGTTSENLDA 260
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les 7; Conserv
A;Residues: 1-352 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T24683 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T26904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: F70682
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conserved hypothetical protein yihF [imported] - Lactococcus lactis subsp. lactis (strair C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bolotin, A; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Reference number: A86625; WUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <370.
A;Residues: 1-38 <370.
A;Cross-references: GB:AE005176; PID:g12723784; PIDN:AAK04954.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                         peroxidase (BC 1.11.1.7) pxdC precursor - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
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                  Score 37; DB 2; Length 290;
Pred. No. 81;
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Pred. No. 1e+02;
                                                                     Indels
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A,Residues: 1-353 <ABR>
A,Cross-references: EMBL:L36157; NID:g537316; PID:g537317
A;Experimental source: subspecies sativa; cultivar Siriver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Kerwords: oxidoreductase
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-353/Product: peroxidase pxdC #status predicted <MAT>
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Pred. No. 1.1e+02;
2; Mismatches 4
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Status: preliminary; translated from GB/EMBL/DDBJ
                                                                        0; Mismatches
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                       53.6%;
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ilarity 63.6%;
Conservative
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Query Match
Best Local Similarity 70...
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGPGTTSNRLD 12
                                                                                                                                                                       236 GGPGTASTTL 245
                                                                                                                         2 GGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: yihF
C;Superfamily: yhaD protein
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;Superfamily: peroxidase
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nes 7; Conserv
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Best Local S
Matches 7
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Best Local S:
Matches 7
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                                                                                                                                                                                                                                                  RESULT 21
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03552
C;Accession: T03552
R;Vlock, C; Paces, V; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
                                                                                                                                                                                                                                                            A;Residues: 1-222 <KAW>
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79545.1; PID:d1043331; PID:g510
A;Experimental source: strain Kl
C;Genetics:
A;Gene: APE0577
                                                                   R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kana, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kana, H.; Camalete Genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-229 <WOO>
A;Cross-references: EMBL:AL022103; PIDN:CAA17889.1; GSPDB:GN00067; SPDB:SPBC2G2.09c
A;Experimental source: strain.972h-; cosmid c2G2
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A;Residues: 1-290 <VLC>
A;Coss-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16205.1; PID:g3128353
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SPBC2G2.09c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40148
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
A;Reference number: Z21842
               C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: A72643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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T03552
maltose transport inner membrane protein - Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2; Length 222;
Pred. No. 62;
2; Mismatches 2; Indels
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A;Map position: 1
C;Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                            53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.6
Best Local Similarity 63.6
Matches 7; Conservative
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A:Introns: 96/3; 150/1; 168/3
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GPGTLASRLTA 184
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Gene: SPDB:SPBC2G2.09c
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 10-Dec-1999
C;Accession: 345318
R;Wu, R.L.; Zhu, G.; Galvin, S.; Xu, C.; Haseba, T.; Chaloin-Dufau, C.; Dhouailly, D.; W Differentiation 55, 137-144, 1994
A;Title: Lineage-specific and differentiation-dependent expression of K12 keratin in rah A;Reference number: 345318; MUID:94192891; PMID:7511548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frmR protein - Streptomyces ambofaciens
C;Species: Streptomyces ambofaciens
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 22-Oct-1999
C;Accession: 525203; 521598
R;Geistlich, M.; Losick, R.; Turner, J.R.; Rao, R.N.
Mol. Microbiol. 6, 2019-2029, 1992
A;Title: Characterization of a novel regulatory gene governing the expression of a polyk
A;Reference number: 525202; MUID:92374852; PMID:1508047
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A;Molecule type: DNA
A;Residues: 1-443 <WIL>
A;Coss-references: EMBL:Z70684; PIDN:CAA94603.1; GSPDB:GN00022; CESP:F28D1.8
A;Experimental source: clone F28D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F28D1.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21499
                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Rosidues: 1-411 <WUR>
A,Cross-references: EMBL:X77665; NID:g495260; PIDN:CAA54741.1; PID:g495261
C,Superfamily: cytoskeletal keratin
C,Superfamily: cytoskeletal keratin
C,Keywords: coiled coil; intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Krebidues: 1-604 <GEI>
A;Cross-references: EMBL:X63451; NID:g46699; PIDN:CAA45051.1; PID:g46701
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 37; DB 2; Length 411; 58.3%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Baynes, C.
submitted to the EMBL Data Library, April 1996
A;Reference number: 219430
A;Accession: T21499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 71/1; 103/3; 162/3; 215/2; 360/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 GGPGEVSVEMDA 207
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGPGTTSNRLDA 13
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April 28, 2005, 17:57:45; Search time 97.9062 Seconds (without alignments) 51.354 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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69
1 EGGPGTTSNRLDA 13
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Gapop 10.0 , Gapext 0.5
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

geneseqp19808:* geneseqp19908:* geneseqp20008:* geneseqp20018:* geneseqp20028:* geneseqp200388:* geneseqp200388:* geneseqp200388:* A Geneseq 16Dec04:* ..........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	Aab68087 An anti-a	Aau64492 Propionib	Abm64701 Propionib	Abm61011 Propionib	Adj70520 Human hea	Abb60469 Drosophil	Adg22481 Cyanophag		Adn22235 Bacterial	Adn24993 Bacterial	Abp76682 Streptomy				Abu41557 Protein e	Aau83139 Novel sec	Abp43778 FLJ14840	Abb68531 Drosophil	Abo68553 Pseudomon	Aab94593 Human pro	Aag67257 Amino aci	Aau35107 Enterococ	Abu29209 Protein e	Adh87666 Enterococ	Aab85503 Human pro
SUMMARIES	OI	AAB68087	AAU64492	ABM64701	ABM61011	ADJ70520	ABB60469	ADG22481	ABO74099	ADN22235	ADN24993	ABP76682	ADG22495	AAY74086	AAM85724	ABU41557	AAU83139	ABP43778	ABB68531	AB068553	AAB94593	AAG67257	AAU35107	ABU29209	ADH87666	AAB85503
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d	Query Match	100.0	63.8	63.8	63.8	63.8	62.3	59.4	. 59.4	σ	59.4	59.4	58.0	58.0	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5
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26-OCT-2000; 2000WO-SE002082.

WO200130854-A2

03-MAY-2001.

99SE-00003895

28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB.

Aac24147 Human kin Aab58459 Lung canc Abb60494 Drosophil Aab50078 Breast an Ad538436 Human nov Abc76902 Human nov Abc76902 Human nov Aac24536 Arabidops Aac24536 Arabidops Aac24556 Arabidops Aac47561 Arabidops Aac47561 Arabidops Aac47561 Arabidops Aac47561 Arabidops Aac47564 Arabidops Aac47564 Arabidops Aac47564 Arabidops	Adhrassa Adk72631 Stereosel Abo78848 Pseudomon Aau44929 Propionib
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## ALIGNMENTS

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23. .33 //note= "Complementarity determining region (CDR) 1 of the light chain" 49. .55
                                                                                                                                                                                                                       186. 98 'note="Complementarity determining region (CDR) 3 of the light chain"
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/note= "Complementarity determining region (CDR) 1 of the
heavy chain"
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/note= "linker"
158. .162
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heavy chain"
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/note= "Complementarity determining region (CDR) 1 of
heavy chain"
                                                                                                                                                                                                            - "Complementarity determining region (CDR) 2 of chain"
                                                                                          Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                          An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                               Location/Qualifiers
                  AAB68087 standard; protein; 249 AA
                                                       (first entry)
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ight f
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Macaca fascicularis.
                                                       09-JUL-2001
                                      AAB68087;
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RESULT 1
           AAB68087
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Tordsson MJ, Kearney PP;

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The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                   Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 69; DB 4; Length 249; 100.0%; Pred. No. 0.0041; Pred. No. 0. 0.0041; ive 0; Mismatches 0; Indels
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological; osteopathic; neuroprotectant.
              Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                       Claim 1; Page 55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU64492 standard; protein; 527 AA.
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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N-PSDB; AAS59645.
                                                                  WPI; 2001-308619/32.
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                                                                                    N-PSDB; AAF84797
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                                 Nilson BHK;
                Brodin TN,
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Gaps

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Bhatia A;

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by content access. The disorders include SAPHO syndrome (synovitis, acne, the disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The access is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting the contactivity of P. acnes polypeptides and therefore treat P. acnes proteins. The antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by canzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was for this intending the directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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Jones R, Carte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 527;
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4; 1
Pred. No. 1.2e+02;
1; Mismatches 1
                                                                                 Example 1; SEQ ID NO 25687; 1069pp; English
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Lodes MJ,
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Zhang Y, Wang S, Jen S, Lodé
Barth B, Vallieve-Douglass J;
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80.0%;
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Best Local Similarity
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                                                                          The invention relates to an isolated polynuclectide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ABMS5624-ABM64356) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymeric comprising a polypeptide of the invention; antibodies against polypeptides of the invention; and an isolated T cell population comprising T cells prepared the method, a vaccine composition (comprising P. acnes polypeptides, this method; a vaccine composition (comprising P. acnes polypeptides, this method; a vaccine composition (comprising P. acnes polypeptides, polymeric composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins, T cell populations or antigen-presenting cells that express the polypeptides polypeptides, polypeptides, polypeptides, polypeptides polypeptides polypeptides polypeptides polypeptides polypeptides polypeptides polypeptides polypeptides polypeptides or antigen-presenting or treating acne polypeptides are useful for diagnosing, preventing or treating acne protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is thought to contain an immunogenic region. Note: The sequence data for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 6; Length 527;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
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Benson DR,
Claim 7; SEQ ID NO 29377; 1481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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Lodes MJ,
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Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
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N-PSDB; ACF64574.
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The invention relates to an instruction also relates to polypeptides and to immunogenic fragments of P. acnes polypeptides The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides The invention and additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising P. acnes polypeptides, on tibodies, fusion proteins, T cell populations, or attigen-presenting cells that express the polypeptide; a method; a vaccine composition (Comprising P. acnes in a cattigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymerlectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the collypeptides are useful for diagnosing, preventing or treating acnes under the polymerlectides, polymerlectides, antibodies, fusion protein. The P. acnes polypeptides, polymerlectides or protein. The polymerlectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a polypeptide predicted to be encoded by an ORF (open cadding frame) contained within the P. acnes polymention and the kit is useful for performing a diagnostic assay. The present cadding frame) contained within the P. acnes polymention to remain a polypeptide predicted to be encoded by an ORF (open cadding frame) contained within the P. acnes polymention. Contained specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pot_engered.
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New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                              polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy: LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                       invention relates to an isolated polynucleotide (ACF64435-ACF64733)
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80.0%; Pred. No. 1.2e+02;
iive 1; Mismatches 1;
                                                                                                                                                                                  Example 1; SEQ ID NO 25687; 1481pp; English
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17-JUN-2002; 2002US-0389987P.
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GGPGTASHRL 16
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                                                                                                                                                                                    for therapeutic intervention in treating a disease associated with adeltered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MBLAS), mycolonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these anticonvolsant, antiarthritic, osteopathic, antidiabetic, antidiabetic, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart
                                                                                                     Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                            This invention relates to novel mitochondrial targets that can be used
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                                                    Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 7.7e+02;
L; Mismatches 1; Indels
                                                    Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 8199.
                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                        Claim 1; SEQ ID NO 2326; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB60469 standard; protein; 749 AA.
                                                     Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                   63.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000; 2000US-00614150
                  (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.(
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                           3 GPGTTSNRLD 12
                                                                                                                                                                                                                                                                                                                                                                                                                               81
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                                                                                                                                                                                                                                                                                                                                                                                                                      GPGSTSRRLD
                                                    Fahy ED,
                                                                                  WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                Sequence 3149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
                                                   Ghosh SS,
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB60469;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher useryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genomic sequence for cyanophage 8-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                      Disclosure; SEQ ID NO 8199; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pochet S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 4; Length 749;
Pred. No. 2.5e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galisson F, Bouzon M,
Robert C, Vico V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 227; 423pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyanophage S-2L encoded protein #226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG22481 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2002; 2002FR-00005424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2002; 2002FR-00005424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marliere P, Kaminski PA,
Weissenbach J, Saurin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 GGPGTASNLLQS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGPGTTSNRLDA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-045746/05.
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Best Local Similarity
N-PSDB; ABL04572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADG22255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyanophage S-2L.
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Gaps

.; 0

Length 305; Indels

Score 41; DB 7; Len Pred. No. 2.1e+02;

59.4%;

Query Match
Best Local Similarity 58.3
Matches 7; Conservative

3; Mismatches

ADN22235 standard; protein; 398 AA.

ADN22235

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:||||| ::||| 224 QGAPGTGASRLD 235

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12

1 EGGPGTTSNRLD

Bacterial polypeptide #4888.

(first entry)

02-DEC-2004

ADN22235;

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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                  ö
                                                                                                                                     Score 41; DB 8; Length 166; Pred. No. 1.1e+02; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nolling J, Deloughery C, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 22845; 455pp; English
                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa polypeptide #6274.
                                                                                                                                                                                                                                                                                           ABO74099 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                       59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0074788P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0094190P
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                      48
                                                                                                                                                                                            1 EGGPGTTSNRLDA 13
                                                                                                                                                    Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                             :|||| ::| |||
36 QGGPGAGADRADA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-615309/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABD07670.
                                                                                                            Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2003
                                                                                   2L genome.
                                                                                                                                                                                                                                                                                                                       ABO74099;
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                              88888888888
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Recombinant DNA construct, transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

bacterial polypeptide

US2003233675-A1

Bacteria.

18-DEC-2003.

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The invention relates to a recombinant DNA construct comprising a prowide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the such as maize or soybean. The method of producing a transformed plant combinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to heabloides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4888; 122pp; English.
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prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as terrgets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Reaudomonas species using blochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at

segdata.uspto.gov/seguence.html

Sequence 305 AA

Goldman BS;

Chen X,

Hinkle GJ, Slater SC,

HINKLE G J. SLATER S C.

(HINK/) (SLAT/) (CHEN/) CAOY/)

GOLDMAN B S.

GOLD/) Cao Y,

20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                 in the
               production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence date for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                  Gaps
improved lignin production or improved galactomannan
                                                                                                                                                                                  ö
                                                                                                                                            Length 398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman BS;
                                                                                                                                            Score 41; DB 8; Pred. No. 2.8e+02;
                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 7646; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                 ADN24993 standard; protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2003; 2003US-00369493
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                                                                                                                                            59.4%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial polypeptide #7646.
                                                                                                                         Query Match
Query Match
Best Local Similarity 72.7.,
Best Local Similarity 72.7.,
                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2004 (first entry)
                                                                                                                                                                                                                  1 EGGPGTTSNRL 11
                                                                                                                                                                                                                                                      77 QGVPGTTVNRL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-061375/06.
                                                                                                          Sequence 398 AA;
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condition,
                                                                                                                                                                                                                                                                                                                                                                                    ADN24993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAOY/)
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                                                                                                                                                                                                                                                                                                             RESULT 10
ADN24993
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tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modifical seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lighth production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ17515-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungicide; infection;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New avilamycin derivatives, useful for treatment of infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avilamycin; antibacterial; virucide; protozoacide; fungicide; infer medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces viridochromogenes Avi gene cluster polypeptide frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 1.6e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                         Score 41; DB 8; Length 400;
Pred. No. 2.8e+02;
!; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bechthold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weitnauer G, Muehlenweg A, Trefzer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 68-301; 319pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP76682 standard; protein; 19938 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COMB-) COMBINATURE BIOPHARM AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                             59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2001; 2001DE-01009166.
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                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                  1 EGGPGTTSNRL
                                                                                                                                                                                                                                                                                                                                                                                   OGVPGTTVNRL
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABZ37516
                                                                                                                                                                                                                                          Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200268436-A1
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ABP76682
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This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (EST) sequences represented in AAZ52858-Z53014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                    New human nucleic acid sequences from pancreatic tumors, and related
                                                                                Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2; Length 224
Pred. No. 2.3e+02;
1; Mismatches 1; Indels
                                             Human prostate tumor EST fragment derived protein #273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:13317.
                                                                                                                                                                                                                                                                                                                                  Schmitt A,
                                                                                                                                                                                                                                                                                                 (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                  Rosenthal A, Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM85724 standard; protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Page 422; 502pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
                                                                                                                                                                                                                                98DE-01020190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.0%;
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               (first entry)
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Best Local Similarity 77.0
77.0
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91 ESGPGTSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 224 AA;
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                                                                                                                                                                DE19820190-A1
                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                28-APR-1998;
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               14-MAR-2000
                                                                                                                                                                                                 04-NOV-1999.
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                                                                                               treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDWP and dDTP, or polymucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxymucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                 genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galisson F, Bouzon M,
Robert C, Vico V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 241; 423pp; French.
                                                                                                                                                                                                                                Cyanophage S-2L encoded protein #240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY74086 standard; protein; 224 AA.
                                                                                                                               ADG22495 standard; protein; 92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2002; 2002FR-00005424
                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2002; 2002FR-00005424.
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                                             4312 GGPGTAEPRRDA 4323
                                                                                                                                                                                               26-FEB-2004 (first entry)
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Weissenbach J, Saurin W,
               13
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               GGPGTTSNRLDA
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                                                                                                                                                                                                                                                                                                  Cyanophage S-2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                  FR2839079-A1
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                                                                                                                                                                ADG22495;
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AAY74086
ID AAY74
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AC AAY74
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ADG22495
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Length 224;

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05-SEP-2000; 2000US-0229509F.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0229513P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-02313413P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-023190P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-023299P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-023399P.
14-SEP-2000; 2000US-023399P.
14-SEP-2000; 2000US-023399P.
15-SEP-2000; 2000US-023399P.
15-SEP-2000; 2000US-023399P.
16-SEP-2000; 2000US-023399P.
16-SEP-2000; 2000US-023423P.
17-SEP-2000; 2000US-023439P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
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18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 200US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P.
18-SEP-2000; 2000US-0234334P
2000US-0186350P.
2000US-0189874P.
2000US-0190176P.
2000US-0205515P.
2000US-0209467P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-021547P.
2000US-0217487P.
2000US-0217487P.
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2000US-0225214P.
2000US-0225264P.
2000US-0225264P.
2000US-0225268P.
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2000US-0225758P.
2000US-0225759P.
2000US-0226279P.
2000US-0226681P.
2000US-0226688P.
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; 2000US-0228924P.
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2000US-0229345P
02-MAR-2000; 2
116-MAR-2000; 2
118-APR-2000; 2
119-MAY-2000; 2
119-MAY-2000; 2
28-JUN-2000; 2
30-JUN-2000; 2
30-JUN-2000; 2
07-JUN-2000; 2
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14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
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11-JUL-2000; 2
14-JUL-2000; 2
26-JUL-2000; 2
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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30-AUG-2000;
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01-SEP-2000;
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S 2000US-0241808P. 2000US-0241809P. 2000US-0241826P. 2000US-0244617P. 2000US-024617P. 2000US-0251479P. 2000US-0251856P. 2000US-0251868P. 2000US-0241221P. 2000US-0241785P. 2000US-0241786P. 2000US-0241787P. 2000US-0246475P. 2000US-0246476P. 2000US-0246477P. 2000US-0246610P. 2000US-0246611P. 2000US-0246613P. 2000US-0249207P. 2000US-0249208P. 2000US-0249209P. 2000US-0249210P. 2000US-0249211P. 2000US-0249212P. 2000US-0249299P. 2000US-0246528P. 2000US-0246532P. 2000US-0249244P. 000US-0249264P 000US-0250391P. Ruben 2000US-0246523P 2000US-0246524P 2000US-0246526P 2000US-0246527P 2000US-0249213P 000US-0249214P 2000US-0249215P 000US-0249216P 000US-0249217P 2000US-0249218P 2000US-0249245P 2000US-0250160P 000US-0256719P 2000US-0251869P 2000US-0251989P 2000US-0251990P 2000US-0246478P 2000US-0246525P SCI Barash SC, HUMAN GENOME WPI; 2001-483426/52. N-PSDB; AAK58505. 02-OCT-2000; 13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 35-JAN-2001; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; NOV-2000; 08-NOV-2000; .7-NOV-2000; .7-NOV-2000; .7-NOV-2000; 7-NOV-2000; .7-NOV-2000; 17-NOV-2000; L7-NOV-2000; Rosen CA, NOV-2 (HUMA-) 

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

+ Sequence Listing; English Claim 11; SEQ ID NO 13317; 3071pp

amino acid sequences given in AAM82170 to AAM891921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expression in a patient's genome complement the patients own produce the secreted (I), by inserting the polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to produce the secreted diseases the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK49942 to AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention AAK54951 to AAK64702 encode the human 8×99999999999999888

Sequence 77 AA;

ö Gaps ö Length 77; 3; Indels Score 39; DB 4; I Pred. No. 1.1e+02; 1; Mismatches 3; 56.5%; Query Match
Best Local Similarity 63.vv.,
7; Conservative

47 EGGPGRASRRV 57 EGGPGTTSNRL 11

ઠ g RESULT 15 ABU41557

ABU41557 standard; protein; 130 AA. 

19-JUN-2003 (first entry) ABU41557;

Protein encoded by Prokaryotic essential gene #27084.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Pseudomonas syringae

WO200277183-A2

03-OCT-2002

21-MAR-2002; 2002WO-US009107

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2001; 2001US-00815242

06-MAR-2002; 2002US-0362699P

(BLIT-) ELITRA PHARM INC.

Malone C, Carr GJ,

'n,

Wang

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Zamudio C, Trawick JD, WPI; 2003-029926/02 N-PSDB; ACA45427

Zyskind JW; Xu HH;

Claim 25; SEQ ID NO 69481; 1766pp; English.

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid The invention relates to an isolated nucleic acid comprising any one of

encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from the proposition of the present from the part of the present sequences. 

Sequence 130 AA;

Gaps ö Length 130; 4; Indels Score 39; DB 6; 1 Pred. No. 1.9e+02; 1; Mismatches 56.5%; ilarity 61.5%; Conservative Query Match Best Local Similarity 8; Conserve

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1 EGGPGTTSNRLDA 13 11 EGTPGSTPRRLGA 23 ద

completed: April 28, 2005, 18:17:31 Job time : 100.906 secs Search

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Perfect score:

Sequence:

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Sequence Sequence Sequence

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Sequence

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
RIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22845
LENGTH: 305
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Pred. No. 47;
3; Mismatches 2; Indels
              US-09-395-936-18
US-09-352-991A-26653
US-09-252-991A-30209
US-09-489-033A-13452
US-09-5489-033A-13755
US-09-489-033A-13755
US-09-489-033A-13755
US-09-489-03391-13755
US-09-919-0391-21
US-08-814-052-2
US-08-814-052-2
US-08-814-052-2
US-08-913-157-4
US-09-919-0139-121
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US-09-919-018-8882
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Sequence 130, Application US/09893737

Patent No. 6822082

GRNERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Ereanell, Scott R.

TITLE OF INVERTION: MAMMALIAN SECRETED PROTEINS

FILE REFERENCE: 00-41

CURRENT APPLICATION NUMBER: US/09/893,737

CURRENT PILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 60/215,446

PRIOR PILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 329

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 130

LENGTH: 219

TYPE: PRI

TYPE: PRI

CRGANISM: Homo sapiens
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Patent No. 6551795
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224 QGAPGTGASRLD 235
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Best Local Similarity 58.3
Matches 7; Conservative
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RESULT 1
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Sequence 1729, A
Sequence 551, Ap
Sequence 2029, A
Sequence 2029, A
Sequence 138, App
Sequence 138, App
Sequence 282, Appli
Sequence 294, App
Sequence 294, App
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Sequence 157, App
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Sequence 10, Appl
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-252-991A-2299
US-09-134-000C-5551
US-09-134-000C-5551
US-09-252-991A-20299
US-09-252-991A-20299
US-09-312-283C-138
US-09-312-283C-138
US-09-312-283C-382
US-09-312-283C-382
US-09-312-283C-384
US-09-312-283C-394
US-09-552-204A-2
US-09-188-930-294
US-09-552-294A-296
US-09-252-991A-29606
US-09-252-991A-29606
US-09-252-991A-29606
US-09-134-000C-4443
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US-09-1352-991A-2927
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 70.0
-ham 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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CURRENT PELICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Patent No. 6617156

GENERAL INFORMATION:
FILL OF INVENTION: BUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BUNERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE OF INVENTION: BUNER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1
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                                   Score 39; DB 4; Length 219; Pred. No. 71;
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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                                                                           2; Indels
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Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                           5; Mismatches
                                                                                                                                                                                                                                            Sequence 17299, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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ORGANISM: Pseudomonas aeruginosa
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US-09-134-000C-5551
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80.0%;
                                     56.5%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                 Query Match
Best Local Similarity 46.2.
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33 QGGPGSTNSKRQA 45
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Best Local Similarity 80...
Best Local 8; Conservative
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US-09-893-737-130
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RESULT

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Sequence 27594, Application US/09252991A

Sequence 27594, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27594
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARGUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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Pred. No. 2.2e+02;
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Pred. No. 3.2e+02;
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PRIOR APPLICATION NUMBER: US 60/074,788
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Gaps
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Fatent No. 662090
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: Piddington, Christopher S.
TITLE OF INVENTION:
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
FILE REFERENCE: 99-08
CURRENT APPLICATION NUMBER: US/09/552,204A.
CURRENT FILING DATE: 2000-04-19
PRIOR PILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PREASEQ for Windows Version 3.0
SEQ ID NO 2.
LINGTH: 285
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Pred. No. 2e+02;
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Oleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
APPLICANT: TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REPERENCE: 11000.1011c2
                                             Score 37; DB 4; ]
Pred. No. 1.4e+02;
0; Mismatches 3
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CURRENT FILING DATE: 1999-05-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 362
LENGTH: 285
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Patent No. 6573095
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                             Query Match
Best Local Similarity 70.0.
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 EGPPGRTGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mouse
      US-09-312-283C-138
                                                                                                                                                                                                                                                                    US-09-312-283C-382
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Factor No. 6573059
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Steaman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Mutison, James G.
APPLICANT: Mutison, James G.
APPLICANT: Mutison, James G.
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APPLICANT: Mutison, James G.
APPLICANT: Mutison, James G.
APPLICANT: Mutison, James G.
APPLICANT: Mutison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions (SI) 99/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 138, Application US/09188930A

Sequence 138, Application US/09188930A

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Sleeman, Matthew

APPLICANT: Sleeman, Matthew

APPLICANT: Ornust, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOGTWANKE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.6%; Score 37; DB 3; Length 198; 70.0%; Pred. No. 1.4e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                         Score 38; DB 4; Length 818; Pred. No. 4.4e+02;
                                                                                                                                                                                                                              4.4e+02;
4.7e+02;
4.7e+12
                                                                                                                                                                                                                                                                    1; Mismatches
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16691
LENGTH: 818
                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                      718 EGGAGEQNARLDA 730
                                                                                                                                                                                                                                                                                                             1 EGGPGTTSNRLDA 13
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Mouse
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US-09-312-283C-138
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US-09-188-930-138
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ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-188-930-138
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Score 37; DB 4; Length 441; Pred. No. 3.3e+02;
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Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                             1; Indels
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rao, Manachandra N
APPLICANT: Turner, Jan R
TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHWARE: Patentin 1.25
SCHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/736,178C
FILING DATE: 19910726
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CONTAM, ROBERT A
                  FILE REFERENCE: 107196.132
CURRENT APPLICATION WUMBER: US/09/248,796A
PURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14545
                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Eli Lilly And Company STREET: Lilly corporate Center CITY: Indianapolis STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07736178C Patent No. 5514544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32089
REFERENCE/DOCKET NUMBER: XE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%;
72.7%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 655 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-14545
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.6
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                       Sequence 2394, Application US/09188930A

Sequence 2594, Application US/09188930A

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: L1000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wateson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muxison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REPRENCE: 11000.1011c2
FULE APPLICANTON NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%; Score 37; DB 3; Length 294; 70.0%; Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
0; Mismatches 3; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 294, Application US/09312283C
Patent No. 6573095
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-312-283C-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-312-283C-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Rat
                                             JS-09-188-930-294
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RESULT 14

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Search completed: April 28, 2005, 18:28:10 Job time : 28.4062 secs

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April 28, 2005, 18:24:46; Search time 80.6406 Seconds (without alignments) 53.700 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1426032 seqs, 333106140 residues
                                                                                                                                                                                                                                                                                                                                                                               US-10-088-639A-2_COPY_226_238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGGPGTTSNRLDA 13
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c	Sequence 2326, Ap	166000,	4888, Ap	Sequence 7646, Ap	8, Appli	163360,	206460,	Sequence 69481, A	Sequence 39568, A	190792,	130, App	Sequence 12542, A	L0700, A
Description	Sequence	Sequence 166000	Sequence 4888,	Sequence	Sequence 8, Appli	Sequence 163360,	Sequence 206460,	Seguence	Sequence	Sequence 190792,	Sequence 130, App	Sequence	Sequence 10700, A
SUMMARIES	US-10-408-765A-2326	US-10-424-599-166000	US-10-369-493-4888	US-10-369-493-7646	US-10-084-846A-8	US-10-424-599-163360	US-10-424-599-206460	US-10-282-122A-69481	<b>ÙS-10-767-701-39568</b>	US-10-437-963-190792	US-09-893-737-130	US-10-156-761-12542	US-09-815-242-10700
DB	16	15	15	15	15	15	15	15	16	16	σ	14	6
å Query Match Length DB ID	3149	266	398	400	19608	69	85	130	188	203	219	385	454
* Query Match	63.8	6.09	59.4	59.4	59.4	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5
Score	44	42	41	41	41	39	39	39	39	39	39	39	39
Result No.	-	8	e	4	S	9	7	æ	6	10	11	12	13

RESULT 2 US-10-424-599-166000

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Sequence 163360, Application US/10424599
Sequence 163360, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
     TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: 2003-02-29
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 400
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                                                                                                                                                                                                                                                                                                                                                                                            Length 400;
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Pred. No. 3.1e+02;
1; Mismatches 2;
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Publication No. US2004006626A1
GENERAL INFORMATION:
APPLICANT: WEITHAUER, GABRIELE
APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREPERR, AXEL
APPLICANT: TREPERR, AXEL
APPLICANT: TREPERR, AXEL
APPLICANT: TERPERR, OS
TITLE OF INVENTION: AVILANYCIN DERIVATIVES
FILE REPRENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN OF: 120
SOFTWARE: PATENTIN OF: 120
SOFTWARE: PATENTIN OF: 120
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SOFTWARE: PATENTIN OF: 120
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TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
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CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                             TYPE: PRT;
ORGANISM: Burkholderia cepacia
US-10-369-493-7646
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGPGTTSNRLDA 13
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Sequence 166000, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 166000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 15; Length 398; Pred. No. 3.1e+02;
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US-10-424-599-166000
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Sequence 7646, Application US/10369493

PUBLICANTON NO. US2003033675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Blater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4888, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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ORGANISM: Burkholderia fungorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.48;
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Best Local Similarity 72.7
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-369-493-4888
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Sequence 39568, Application US/10767701
Publication No. US20040172684A1
GRNERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement File REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 39568
LENGTH: 188
                                                                             PRIOR PILING NUMBER: 50/200, 848
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
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PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
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Similarity 61.5%; Score 39; DB 15; Length 130;
Similarity 61.5%; Pred. No. 2e+02;
8; Conservative 1; Mismatches 4; Indels
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US-10-767-701-39568
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Pred. No. 2.9e+02;
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; Sequence 190792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 69481
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63.6%;
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Best Local Similarity 63.67
Local 77, Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GPSTTDEKLDA 119
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Best Local Similarity
Matches 8; Conserv
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US-10-767-701-39568
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERIOR: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Experiment of Application No. Vibration No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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US-10-424-599-163360
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 15;
Pred. No. 1.1e+02;
2; Mismatches 2
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163360
LENGTH: 69
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APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblesn, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGGPGTTSNRL 11
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ORGANISM: Glycine max
                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-206460
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APPLICANT:
APPLICANT:
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Gaps
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0
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APPLICANT: Oblien, Kari L.
APPLICANT: Oblien, Kari L.
APPLICANT: Oblien, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramanoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: IDENATYORES
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: OF SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOUR
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 14;
Pred. No. 6.1e+02;
1; Mismatches 1;
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: UP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR PILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12542
; LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10700, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis US-09-815-242-10700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.5
Best Local Similarity 80.0
Matches 8; Conservative
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                                       TITLE OF INVENTION: Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190792
LENGTH: 203
TYPE: PPT
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Pred. No. 3.2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: PAT_MRT4530_87172C.1.pep
US-10-437-963-190792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 130, Application US/09893737
Patent No. US20020110855A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS;
FILE REFRENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR PUPLICATION NUMBER: US 60/215,446
PRIOR PRICRATION NUMBER: US 60/215,446
NUMBER OF SEQ ID NOS: 329
SOFTWARE FRANCEO FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISBA, HARUO
APPLICANT: ISBA, HARUO
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.5%;
     La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.v-
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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US-10-156-761-12542
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/203,335

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLICATION NUMBER: 60/230,233

PRIOR PLICATION NUMBER: 60/233,625

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,636

PRIOR PLICATION NUMBER: 60/253,636

PRIOR PLICATION NUMBER: 60/267,636

PRIOR PLICATION NUMBER: 60/269,308

PRIOR PLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

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PRIOR APPLICATION NUMBER: 60/269,308
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Publication No. US20040048310A1
Publication No. US20040048310A1
Publication No. US20040048310A1
APPLICANT: PHUMPAN, GRECORY D. APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WARTINEZ, RICARDO
APPLICANT: WARTINEZ, RICARDO
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE-LIKE
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: 038602/1366
CURRENT APPLICATION NUMBER: US/10/182,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sequence 57133, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Enterococcus faecalis
US-10-282-122A-57133
                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 80.0
Matches 8; Conservative
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LENGTH: 454
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US-10-182-243-45
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; CURRENT FILING DATE: 2003-07-07; PRIOR PAPPLICATION NUMBER: PCT/US01/02337; PRIOR FILING DATE: 2001-01-25; NUMBER OF SEQ ID NOS: 84; SCOTURARE: Patentin Ver. 2.1; SEQ ID NO 45; LENGTH: 600; TYPE: PRT ; ORGANISM: Homo sapiens US-10-182-243-45

Query Match

Query Match

Patches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps O; Beat Local Similarity 87.5%; Pred: No. 9.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps O; Search completed: April 28, 2005, 19:02:17
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55; Search time 17.875 Seconds Run on:

(without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_226_238 69 1 EGGPGTTSNRLDA 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ΩI	Description
1 1	43	62.3	149	~	C87666	ribonuclease HI [1
8	40	58.0	249	7	AG0618	probable DNA repli
m	40	58.0	249	~	T03011	dnaC protein homol
4	40		344	7	S57901	estradiol 17beta-c
ß	40	58.0	351	~	T36010	
9	39	56.5	1073	~	T33764	hypothetical prote
7	39	56.5	1112	~	H95964	Ψ
80	39	56.5	3938	~	T42761	Bassoon protein -
6	38	55.1	293	N	E69174	succinate-CoA liga
10	38	55.1	293	N	F83618	conserved hypothet
11	38	55.1	312	~	AG2884	hypothetical prote
12	38	55.1	312	7	D97660	hypothetical prote
13	38	55.1	352	~	F70134	flagellar motor sv
14	38	55.1	667	~	F70682	probable membrane
15	38	55.1	1872	7	T24683	hypothetical prote
16	37	53.6	139	7	E75346	organic hydroperox
17	37	53.6	194	7	157523	HSP90 - mouse (fra
18	37		222	7	A72643	hypothetical prote
19	37	53.6	229	7	T40148	hypothetical prote
20	37	53.6	290	7	T03552	ä
21	37	53.6	353	N	T09665	peroxidase (EC 1.1
22	37	53.6	385	~	H86731	Š
23	37	53.6	411	~	845318	keratin 12 - rabbi
24	37		443	7	T21499	
25	37	53.6	604	~	S25203	srmR protein - Str
56	37	53.6	919	~	A72627	probable 2-oxoacid
27	36	52.2	143	~	A49438	Ę,
28	36	52.2	148	0	m	ribonuclease H PA1
29	36	52.2	159	7	I49023	tumor suppressor p

hypothetical prote hypothetical prote	Holliday junction DNA-binding protei	syntaxin synt4 [im peroxidase (EC 1.1	probable methionin probable beta-keto	carboxypeptidase A ADK1 [imported] -	conserved hypothet hypothetical prote	hypothetical prote fibrinogen alpha c	chemotaxis protein
A82783 T33010	E81717 C71565	108433 T48847 JC4779	T40384 E96029	A56171 B86170	E83085 T23624	T23623 FGHUA	E84253
00	000	900	0 0	0 0	0 0	7 7	0
240 313	334	341 351	379 400	417	549 582	617 644	668
52.2 52.2	22.2	52.2	52.2 52.2	52.2 52.2	52.2 52.2	52.2 52.2	52.2
36	36	9 9 9	36	36 36	36 36	36 36	36
30 31	335	# 15 19 10 10 11 10 10 11	37	39 40	41	4 4 4	45

## ALIGNMENTS

PRSIII.T 1
C87666
ribonuclease HI [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: C87666
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: C87666
A;Status: preliminary
A; Molecule type: DNA
A;Residues: 1-149 <sto></sto>
A.Cross_references.INIDBOT.Oga341. GR.AR005673. NID.c13425071. PIDN.AAK25327.1. GSPDB.GN

A;Cross-references: UNIPROT:09A341; GB:AE005673; NID:913425071; PIDN:AAK25327.1; GSPDB:GR C;Genetics: A;Gene: CC3365 C;Superfamily: ribonuclease H

Gaps . , Length 149; 1; Indels Score 43; DB 2; Pred. No. 3.7; 3; Mismatches Query Match 62.3%; Best Local Similarity 63.6%; Matches 7; Conservative ઠે

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2 GGPGTTSNRLD 12 | ||||: 38 GEPGTTNNRME 48 g

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Auchable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterics probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica serovar Typhi Sybotes: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0618 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Comnerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Tile: Drainiary A;Molecule type: DNA A;Residues: 1-249 <PAR> A;Cross-references: GB:AL513382; PIDN:CAD05417.1; PID:g16502178; GSPDB:GN00176 C;Genetics: STY1023 C;Superfamily: DNA replication protein dnaC

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RESULT 3 T03011

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: Last <SEE>
A;Cross-references: UNIPROT:Q9XABB; EMBL:AL096839; PIDN:CAB50763.1; GSPDB:GN00070; SCOEDE
C;Genetics:
A;Gene: SCOEDB:SCC22.20
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 1-1073 - PAUJ-
A,Residues: 1-1073 - PAUJ-
A,Status: UNIPROT: OBITWO; UNIPROT: O9UAN9; EMBL: AF101304; PIDN: AAC69200.1; GSPDE
A,Experimental source: strain Bristol N2; clone C02E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable outer membrane secretion protein SMb21543 [imported] - Sinorhizobium meliloti (f C)Species: Sinorhizobium meliloti (c)Species: Sinorhizobium meliloti (c)Species: Sinorhizobium meliloti (c)Species: Old #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 (C)Accession: H95964 (R)Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, Z001 M.S.A. 98, A;Fitle: The complete sequence of the 1,683-kD pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-112 cKUR>
A;Molecule type: DNA
A;Rosidues: 1-112 cKUR>
A;Cross-references: UNIPROT:092UV3; GB:AL591985; PIDN:CAC49384.1; PID:g15140870; GSPDB:GR
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Polain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M.L.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C02B11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                  Score 40; DB 2; Length 351;
Pred. No. 30;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Pauley, A.; Harper, M. submitted to the EMBL Data Library, October 1998 A.Description: The sequence of C. elegans cosmid CO2EII. A.Reference number: 221403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 37/1; 174/3; 248/3; 511/3; 702/2; 1043/3
                                                                                                                                                                                                                                                        58.0%;
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Best Local Similarity 80.0°
Matches 8, Conservative
                                                                                                                                                                                                                                                        Query Match 58.0
Best Local Similarity 63.6
Matches 7; Conservative
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Cross-references: UNIPROT:P51657; EMBL:X78811; NID:9561532; PIDN:CAA55389.1; PID:95615
Supering: 17beta-dehydrogenase; short-chain alcohol dehydrogenase homology
;Keywords: oxidoreductase
;4-189/Domain: short-chain alcohol dehydrogenase homology <SADH>
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R;Accession: S57901
R;Accession: S57901
R;Accession: S7901
R;Accession: S7901
R;Accession: S57901
A;Title: Rat 17-beta-hydroxysteroid dehydrogenase type 1: primary structure and regulati A;Reference number: S57901; MUID:95009707; PMID:7925110
A;Accession: S57901
A;Accession: S57901
A;Accession: S57901
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A;Accession: S7901
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C;Superfamily: DNA replication protein dnaC
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36010
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
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                                                                                                                                                                                                                                                                                                                                                                           dnaC protein homolog - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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                                                                                               Gaps
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                                      Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2; Length 249;
Pred. No. 21;
                                                                                                      4; Indels
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                                      DB 2;
21;
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C;Accession: T03011 #sequence_revision 24-Mar-1999 #
R;Piqueroa-Bossi, N.; Bossi, L.
R;Piqueroa-Bossi, N.; Bossi, L.
R;Reference number: 214818
A;Recession: T03011
A;Accession: T03011
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-249 <FIG>
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                                                                                                  0; Mismatches
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                                      Score 40;
Pred. No.
                               58.0%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                            Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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56.5%;

Query Match 56.5 Best Local Similarity 77.8 Matches 7; Conservative

A;Gene: SMb21543 A;Genome: plasmid

913 GDPGSTSNR 921

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RESULT 8 T42761 Bassoon protein - rat

2 GGPGTTSNR 10

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Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cipaccession: F83618
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Broadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 <STO>
A;Cross-references: UND:0916S9; GB:AE004459; GB:AE004091; NID:g9946043; PIDN:AAG03599
A;Experimental source: strain PAO1
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
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A;Cross-references: UNIPROT:Q8UCI1; G8:AE008688; PIDN:AAL43493.1; PID:g17741000; GSPDB:G?
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu2506 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                     conserved hypothetical protein PA0209 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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59;
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Pred. No. 55;
1; Mismatches
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Pred. No.
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C;Superfamily: inner membrane protein ugpA
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                              Pseudomonas aeruginosa
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255 EGGTGTASSKREA 267
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252 QGGPGTASETIN 263
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Rattus norvegicus (Norway rat)
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C; Accession: T42761
C; Accession: T42761
S; Sammarti-Vila, L; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A; Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A; Reference number: Z22249; MUID: 98345363; PMID: 9679147
A; Accession: T42761
A; Status: preliminary; translated from GB/EMBL/DDBJ
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R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K., S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: Succinyl-CoA synthetase, alpha subunit
Keywords: acid-thiol ligase; ATP; coenzyme A; phosphohistidine; phosphoprotein; tricar
249/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
*Kesidues: 1-3938 *OLIE:
A;Cross-references: UNIPROT:088778; EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g341
A;Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Function:
A;Description: may be involved in cytomatrix organization at the site of neurotransmitte
A;Note: component of the presynaptic cytoskeleton
C;Keywords: coiled coil; zinc finger
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
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A;Experimental source: strain Delta H
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                        Score 39, DB 2; Length 1112;
Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ternate names: brain-specific synapse-associated protein
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69 GPGSVSRRLD 78

ઠે 원 EGGPGTTSNRLDA 13

A; Residues: 1-293 <MTH>

A; Note: MTH563 Genetics:

A;Molecule type: DNA

A; Experimental source: strain H37Rv

A;Gene: AGR C 4553 A;Map position: circular chromosome C;Superfamily; inner membrane protein ugpA

:Genetics:

Query Match 55.1%; Best Local Similarity 50.0%; Matches 6; Conservative

:||||| :: 252 QGGPGTASETIN 263

1 EGGPGTTSNRLD 12

ठ В Best Local Similarity 72.7 Matches 8; Conservative

Query Match

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Residues: 1-1872 <WIL>
| Cross-references: UNIPROT:Q9XTE2; EMBL:Z50875; PIDN:CAA90776.1; GSPDB:GN00021; CESP:T08
| Experimental source: clone T08A11
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;Molecule type: DNA
;Residues: 1-1872 <MI2>
;Cross-references: EMBL:ALO21180; PIDN:CAA15982.1; GSPDB:GN00021; CESP:T08A11.1
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24683; T26904
R;Chui, C.; Sulaton, J.
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   C;Genetics:
A;Gene: Rv2395
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0361
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                                                                                                                                       Length 667;
                                                                                                                                    Score 38; DB 2; I
Pred. No. 1.3e+02;
2; Mismatches 4;
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                                                                                                                                       Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: F70134

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Bowman, C.; Garland, S.; Fuji, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hanson, M.; Vugt, Salzuses Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-312 <KUR>
A;Cross-references: UNIPROT:Q8UCI1; GB:AE007869; PIDN:AAK88237.1; PID:g15157693; GSPDB:G
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C,Species: Mycobacterium tuberculosis
C,Species: Mycobacterium tuberculosis
C,Accession: F70682
R,Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A,Authors: Sqares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MUID:98295987; PMID:9634230
A,Accession: F70682
A,Status: preliminary, nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Euroscopia 1-667 cCOL>
A,Cross-references: UNIPROT:P71749; GB:Z81368; GB:AL123456; NID:g3261656; PIDN:CAB03731.
Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A,Reference number: A97359; MUD:21608551; PMID:11743194
A,Accession: D97660
A,Status: preliminary
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A;Residues: 1-352 <KLE>
A;Residues: 1-352 <KLE>
A;Cross-references: UNIPROT:O57511; GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC6667
A;Experimental source: strain B31
C;Superfamily: flagellar motor switch protein flim
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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59;
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Pred. No. 59;
3; Mismatches
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ATPB CLOPE

CN93 MOUSE

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SYR_WYCLE
SASO BRANA
BDF1_YEAST
MGD1_MOUSE
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IRS2_MOUSE
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                                                                                                                                     September 24, 2004, 01:42:46; Search time 10.7925 Seconds (without alignments) 62.721 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                          rattus norv
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                                                                                          ovis aries
drosophila
                                                                                                                                           microlepia
                                                                                                                                                                                                                                                                                                                                                        halobacteri
                               taurus
                                                                     sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales,
Caulobacteraceae, Caulobacter.
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Q9uls6
O35174
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O03068
O84709
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P12370
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
RNHA OR CC3365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 AA
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                                                                                                                                                                                                                                                                               ATPB_PTEES
GTR8_HUMAN
KCS2_HUMAN
KCS2_HUMAN
KCS2_RAT
ATPB_DENPU
BNGA_CHLTR
GVD2_HALN1
GVD2_HALN1
GVD2_HALN2
DCMC_HUMAN
ATPB_PTEAQ
XXNB STRLI
KAPA_CANFA
KAPA_GANFA
KAPA_BOVIN
KAPA_HUAN
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 Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=155892;
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SEQUENCE FROM N.A.
47.8
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Q9A341;
 RESULT 1
RNH_CAUCR
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SEQUENCE FROM N.A.

SEQUENCE TO Columbia;

MEDINNE-210670; PubMed=11130713;

MEDINNE-210670; PubMed=11130713;

A salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Balanoubat M., Lemcke K., Rieger M., Ansorge W., Obermaier B.,

Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

De Simone V., Choisne N., Artiguenave F., Robert C., Erothier P.,

Mincker P., Cattolico L., Waissenbach J., Saurin W., Quetier F.,

A wincker P., Cattolico L., Waissenbach J., Saurin W., Benes V.,

A windbach E., Drzonek H., Faffle H., Holland R., Brander S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

Conzad A., Hornischer K., Kauer G., Lochnert T.-H., Nordsiek G.,

Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
                                                                                                                                     of
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
17-OCT-2001 (Rel. 20, Last annotation update)
18-OCT-2001 (Rel. 20, Last annotation u
"Complete genome sequence of Caulobacter crescentus.";
Proc. Nacl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: This enzyme is an endonuclease that degrades the RNA RNA-DNA hybrids specifically (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                   proteome.
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PIR; C87666, C87666.
HISP: P000647; 1RBR.
TIGS: CC3365; -.
HAMAP; MF 00042; -; 1.
InterPro; IPR001156; RNaseH.
InterPro; IPR00715; RNaseH.
InterPro; IPR00715; RNaseH.
Hydrolase; Nuclease; Endonuclease; Magnesium; Complete prot METAL
METAL
10 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
SEQUENCE 149 AA; 16674 MW; CB2271A33782435C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 63.6%;
Matches 7; Conservative
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GL12_ARATH
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Rattus norvegicus (Rat).
     HSD17B1 OR EDH17B1.
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Matches
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de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Mannhaupt G., Haase D., Schoof H., Nudd S., Zaccaria P., Mewes H.-W.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Roomey T., Rizzo M., Walts A., Utterback T., Fuji C.Y., Shea T.P.,
A Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B.,
A Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE NON-FUNCTIONAL MANGANESE-BINDING
                                                                                                                                                                                                  -!- FUNCTION: May play a role in plant defense. Has probably no oxalate oxidase activity even if the active site is conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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InterPro; IPR00113; Cupin.
InterPro; IPR00113; Cupin.sup.
InterPro; IPR001929; Germin.
Print; PR00130; GERMIN; I.
PRINTS; PR00125; GERMIN; FALSE_NEG.
Apoplast; Cell wall; Signal; Glycoprotein; Manganese; Metal-binding;
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P51657;
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Estradiol 17 beta-dehydrogenase 1 (EC 1.1.1.62) (17-beta-HSD 1)
(17-beta-hydroxysteroid dehydrogenase 1).
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
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BY SIMILARITY.
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                                                                                                                                                                                                                                    (By similarity).
--- SUBCELLULAR LOCATION: Apoplast (By similarity).
--- SIMILARITY: Belongs to the germin family.
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0; Mismatches
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50 BY
38 N-
71 N-
139 N-
24648 MW;
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71
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129 AA;
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Best Local Similarity
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114
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SEQUENCE
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DHB1_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akinola L.A., Poutanen M., Vihko R., "Cloning of rat 17 beta-hydroxysteroid dehydrogenase type 2 and characterization of tissue distribution and catalytic activity of rat
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley, TISSUE=Testis, MEDLINE=98201618; PubMed=9524272; Akinola L.A., Poutanen M., Peltoketo H., Vihko R., Vihko P.; "Characterization of rat 17 beta-hydroxysteroid dehydrogenase type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Ovary;
MEDIAINE=$5009707; PubMed=7925110;
Ghersevich S., Nokelainen P., Poutanen M., Orava M.,
Autio-Harmainen H., Rajaniemi H., Vihko R.;
"Rat 17 beta-hydroxysteroid dehydrogenase type 1: primary structure and regulation of enzyme expression in rat ovary by diethylstilbestrol and gonadotropins in vivo.";
Endocrinology 135:1477-1487(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene and mRNA transcripts.";
Gene 208:229-238(1998).
-!- FUNCTION: FAVORS TREDUCTION OF ESTROGENS AND ANDROGENS.
-USES PREFERENTIALLY NADH.
-!- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P) (+) = estrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00061; ADH_SHORT; 1.
iosyntheeis; Oxidoreductase; NAD; Multigene family.
iosyntheeis; Oxidoreductase; NAD; Multigene family.
143 t43 SUBSTRATE BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
CBSFC139FBB3995E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Kidney;
MEDLINE=96198748; Pubmed=8612487;

    -!- PATHWAY: Estrogens biosynthesis.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinology 137:1572-1579(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR002198; ADH_short.
Pfam; PF00106; adh short; 1.
PRINTS; PF000080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA; 36967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X78811; CAA55389.1; -. EMBL; X97754; CAA66349.1; -. EMBL; X98038; CAA66657.1; -. PIR; S57901; S7901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 1 and type 2 enzymes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 EGGPGGALERADÁ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 61.5
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steroid biosynthesis; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SDR) family.
                                                                      NCBI_TaxID=10116;
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EMBL; AE000839; AAB85069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| || |:::|
255 EGGTGTASSKREA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                      PIR; E69174; E69174.
                                                                                                                                                                                                                                    subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P07459; 1SCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
ACT_SITE 249
           SEOUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                          phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLIM_BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Lucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Involved in the formation of 2-(5''-phosphoribosyl)-3'-dephosphocoenzyme-A, the prosthetic group of the acyl-carrier protein of the malonate decarboxylase (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 3-dephospho-CoA = 2'-(5''-triphosphoribosyl)-3'-dephospho-CoA + adenine.
-!- SIMILARITY: Belongs to the citG/mdcB family.
                                                               16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable 2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase
(EC 2.7.8.25) (2-(5''-triphosphoribosyl)-3'-dephospho-CoA synthase)
MDCB OR PA0209.
                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Succinyl-CoA synthetase alpha chain (EC 6.2.1.5) (SCS-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%; Score 38; DB 1; Length 293; 61.5%; Pred. No. 27; 1. Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE004459; AAG03598.1; -.
PIR; F83618; F83618.
HAWAP; MF 00397; -; 1.
InterPro; IPR002736; CitG.
Pfam; PP091, CitG.
Transferae; Complete proteome.
SEQUENCE 293 AA; 30533 MW; A9A085F070C680B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AA:
                                      293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                            Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGGAGEQNARLDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen."
Nature 406:959-964(2000)
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                          NCBI_TaxID=287;
                                     MDCB PSEAE
Q91659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUCD METTH 026663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
SUCD_METTH
                         MDCB PSEAE
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                                             Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-98037514; pubMed=9371463; Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J. Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .!- SIMILARITY: Belongs to the succinate/malate CoA ligase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003781; CoA_lig_alpha.
InterPro; IPR005811; CoA_lig_alpha.
InterPro; IPR005811; CoA_lig_ase.
Pfam; PF02629; CoA_binding; 1.
Pfam; PF03649; ligase-CoA; 1.
PRINTS; PR01799; SCOASYNTHASE.
TIGRAPAS; TIGRO1019; succoAalpha; 1.
PROSITE; PS00399; SUCCINYL COA_LIG_2; 1.
PROSITE; PS01216; SUCCINYL COA_LIG_1; 1.
Ligase; Tricarboxylic acid cycle; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELE-PHOSPHOHISTIDINE INTERMEDIATE
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Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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293 AA; 30810 MW; 2E9769305CE51DA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05751;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DEC-2091 (Rel. 40, Last annotation update)
Flagellar motor switch protein flim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Golobori T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPD1 COF
Q8FUC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPD1_C
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                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            STRAIN=ATCC 35210 / B31;
MBDLINE=8066543; PubMed=9403685;
Fraesr C.M., Casjen B.M., Hung W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-P., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Uterbosck T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-dehydroquinate dehydratase (BC 4.2.1.10) (3-dehydroquinase) (Type I
                                                                                                                                                                                                                      NATURE 330:580-586 (1997).

-!- FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Membrane-associated (Potential). SIMILARITY: Belongs to the flim family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.1%; Score 38; DB 1; Length 352; 72.7%; Pred. No. 33; indels iive 0; Mismatches 3; Indels
                                                                                                                                                                                              "Genomic sequence of a Lyme disease spirochaete, Borrelia
            Ge Y., Charon N.W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AA; 39284 MW; 2454D37BBF51C977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemotaxis; Flagellum; Flagellar rotation; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO0955; FLGMOTORFLIM.
ProDom; PD001777; SpoA; 1.
TIGRFAMB; TIGR01397; flim_ewitch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001689; Flag Flim.
InterPro; IPR001543; SpoA.
Pfam; PF02154; Flim; 1.
Pfam; PF01052; SpoA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001137; AAC66670.1; -.
PIR; F70134; F70134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desulfurococcaceae; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U43739; AAA85602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L75945; AAB58965.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 GVGTTSENLDA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
SEQUENCE 352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AROD OR APE0577.
                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; BB0278; -
STRAIN=212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AROD AERPE
09YEK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ОНОаве)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AROD AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       -i - CATALYTIC ACTIVITY: 3-dehydroquinate = 3-dehydroshikimate + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AP000060; BAA79545.1; -.

PIR, A72643; A72643.

HAMAP, ME 00214; -; 1.

InterPro, IPR001381; DHQuinase I.

PROSITE; PS01028; DEHYDROQUINASE I; FALSE NEG.

Aromatic amino acid biosynthesis; Lyase; Complete proteome.

ACT SITE 117 117 BY SIMILARITY.

ACT SITE 143 143 SCHIFF-BASE INTERNEDIATE (BY SIMILARITY).

SEQÜENCE 222 AA; 23153 MW; A77F9F32E3303823 CRC64;
                                                                                                                                         Ή.
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-!- FUNCTION: Modulates the activities of several enzymes which are inactive in their acetylated form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS-WAR-2004 (Rel. 43, Created)
IS-WAR-2004 (Rel. 43, Last sequence update)
IS-WAR-2004 (Rel. 43, Last amotation update)
NAD-dependent deacetylase 1 (EC 3.5.1.-) (Regulatory protein SIR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 third step. -- SIMILARITY: Belongs to the type-1 3-dehydroquinase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                            Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ahkai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Makuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Rubota K., Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%; Score 37; DB 1; Length 222; 63.6%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 AA
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                                                                                                                                                                                                                                                                                                                                                    crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                      MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 GPGTLASRLTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPGTTSNRLDA 13
FROM N.A.
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285 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
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Q28706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
K1CL_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C TISSUE-Brain, and Muscle;
X MEDLINE-21388227; PubMed=12477932;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: NAD(+) + an acetylprotein = nicotinamide + O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Complement-ciq tumor necrosis factor-related protein 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                      1; Zinc; Complete proteome.
DEACETYLASE SIRTUIN-TYPE.
NAD BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                   acetyl-ADP-ribose + a protein.
COPACTOR: Binds 1 zinc ion and NAD (By similarity).
SUBCELLUAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the sirtuin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7EF99C2DE0012680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                   EMBL; AP005214; BAC16902.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                    HAMAP; MF 01121; -; 1.
InterPro; IPR003000; SIR2.
Pfam; PF02146; SIR2; 1.
PROSITE; PS50305; SIRTUIN; 1.
Hydrolase; NAD; Metal-binding;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GGPGRADHRVD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQT2 HUMAN
Q9BXJS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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-i- SUBUNIT: Heterotetramer of two type I and two type II keratins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu R.-L., Zhu G., Galvin S., Xu C., Haseba T., Chaloin-Dufau C., Dhouailly D., Wei Z.-G., Lavker R.M., Kao W.-Y., Sun T.-T.; "Lineage-specific and differentiation-dependent expression of K12 keratin in rabbit corneal/limbal epithelial cells: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 2.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnetrield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnetrield Y.S.M., E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99116899-16903 (2002).
-!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Keratin, type I cytoskeletal 12 (Cytokeratin 12) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; Length 285;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C1Q.
7E31FF9868D4EDFA CRC64;
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MEDLINE=94192891; PubMed=7511548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              northern blot analysis.";
Differentiation 55:137-144(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew, HGNC:14325; CIQTNE2.
InterPro; IPR001073; CIQ.
InterPro; IPR008166; Collagen.
InterPro; IPR008168; TNF like.
Pfam; PF01386; CIQ; 1.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTCIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF329836; AAK17960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC011699; AAH11699.1; -. BC054506; AAH54506.1; -.
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70.0%;
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Matches 7; Conservative
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its an example of this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                   MISCELLANDOUS: There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and II (neutral to basic) (40-55 and 56-70 kDa, respectively).
SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98153623; PubMed=9399908;
Nishida K., Honma Y., Dota A., Kawasaki S., Adachi W., Nakamura T.,
Quantock A.J., Hosotani H., Yamamoto S., Okada M., Shimomura Y.,
                Associated mainly with all
           TISSUE SPECIFICITY: Cornea specific. Associated mainly with all layers of the central corneal epithelium and also found in the suprabasal limbal epithelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS MCD GLY-135; ILE-135; ARG-140 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Keratin, type I cytoskeletal 12 (Cytokeratin 12) (KI2) (CK 12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cornea,
MEDLINE=96335085; PubMed=8759347;
Nishida K., Adachi W., Shimizu-Matsumoto A., Kinoshita S.,
Mizuno K., Matsubara K., Okubo K.,
"A gene expression profile of human corneal epithelium and
isolation of human keratin 12 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.6%; Score 37; DB 1; Length 411; 58.3%; Pred. No. 58; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER 12.
COIL 2.
0B22E9A4D9DCC250 CRC64;
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                                                                                                                                                                                                                                                                                                 Pfam; PF00038; filament; 1. –
PRINTS; PR01248; TYPEIKERATIN.
PROSITE: PS0026; IF; 1.
Intermediate filament; Coiled coil; Keratin.
Keratin 3 associates with keratin 12.
                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
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                                                                                                                                                                                                                                                                  InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
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les 7; Conservative
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ALC HUMAN
ALC Q99456,
DT 01-NOV-
DT 15-MAR-
DE Keraelt
BE Keraelt
BE Keraelt
COC BEUKARY
COC Mammal)
OX NCBL T?
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RN KILLIN
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The Transfer Fractin I. Mucation in a German Kindred with meebmain B corneal dystrophy.";

Br. J. Ophthalmol. 84:527-530(2000).

-!- FUNCTION: May play a unique role in maintaining the normal corneal epithelial function (By similarity).

-!- SUBUNIT: Heterotetramer of two type I and two type II keratins.

Keratin 3 associates with keratin 12.

-!- TISSUE SPECIFICITY: Cornea specific.

-!- DISEASE: Defects in KRT12 are a cause of juvenile epithelial corneal dystrophy of Meesmann (MCD) [MIM:122100]. MCD is an autosomal dominant disease that causes fragility of the anterior corneal epithelium. Patients are usually asymptomatic until adulthood when rupture of the corneal microcysts may cause erosions, producing clinical symptoms such as photophobia, contact lens intolerance and intermittent diminution of visual acuity.

Rarely, subepithelial scarring causes irregular corneal astigmatism and permanent visual impairment. Histological examination shows a disorganized and thickened epithelium with with examination shows a disorganized and thickened epithelium with examination shows a disorganized and thickened epithelium with
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--- MISCELLAMBOUS: There are two types of cytoskeletal and microfibrillar Keratin, I (acidic) and II (neutral to basic) (40-55 and 56-70 kDa, respectively).
--- SIMILARITY: Belongs to the intermediate filament family.
Kinoshita S.; and chromosomal localization of a cornea-specific human "Isolation and detection of four mutations in Meesmann corneal epithelial dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular genetics of Meesmann's corneal dystrophy: ancestral and novel mutations in keratin 12 (K12) and complete sequence of the
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., VARIANTS MCD THR-129 AND THR-135, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20245342; PubMed=10781519; Corden L.D., Swensson O., Swensson B., Rochels R., Wannke B., Thiel H.J., McLean W.H.I.; Thiel H.J., McLean W.H.I.; Anovel keratin 12 mutation in a German kindred with Meesmann's
                                                                                                                                                                                                                                                                                                                                                                                                                                    Corden L.D., Swensson O., Swensson B., Smith F.J.D., Rochels R., Uitto J., McLean W.H.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Irvine A.D., Corden L.D., Swensson O., Swensson B., Moore J.E. Frazer D.G., Smith F.J.D., Knowlton R.G., Christophers E., Rochels R., Uitto J., McLean W.H.I.; "Mutations in cornea-specific keratin K3 or K12 genes cause Meesmann's corneal dystrophy."; Nat. Genet. 16:184-187(1997).
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                                                                                                                                                                                    Am. J. Hum. Genet. 61:1268-1275(1997).
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AB007119; BAA25063.1; -.
AB007115; BAA25063.1; JOINED.
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EMBL; AB007117; BAA25063.1; JOINED.
EMBL; AB007118; BAA25063.1; JOINED.
EMBL; AF137286; AAF61432.1;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20113327; PubMed=10644419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS MCD THR-135 AND LEU-143.
MEDLINE=97315826; PubMed=9171831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human KRT12 gene.";
Exp. Eye Res. 70:41-49(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CS7BL/6J; TISSUB-Medulla oblongata, and Testis;
MEDLINE-22354683; PubMed-12466851;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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                                          PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 494;
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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CUB and sushi multiple domains protein 3 (Fragment).
                                                                                                                                                                                                                  / FTIG=VAR 008525.
/FTIG=VAR 008525.
R -> G (in MCD).
/FTIG=VAR 008526.
                                                                                                                                                                 /FTId=VAR 009547.
M -> T (in MCD).
/FTId=VAR 013126.
                                                                                                                                                                                                                                                                             FTIG=VAR 003834
                                                                                                                                                                                                                                                                                                  FTId=VAR 008527
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D (in MCD).
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FTId=VAR 01312
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1; Mismatches
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COIL 1B.
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COIL 1A.
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InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
PRIMTS; PR01248; TYPELKERATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               277 GGPGEVSVEMDA 288
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Matches 7; Conservative
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Parallerical Tr., Commany Y., Ristogram A., Schonbach C., Goldberl T., Radiarelli R., Mrangila A., Matenda H., Schonbach C., Goldberl T., Radiarelli R., Hill D., Bull C., Wogami A., Schonbach C., Goldberl T., Radiarelli R., Hill D., Waterda B., Matenda H., Batelow S., Beisels K.W., Dalla E., Dreagani T.M., Ranapin A., Matenda H., Batelow S., Beisels K.W., Dalla E., Dreagani T.M., Pletcher C.E., Porrett A., Prace K.S., Dalla E., Dreagani T.M., Pletcher C.E., Porrett A., Prace K.S., Dalla E., Dreagani T.M., Pletcher C.E., Porrett A., Prace K.S., Dalla E., Dreagani T.M., Pletcher C.E., Porrett A., Prace K.S., Bitcher C.E., Matenda M., Pletcher C.E., Porrett A., Prace K.S., Bitcher C.E., Matenda M., Dalla E., Matenda M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M., Canglo, M.,

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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

A Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,

A Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,

A Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

A Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

A Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

R Nagatsuma M., Takhashi-Fuji A., Oshima A., Sugiyama A., Kawakami B.,

R Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RI NEDO human cDNA sequencing project.";

RI Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

C -! - SUBCELULAR LOCATION: Type I membrane protein (Potential).

CC -! - ALTERNATIVE PRODUCTS:

CC -! - ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND VARIANTS MET-182 AND HIS-3584.
TISSUE=Brain, and Teefils;
MEDLINE=22824680; PubMed=12943675;
Shimizu A., Asakawa S., Shimizu N.;
A novel giant gene CSMD3 encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1.";
Blochem. Biophys. Res. Commun. 309:143-154(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase T., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 624-3670 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                    4
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=22788796; PubMed=12906867;
Lau W.L., Scholnick S.B.;
"Identification of two new members of the CSMD gene family.";
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=3;
IsoId=072407-3; Sequence=VSP_009048, VSP_009049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=07Z407-5; Sequence=VSP 009051, VSP 009052; Note=No experimental confirmation available;
                                                                                                                                                                                                       Q72407; Q96P23;
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
CUB and sushi multiple domains protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q7Z407-4; Sequence=VSP 009050;
Note=No experimental confirmation available;
53.3%; Pred. No. 4.8e+02; wiematches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
IsoId=Q7Z407-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21456161; PubMed=11572484;
                                                                                           2204 GNPGTTANGKVFRID 2218
                                                                   2 GGPGTTSN----RLD 12
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DNA Res. 8:179-187(2001).
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                                  8; Conservative
                                                                                                                                                                                          STANDARD;
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Homo sapiens (Human).
                  Best Local Similarity
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AISCGIPKAPTWGGILTDYLVGTRVTYFCNDGYRLSSKEL
TTAVCO -> GEVYYAKOMKOMNVELAPFNVFIWITNFSEN
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2; Mismatches 1; Indels
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/FTId=VSP 009049.
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUB AND SUSHI MULTIPLE DOMAINS PROTEIN 3. EXTRACELLULAR (POTENTIAL).
TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substantia nigra, thalamus, spinal cord, hippocampus and fetal brain. Also expressed in testis.

SIMILARITY: Belongs to the CSMD family.

SIMILARITY: Contains 14 CUB domains.

SIMILARITY: Contains 19 Sushi (SCR) domains.
                                                                                                                                                                                                                                                                                                                                    EMBL; AV210419; AA034702.1; -...

REMBL; AB114604; BAC82443.1; -...

REMBL; AB114605; BAC82444.1; -...

REMBL; AB067491; BAS67787.2; -...

REMBL; AR067491; BAS67587.2; -...

REMBL; ARC6252; BAC68505.1; ALT_INIT.

Genew; HGNC:19291; CSMD3.

RITCEPTO; IPRO000459; CUB.

RITCEPTO; IPRO00045; Sushi_SCR_CCP.

REMBL; SMO0043; Sushi, 27.

RANART; SMO0042; CUB; 14.

REPGAL; SMART; SMO0042; CUB; 14.

REPGAL; SMART; SMO0042; CUB; 14.

REPGAL; Signal; Transmembrane; Sushi; Alternative splicing; Polymorphism.

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                                                                                                                                                                       STRAIN-ATCC 15622 / PAO1;

MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                          -!- FUNCTION: This enzyme is an endonuclease that degrades the RNA RNA-DNA hybrids specifically (By similarity).
                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 148; Pred. No. 28;
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dagnesium (BY Similarity).
1171AF5A9D267CDB CRC64;
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PIR, A83418; A83418.
HSSP; P00647; 1RBS.
HAWARP; MF 00042; -; 1.
InterPro; 1PR000156; RNaseH.
Pfam; PF00075; rnaseH; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium; ' A84078SIUM, BY SIM
                                                 28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ribonuclease HI (EC 3.1.26.4) (RNase HI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                               148 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.2%;
                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 54.9
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                             RNHA OR PA1815.
Pseudomonas aeruginosa.
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=287;
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28-FEB-2003
10-OCT-2003
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1D PAZH AUSSU
AC Q9PUĞ7;
DT 28-FEB-2003
DT 10-OCT-2003
                               RNH PSEAE
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                                                                                                                                                                                                                                      TISSUE-Venom gland;
MEDLINE=20166950; PubMed=10700385;
Singh S.B., Armugam A., Kini R.M., Jeyaseelan K.;
Singh S.B., Armugam A., Kini R.M., Jeyaseelan K.;
Phospholipase A(2) with platelet aggregation inhibitor activity from Austrelaps superbus venom: protein purification and cDNA cloning.";
Arch. Biochem. Biophys. 375:289-303(2000).
-!- FONCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Inhibits collagen-induced platelet aggregation (By similarity).
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acylglycerophosphocholine + a fatty acid anion.
-! CORACTOR: Calcium (Probable)
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SUBCELLULAR LOCATION: Corrected (By similarity).
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                                  Austrelaps Superbus (Australian copperhead).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostc Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Acanthophiinae; Austrelaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 152;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
Phospholipase A2 isozyme S17-58 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase) (ASPLA17).
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PRINTS; PR00189; PHPHLIPAGRA2.
PRODOW; PD000303; PAPHLIPAGRA2.
SWART; SW00085; PA2c; 1.
PROSTITS; PS00119; PA2 ASP; 1.
ERGSTITE; PS001119; PA2 HIS; 1.
Lipid degradation; Hydrolase; Toxin; Signal; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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InterPro; IPR001211; PhospholipaseA2.
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16641 MW;
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)
(Melanoma differentiation associated protein).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D., Burell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W., Vogelstein B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
S
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MEDLINE=94061997; PubMed=8242752;

Bl-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,

Irnt J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;

"WAFI, a potential mediator of p53 tumor suppression.";

Cell 75:817-825(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BXSB; TISSUE=Spleen;
MEDLINE=94366751; PubMed=8084607;
Hupph K., Siwarski D., Dosik J., Michieli P., Chedid M., Reed Mock B., Givol D., Mushinski J.F.;
"Mock B., Givol D., Mishinski J.F.;
"Molecular cloning, sequencing, chromosomal localization and expression of mouse p21 (Waf1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Topological control of p21WAF1/CIP1 expression in normal and neoplastic tissues.";
Cancer Res. 55:2910-2919(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.2%; Score 36; DB 1; Length 159; 66.7%; Pred. No. 31;
                                                                                                159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the CDI family.
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95316868; PubMed=7796420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U09507; AAB60456.1; -. EMBL; U24173; AAC52220.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 9:3017-3020(1994).
                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A49438; A49438.
PIR; I49023; I49023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                            CDNA MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Local Similarity

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B., Gardiner D.M.;
Distal-less and FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mullen L.M., Bryant S.V., Torok M.A., Blumberg B., Gardiner W.Nerve dependency of regeneration: the role of Distal-less signaling in amphibian limb regeneration."; Development 122:1487-3497(1996).

-!- SUBCELLULAR LOCATION: Nuclear (Potential).

-!- SIMILARITY: Belongs to the distal-less homeobox family.

-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 280;
Pred. No. 57;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UP3B_HUMAN STANDARD; PRT; 320 AA.
09BT76; 086W06;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last senotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Uroplakin 3B precursor (Uroplakin IIIb) (UPIIIb) (P35).
UP38B.
5
                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                          280 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
Probom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97108743; PubMed=8951064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS50071; HOMEOBOX 2; 1.
1;
                                                                                                                                                                                                                                                                                                                                                                                                            Ambystoma mexicanum (Axolotl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; US9480; AAB49668.1; -. HSSP; P02836; 3HDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.2°
Best Local Similarity 63.6
Matches 7; Conservative
6; Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Homeobox protein DLX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGPGTTSNRLD 12
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                                                                                                 127 GGPGTSQGR 135
                                             2 GGPGTTSNR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8296;
                                                                                                                                                                                                                             DLX3 AMBME
                                                                                                                                                                                                                                                  090229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
UP3B_HUMAN
                                                                                                                                                                                                  DLX3_AMBME
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Indels

2;

2; Mismatches

6; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";

T and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

L FUNCTION: Component of the asymmetric unit membrane (AUM); a highly specialized biomembrane elaborated by terminally differentiated urothelial cells. May play an important role in AUM-cycoskeleton interaction in terminally differentiated urothelial glycocalyx which may play an important role in preventing bacterial adherence (By smillarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Heterodimer formation with Uroplakin Ib.

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Heterodimer formation with Uroplakin Ib is a prerequisite to exit out of the endoplasmic reticulum (ER).

-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A., Whiting W., Madan A.Y., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                        Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratine P.H.,
                                                                                                    SEQUENCE FROM N.A., SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=22336509; PubMed=12446744;
Deng F.-M., Liang F.-X., Tu L., Resing K.A., Hu P., Supino M.,
Hu C.-C.A., Zhou G., Dimy M., Krebisch G., Sun T.-T.;
"Uroplakin IIIb, a urothelial differentiation marker, dimerizes with uroplakin Ib as an early step of urothelial plaque assembly.";
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 1).
64A68E268A8BB0EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:21444; UPK3B.
Endoplasmic reticulum; Signal; Transmembrane; Glycoprotein.
SIGNAL 1 29 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UROPLAKIN 3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY233462; AAO89507.1; ALT_FRAME.
EMBL; BC004304; AAH04304.1; -.
                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                           Cell Biol. 159:685-694(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33851 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
320
240
266
320
133
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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DB 1; Length 320;

Score 36; DB Pred. No. 66;

52.2%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome Bequences v.
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).

-!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palliadronic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reanneling (By similarity).
-!- SUBUNIT: Forms a complex with ruvA (By similarity).
-!- SIMILARITY: Belongs to the ruvB family.
                                                                                                                                                                                                                                                                                                                                       Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L. Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR00635; ruvB; 1.
DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.2%; Score 36; DB 1; Length 330; 58.3%; Pred. No. 69; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 64 ATP (POTENTIAL).
330 AA; 36875 MW; B734E54AEEC04C67 CRC64;
                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                    330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPase_centr.
                                                                                                                                                                                   Holliday junction DNA helicase ruvB.
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                             MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002298; AAF39175.1; -.
                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EGGPGTTSNRLD 12 : | | | | | | | |
                                                                                                      STANDARD;
                          260 GGPGAAADRL 269
2 GGPGTTSNRL 11
                                                                                                                                  16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; E81717; E81717.
                                                                                                                                                                                                                                                                                                          STRAIN-MoPn / Nigg;
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=83560;
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                                                                                                       CHLM
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SEQUENCE
                                                                                                                     Q9PKZ8;
                                                                                                       RUVB
                                                                                      CHLMU
                                                                      RESULT 19
                                                                                        RUVB .
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RESULT 20

RUVB OR

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RA Salanoubar M., Lemcke R., Rieger M., Ansorge W., Unseld M.,
RA Salanoubar M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
RA Balanoubar M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
RA Delseny M., Soluty M. Grivell L.A., Mache R., Pulgdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Mincker P., Cattolico L., Waissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vedelmann R., Franz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionari B.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent B.,
RA Gooke R., Laudie M., Berger-Llauuro C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoef H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoef H., Rudd S., Zaccaria P., Mannhaupt G., Haas B., Maiti R., Wu D., Peterson J., Vonter J.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Praser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Rimura T., Ideasma R., Ravashima K., Kishida Y.,
Rabayama C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Rabayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Nasanaha A., Vanasaki M., Panasaki M., Panasaki C., Watsanaki A.,
Nasanahaba A., Vanasaki M., Panasaki M., Panasaki C., Watsanaki P.,
Nasanahaba A., Vanasaki M., Panasaki M., Panasaki C., Watsanaki C., Watsanaki A.,
Nasanahaba A., Vanasaki M., Panasaki M., Panasaki C., Watsanaki C., Watsanaki A.,
Nasanahaba A., Vanasaki M., Panasaki M., Panasaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki C., Watsanaki
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X Amada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Hansen N.F.,

A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Ramiya A., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Khan S., Koesema E., Vayabberg M., Wallender E.K., Wong C., Yamamura Y.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                               SYPIZZOR ANGESTAL (SYPICA).
SYPIZZOR ANGESTAL (STATES).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stracke R., Palme K.; signal peptide selection derived cDNAs from Arabidopsis thaliana leaves and guard cells."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
Gansel X., Sticher L.;
"Vesicle traffic in Arabidopsis thaliana: characterization of
ALSMARB3; a novel plant t-SMARB that interacts with syntaxins.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 43, Last annotation update)
Syntaxin 122 (AtSYP122) (Synt4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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       HERE BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERNER BERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=D/UW-3/Cx;
MEDLINE=990000809; PubMed=9784136;
Stephens R.S. Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin B.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: The runA-runB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RunAB is an helicase that mediates the Holliday junction migration by localized denaturation and seanelling (By similarity).

SUBUNIT: Forms a complex with runA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%; Score 36; DB 1; Length 334; 58.3%; Pred. No. 69;
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                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Holliday junction DNA helicase ruvB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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HAWAP; MF 00016; -; 1.
InterPro; IPR003593; AAA ATPasse.
InterPro; IPR0035959; AAA ATPasse.
InterPro; IPR004605; RuvB.
InterPro; IPR008823; RuvB.C.
InterPro; IPR008824; RuvB.N.
Pfam; PF000004; AAA; 1.
Pfam; PF005491; RuvB.C; 1.
Pfam; PF05496; RuvB.N; 1.
                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq.
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.";
Science 282:754-759(1998).
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DSGPGARSVRLD 146
       135 DSGPGARSVRLD 146
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Matches 7; Conservative
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                                                                                                                                                                                                   STANDARD;
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ID S122 ARATH
AC Q9SVC2, Q9SUJ2;
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                                                                                                                                                                                               RUVB CHLTR
084044;
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341 AA.

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STANDARD;

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RESULT 21

Query Match

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4 PGTTSNRLDA 13
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 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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10-OCT-2003 (Rel. 42, Last annotation update)
Probable methionine aminopeptidase 1 (EC 3.4.11.18) (MetAP 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%; Score 36; DB 1; Length 341; 60.0%; Pred. No. 71; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      InterPro; IRN006012; Syntaxin.
InterPro; IRN006012; Syntaxin.
InterPro; IRN00727; T SNARE.
Pfam; PF05739; SNARE; T
Pfam; PF05739; SNARE; 1.
SMART; SM00397; t SNARE; 1.
PROSITE; PS001914; SYNTXIN; 1.
PROSITE; PS00192; T SNARE; 1.
Transport; Protein transport; Transmembrane; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                         306 341 VESICULAR (POTENTIAL).
64 185 COLIED COIL (POTENTIAL).
213 275 T-SNARR COLLED-COIL HOMOLOGY.
214 214 N -> S (IN RRF 2 AND 5).
341 AA; 37837 MW; 65817034D954ABFF CRC64;
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Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 AA.
                                                                                                                                                                                                                                                EMBL; AY050907; AAK93584.1; -. EMBL; AY091410; AAM14349.1; -. EMBL; AY087633; AAM65172.1; -.
                                                                                                                                                                                                                       EMBL; AF083808; AAN60366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                       AL050300; CAB43444.1; -.
        Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 60.0
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SPBC3E7.10.
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123 ESGPGSSSDR 132
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                                                                                                                                                                                                                                                                                                                                                                                                   305
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PIR; T48847; T48847.
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
                                                                                                                                                                                                                                EMBL; AJ245407;
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059730;
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Matches
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11D AC
DT DT DT DT OCC
OCC OCC
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                                                                                                                                                                                               RA WOOD V., Gwilliam R., Rajandeal 189350.

RA WOOD V., Gwilliam R., Rajandeal 189350.

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

ROLLING M., Connor R., Cronin A., Davis P., Feltwell T., Frager A.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Frager A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,

Amens K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Saunders D., Seeger K., Sharp S.,

RA Nother K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Barlon J., Simmonds M., Squares R., Squares S., Stewens K.,

RA Andraw J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Meltjens I., Vanstreels B., Rieger M., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,

RA Goffeu A., Cadieu B., Nang Z., Hunt C., Moore K., Hurst S.M.,

Bager P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

R. Lucas M., Rochet M., Gaillardh C., Parlada V.A., Garzon A., Thode G.,

Baga R.R., Cruado L., Jimenez J., Sanchez M., Galzon A., Thode G.,

Baga R.R., Cruado L., Jimenez J., Sanchez M., Galzon A., Thode G.,

Baga R.R., Cruado L., Jimenez J., Sanchez M., Galzon A., Thode G.,

Baga R.R., Cruado L., Jimenez J., Sanchez M., Garzon A., Thode G.,

Baga R.R., Cruado L., Moreno S., Armstrong J., Foreburg S.L.,

Ra Daga R.R., Cruado L., Moreno S., Armstrong J., Rutsetrong S.,

R. The genome sequence of Schizosaccharomyces pombe.",

Rature 415:871-880(2002).

R. Copacines G. Schizosaccharomyces pombe.",

R. Copacines G. Copacines F. Morentially Methionine, from peptides and
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COBALT 1 AND 2 (By similarity)
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InterPro; IPR001714; Pept M24 MAP.
InterPro; IPR001746; Pept M24A MAP1.
InterPro; IPR000994; Pept[dase M24.
Pfam, PF00557; Peptidase M24; I.
PRINTS; PR00599; MAPEPTIDASE.
TIGRPAM; TIGR00500; met_pdase I; I.
PROSITE; PS00680; MAP 1; PALSE NEG.
Hydrolase; Aminopeptidase; Cobalt.
                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360;
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60.0%;
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Best Local Similarity
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M24.001;
WCBI_TaxID=4896
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FIBA HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUEENCE FROM N.A.

TISSUEENCE TROM N.A.

TISSUEENCE, pubmed=1247932;

MEDLINE=22388257; Pubmed=1247932;

MEDLINE=22388257; Pubmed=1247932;

Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F., Bhat N.K.;

Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F., Bhat N.K.;

Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F., Bhat N.K.;

A pleton M.; Soares M.B.; Bonaldo M.F.; Caraninci P.; Prange C.;

Brownstein M.J.; Uddin T.B.; Toshiyuki S., Caraninci P.; Prange C.;

Raha S.S., Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Broak S.A.; McKennan F.J.; Malek J.A.; Gunaratne P.H.;

Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

An iting M.; Madan A.; Sodergren B.J.; Lu X.; Gibbs R.A.;

Ratesley J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A. Miting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

Ratesley R.W.; Touchman J.W.; Grhmutz J.; Dickson M.C.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

Schnetch A.; Schein J.E.; Jones S.J. M.; Marra M.A.;

Human and mouse CDNA sequences.";

Process A. School S.J. Marra M.A.;

Human and mouse CDNA sequences.";

Human and mouse CDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98046021; PubMed=9384570;
Garcia-Saez I., Reverter D., Vendrell J., Aviles F.X., Coll M.;
"The three-dimensional structure of human procarboxypeptidase A2.
Deciphering the basis of the inhibition, activation and intrinsic activity of the zymogen.";
EMBO J. 16:6906-6913(1997).
-!- CATALVITC ACTIVITY: Similar to that of carboxypeptidase A (EC 3.4.17.1), but with a preference for bulkier C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pancreas;
MEDLINE=95204457; PubMed=7896805;
Catasus L., Vendrell J., Aviles F.X., Carreira S., Puigserver A.,
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-98111000; PubMed-9450539;
Reverter D., Garcia-Saez I., Catasus L., Vendrell J., Coll M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence and conformation of human pancreatic procarboxypeptidase A2. cDNA cloning, sequence analysis, and three-dimensional model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

    -!- SIMILARITY: Belongs to peptidase family M14.

                                                                                                                                                     P48052; Q96A12; Q96QN3; O1-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) Carbocr-2003 (Rel. 42, Last annotation update) Carboxypeptidase A2 precursor (EC 3.4.17.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING
                                                                                                                                 417 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 270:6651-6657(1995)
                                                                                                                                 STANDARD:
  148 PGTTTDELDS 157
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                 HUMAN
                                                                             RESULT 23
CBP2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase, Carboxypeptidase, Metalloprotease, Zinc, Zymogen, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93090725; PubMed=1457396; Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J., Ray S.N., Redman C.M., Grieninger G.; "Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel exon conferring marked homology to beta and gamma subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> G (IN REF. 2; AAH07009).
-> I (IN REF. 1).
3D9C073A98700A83 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                           GG), GO:000182; F:carboxypeptidase A activity; TAS GO; GO:0007039; P:vacuolar protein catabolism; TAS InterPro; IPR003146; Pept Mi4A_propep.
InterPro; IPR00314; Peptidase Mi4.
InterPro; IPR009034; Peptidase Mi4.
InterPro; IPR009020; Protease Jnhib.
Pfam; PF00244; Propep_Mi4; 1.
Pfam; PF00246; Zn carbOpept; 1.
PRINTS; PR00765; GRBOXYPTASEA.
SWART; SM0613; Zn Dept; 1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE. CARBOXYPEPTIDASE A2
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NUCLEOPHILE.
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SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
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                                                                                                                                   EMBL, U19977; AAA74425.1; -.
EMBL, BC007009; AAH07009.1; -.
EMBL, BC014571; AAH14571.1; -.
EMBL, BC015140; AAH1511.1; -.
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112
417
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1180
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Genew; HGNC:2297; CPA2
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PDB; 1AYE; 13-JAN-99.
PDB; 1DTD; 12-JUL-00.
PDB; 106X; 30-JAN-03.
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417 AA;
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es 6; Conserv
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SIGNAL
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"Amino acid sequence studies on the alpha chain of human fibrinogen
                                                                          Fretto L.J
                                                                                                    fibrin."
 Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
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Overlapping sequences providing the complete sequence.";
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MEDLINE=80088230; PubMed=518845;
Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
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Henschen A., Lottsp
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                                                                                                                   CROSS-LINKING ACCEPTOR SITES
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

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Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Pred. No. 2e+02;
1; Mismatches 1; Indels
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Maekkawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata
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Arocha-Pinango C.L., Matsuda M.;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA translocase ftsK.
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75.0%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   SUBSCRIBILIARY LOCATION: Integral membrane protein. Located at the septum. The large C-terminal part of the protein is cytoplasmic
generating positive supercoils in front of it and negative supercoils behind it (By similarity).
SUBUNIT: Homohexamer. This suggests the formation of a ring between the two cells at the septum that surrounds DNA (By
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; FtsK_SpoiliE.
Pfam; PF01580; FtsK_SpoiliE; 1.
SMART; SM00382; AAA; 1.
PR051TE; PS50901; FTSK; 1.
Chromosome partition; Cell division; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 881;
Pred. No. 2e+02;
1; Mismatches 4; Indels
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-!- SIMILARITY: Contains 1 FtsK domain.
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Q9149 drosophila
Q89149 drosophila
Q8910 bradyrhizob
Q8bxm8 musculu
Q8c017 mus musculu
Q8c42 mus musculu
Q8c078 mus musculu
Q9c070 brachydanio
Q8wpu6 trypanosoma
O84893 salmonella
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Q9xab8 streptomyce
Q82wd2 nitrosomona
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                GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Q805GJO
Q8EXM8
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Q8CC0G3
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"Cloning and mapping of ZNF231, a novel brain-specific gene encoding neuronal double zinc finger protein whose expression is enhanced in a neuronal double zinc finger protein whose expression is enhanced in a neurodegenerative disorder, multiple system atrophy.";

Genomics 54:50-58(1998).

EMBL, APO52224; AAC83555.1;

Genew; HGNC:1117; BSN.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0007268; P:synappic transmission; TAS.

InterPro; IRP08899; Znf_piccolo.

InterPro; IRP08899; Znf_piccolo.

Pfam; PF05715; Zf_piccolo.

Pfam; PF05715; Zf_piccolo.
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                                                                                                                     STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99026125; PubMed=9806829;
Hashida H., Goto J., Zhao N., Takahashi N., Hirai M., Kanazawa I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               NIFS OR RB7424.
Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                               63.8%; Score 44; DB 16; Length 419; 66.7%; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                            1; Indels
 Aminotransferase NifS-putative NifS homolog (EC 4.4.1.-)
                                                                                                                                                                                                              strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL: BX204146; CAD75352.1; -.
Aminotransferase; Lyase; Transferase; Complete proteome.
SEQUENCE 419 AA; 43485 MW; B91E67E8F2C62D79 CRC64;
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Last annotation update)
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01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last and
Neuronal double zinc finger protein.
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392 GGHGTTSDQIDA 403
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Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                       SEQUENCE FROM N.A.
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AC Q9Y1-
DT 01-N
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Q7v067 prochloroco
Q88dp8 pseudomonas
Q951j2 macaca fasc
Q40366 medicago sa
Q19879 caenorhabdi
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Q9ch82 lactococcus
Q8rx70 arabidopsis
Q8rx70 arabidopsis
Q9r599 arabidopsis
Q9x20 drosophila
Q9w8b7 mesostigma
Q9w8b7 dloscorea a
Q00509 streptomyce
Q7uj59 rhodopirell
Q9bx7 aeropyrum p
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Q'yani5 bradyrhizob
Q9770 pseudomonas
Q96417 human immun
Q9p819 suillus bov
Q'zz62 brachydanio
Q'2z62 brachydmonas
Q8124 enterococu
Q9125 streptomyce
Q95fm2 xylella fas
Q95fm2 xylella fas
Q9679 pramodium
Q96m8 homo sapien
Q8600 lattobacter
Q8900 lattobacter
Q80812 rhodobacter
Q8125 caenorhabdi
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09vp88 drosophila
080t79 mus musculu
080dq3 kamiti rive
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072407 homo sapien
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0845j8 pseudomonas
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Q889t4 pseudomonas
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Q86X98
Q9D8U4
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749 AA.

09Y149; 01-NOV-1999 (TrEMBLrel. 12, Created)

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RESULT 1 Q7UNR6 ID Q7UN AC Q7UN DT 01-C DT 01-C

127 GGPGTASNLLQS 138

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RESULT 4 089670

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                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota; Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
  01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                      01-OCT-2002 (TrEMBLrel. 22, Last a
BCDNA:GH03922 protein.
ARC105 OR BCDNA:GH03922 OR CG4184.
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EMBL; AF145620; AAD38595.1; -.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI TaxID=7227;
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The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs."; Nature 420:563-573(2002).

EMBL; AKO44660; BAC32023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic sequence of nitrogen-fixing symbiotic bacterium
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
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                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA; 34112 MW; AE97D4548E8394A0 CRC64;
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                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005958; BAC51620.1; -.
GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
313 AA.
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PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
PRT;
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                                                                                                                                                                 ABC transporter permease protein.
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                                                                                                                                                                                                                                 Bradyrhizobium japonicum.
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-USDA 110;
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rabata S.;
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089670
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8; Conservative

Matches

Query Match Best Local Similarity

7

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Gaps

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62.3%; Score 43; DB 5; Length 749; 66.7%; Pred. No. 62; ive 1; Mismatches 3; Indels

FBG00027592; Arc105. 749 AA; 80526 MW; 42375AEB7C13A1DF CRC64;

FlyBase; SEQUENCE

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SEQUENCE FROM N.A.
STRAINE-SCABL/60; IISSUE=Testis;
MEDIINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                          R MGD; MG1:2444812; CamkEr.

R MGD; MG1:2444812; CamkEr.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/theonine kinase activity; IEA.

GO; GO:0004713; F:protein aerine/thase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00019; Prot kinase.

R InterPro; IPR00229; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Prodom; P000009; pkinase; 1.

R Prodom; P0000001; Prot kinase; 1.

R SMART; SM00220; S_TKc; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:000413; F:protein tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR002209; Ser thr pkinase.

InterPro; IPR008271; Ser thr pkinase.

InterPro; IPR008271; Ser thr pkinase.

InterPro; IPR008271; Ser thr pkinase.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF453383; AAN75696.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE T; 1.
SEQUENCE 579 AA; 63477 WW; A79C6F3E1CEGDDCA CRC64;
                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) CA+/calmodulin-dependent protein kinase kinase beta
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01-MAR-2003 (TrEMBLrel. 23, Last seq
  01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK031399; BAC27387.1; -.
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                                                                                       CAMKK2 OR 6330570N16RIK. Mus musculus (Mouse).
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                                                                                                                                                                                  NCBI_TaxID=10090;
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Q8CH42
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R MGO; MGI:2444812; Carakto.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006474; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00219; Ser_thr_pkinase.

R InterPro; IPR00211; Ser_thr_pkinase.

R Probon; PD00001; Prote kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE Dom; 1.

R PROSITE; PS00101; PROTEIN KINASE Dom; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
51-OCT-2003 (TrEMBLrel. 25, Last annotation update)
85-millar to Ca+/calmodulin-dependent protein kinase kinase beta (CaM-kinase kinase beta)
CAMKK2 OR 6330570N16RIK.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                  Score 42; DB 11; Length 503;
Pred. No. 62;
3; Mismatches 2; Indels
                  InterPro; IPR000715; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
Fam; PF00069; pkinase; 1.
Probom; PF000001; Prot kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
SEQUENCE 503 AA; 55501 MM; 8GS96D6839649F42 CRC64;
GO; GO:0006468; P:protein amino acid phosphorylation; IEA
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58.3%;
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105 QGGPASSSNSLD 116
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les 7; Conservative
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Q8COG3
ID Q8COG3
AC Q8COG3;
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MEDLINE=21270059; PubMed=11376489;
Lee J.S., Ray R., Chien C.B.;
"Cloning and expression of three zebrafish roundabout homologs suggest roles in axon guidance and cell migration.";
Dev. Dyn. 221:216-230(2001).
EMBL; AF337035; AAKS8427.1;
                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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NCBI _TaxID=5691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berriman M., Hall N., Sheader K., Bringaud F., Tiwari B., Isobe T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P., Rudenko G.;
of Variant Surface Glycoprotein gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Pred. No. 1.9e+02;
0; Mismatches 3;
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PROSITE; PS50835; IG_LIKE; 5.
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InterPro; IPR008957; FN III-11ke.
InterPro; IPR00216; GPGR Rhodpsn.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig-c2.
Pfam; PF00041; fn3; 3.
Pfam; PF00047; ig; 5.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei.
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                                                                                                  Roundabout 2.
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; AK032070; BAC27681.1; -.

MGD; MG1:2444812; CankK2.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                         Score 42; DB 11; Length 588;
Pred. No. 72;
3; Mismatches 2; Indels
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SMART; SM00210; S_TKC; 1.
SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
SEQUENCE S88 AA; 64598 WW; 95813E1C28FC614F CRC64;
                                                                                                                                                                                                                                                               588 AA; 64753 MW; 8026EE485C3BA06A CRC64;
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CAMKK2 OR 6330570N16RIK.
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Last annotation update)
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                       Prodom; PD000001; Prot Kinase; 1.
SMART; SM00220; S TKc; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00011; PROTEIN KINASE ATP; 1.
PROSITE; PS000108; PROTEIN KINASE DOM; 1.
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
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58.3%;
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Pfam; PF00069; pkinase; 1
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Best Local Similarity 58.3
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les 7; Conservative
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Q9XSZ8;
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Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=S. typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677668;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
                                                                                                genomic
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720, MEDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601, 602;
                                                                                                                                                                                                                                                                                                                         on-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative DNA replication protein (Hypothetical protein) (Gifsy-2 prophage, ATPase involved in DNA replication initiation).
T1917 OR STM2625 OR STM1015 OR STY1023.
Salmonella typhi, and
                                           STRAIN-427;

MEDLINE-21429110; PubMed=11543629;

Zeng C., Kouprina N., Zhu B., Cairo A., Hoek M., Cross G.A.M,

Soogawa K., Larionov V., de Jong P.;

"Large-insert BAC/YAC libraries for selective re-isolation of ergions by homologous recombination in yeast.";

Genomics 77:27-34(2001).

EMBL; ALG70322; CAD21450.1;

Hypothetical protein.

SEQUENCE 105 AA; 11507 MW; 1C875F8030278B66 CRC64;
                                                                                                                                                                                                      ó
                                                                                                                                                                              Score 40; DB 5; Length 105;
Pred. No. 28;
0; Mismatches 4; Indels
Chromosome Libraries for Trypanosoma brucei.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.typhimurium; STRAIN=LT2;
Figueroa-Bossi N., Bossi L.;
"Prophage genes in Salmonella.";
Submitted (UNN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhi, STRAIN=TY2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                              58.0%;
                                                                                                                                                                Query Match
Best Local Similarity 60....
Best Local Similarity - 7...
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                                                                                                                                                                                                                             1 EGGPGTTSNRLD 12
                                                                                                                                                                                                                                                   77 EGGGGTKKNRKD 88
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                  SEQUENCE FROM N.A.
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Foster T.P., Chouljenko V.N., Kousoulas K.G.; "Functional characterization of the HveA homolog specified by African
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EMBL, AF147720; ABD37381.1; -.

HSSP, Q92956; LJMA.
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Elebwell T., Hamilin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Micehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus aethiops (Green monkey) (Grivet).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:appoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_GC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00061; ADH_SHORT; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 249 AA; 27568 MW; 6D5D99B79B696BA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397951C6617FE3AA CRC64;
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Last annotation update)
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Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002611; IstB_ATPbind.
Pfam; PF01695; IstB; 1.
SMART; SM00382; AAA; 1.
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MEDLINE=99296730; PubMed=10366573;
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                                                                                                                                                                                                                          Nature 413:848-852(2001).
EMBL; AR016840; AR059533.1; -.
EMBL; AR010386; ARC26072.1; -.
EMBL; AR008819; AAL21519.1; -.
                                                                                                                                                                                                                                                                                                                                                        EMBL; AE008743; AAL19949.1; -. EMBL; AL627268; CAD05417.1; -.
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
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Query Match
Best Local Similarity 63.00
Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1115 MEMBRANG (BI SIMILMANIII).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21996410; PubMed=12000953; MEDLINE=21996410; PubMed=12000953; Bentley S.D.; Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Rabbinowitsch E., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
             Score 40; DB 6; Length 283;
Pred. No. 77;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                       1; Indels
                                                                                                                                                                                                                                                                                                                                              Murphy L., Harris D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00528; BPD transp; 1.
PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
Transmembrane; Transport; Complete proteome.
SEQUENCE 313 AA; 33365 MW; 2AE7PAEDF5AC56B0 CRC64;
                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Binding-protein dependent transport protein.
SCO0454 OR SCF51A.32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL919105; CAB56684.1; -. GO: 00.1001021; C.integral to membrane; IEA. GO; GO: 00105215; F:transporter activity; IEA. GO; GO: 0006810; P:transport; IEA.
                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
             58.0%;
70.0%;
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Nature 417:141-147(2002).
                                      Conservative
                                                                                                                                                                                                                                                     Streptomyces coelicolor.
                                                                                                                                                          PRELIMINARY;
                                                                                          192 EAGPGTSSSR 201
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 Query Match
Best Local Similarity
'''' 7; Conserv
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                                                                                                                                RESULT 14
Q9RL33
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Length 313;
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                 Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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TIGRRAMs; TIGR00534; OpcA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 351 AA; 37677 MW; EE133DFBF2651577 CRC64;
                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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DB 16;
85;
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Pred. No. 96;
                                                 Mismatches
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Score 40;
Pred. No.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=21996410; PubMed=12000953;
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MEDLINE=97000351; PubMed=8843436;
                                                 2;
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EMBL; AL939110; CAB50763.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SC01938.
SC01938 OR SCC22.20.
58.0%;
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                                                                                                                              :[||||:|
260 QGGPGTSSTTL 270
                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                               1 EGGPGTTSNRL
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Best Local Similarity
7; Conserve
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Conserved hypothetical protein.
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146 AA; 16049 MW;
  56.5%;
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Gramene; Q8LR30; -
SEQUENCE 146 AA; 16049 MW
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Best Local Similarity 61.5
Matches 8; Conservative
Query Match 56.5
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                         1 EGGPGTTSNRL 11
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29 KGGSGNTSNKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=323;
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                                                                                                                                                                                                                                               Q883M3
                                                                                                                                                                                                   RESULT 18
Q883M3
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Q8LR30
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Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
A Arciero D.W., Hommes N.G., Whittaker M.M., Arp D.J.,
T. "Complete genome sequence of the ammonia-oxidizing bacterium and
tobligate chemolithoautotroph Nitrosomonas europaea.";
L.J. Bacteriol. 185:2759-2773 (2003).
R. Rabi BX321858; CAB64669.1 --
R. GO; GO:001620; C:membrane; IEA.
R. GO; GO:0016215; F:transport: IEA.
R. GO; GO:0005215; F:transport: IEA.
R. GO; GO:0005315; P:transport: IEA.
R. GO; GO:0005315; TonB_Oxc.
R. PROBITE: PROBIJES; TONB_DEPENDENT_REC_2; 1.
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Hypothetical protein; Complete protecome.

SEQUENCE 67 AA; 7030 MW; 781F9A0C593FBF85 CRC64;
                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI_TaxID=915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.0%; Score 40; DB 16; Length 757; 60.0%; Pred. No. 2.1e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83756 MW; CD4E8F4FD5B2B891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical transmembrane protein SMC00732.
                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                  757 AA
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Rhizobium meliloti (Sinorhizobium meliloti)
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MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22586410; PubMed=12700255;
                                                                                                                                                                                   TonB-dependent receptor protein.
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SEQUENCE 757 AA; 83756 M
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Matches 6; Conservative
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                                                                  PRELIMINARY;
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384 DGGPGTSAHR 393
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STRAIN=ATCC 19718 /
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                                                                                            Q82WD2;
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                                                                Q82WD2
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Q92MH7
                       RESULT 16
Q82WD2
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DTT ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE ACCOUNT OF THE
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Noryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0671D01.";
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AE016864; AAO55845.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Pseudomonadales;
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DB 16; Length 67;
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                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein; Complete proteome.
130 AA; 14087 MW; 8B290C4A55E86010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE25E9C7AA95B0B7 CRC64;
                                                                                                                                                                                                                                                                                                          0893M3;
01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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58;
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Pred. No. 52;
1; Mismatches 4
                                                                                                                                                                                                                                                                                     130 AA
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                     Pred. No. 26;
2; Mismatches
  Score 39;
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Pred. No.
                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammapro
Pseudomonadaceae, Pseudomonas.
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Best Local Similarity
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Gaps

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Indels

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TISSUE=Brain;
OBada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.5%; Score 39; DB 11; Length 278; 53.8%; Pred. No. 1.1e+02;
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050521; BAB17289.1; -.
EMBL; AB050521; BAB17289.1; -.
GO; GO:0005489; F:zinc transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; CytC, heme. BS.
InterPro; IPR000306; Znf. FyvE.
InterPro; IPR001841; Znf. FyvE.
Pfam; PF01363; FyvE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 AA; 30546 MW; E7BBBCB8F565EC28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSGLY9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical Treatein.
                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to LIM domains containing 1 (Fragment).
                                                                                                                                                                                     278 AA.
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                              Mismatches
                Pred. No.
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PROSITE; PS50023; LIM DOMAIN 2; 3.
100.08; P1.
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InterPro; IPR001781; LIM.
Pfam; PP00412; LIM; 3.
ProDom; PD000094; LIM; 3.
SMART; SM00132; LIM; 3.
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Best Local Similarity 53.8<sup>3</sup>
Matches 7, Conservative
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                                7; Conservative
                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                 54 GPGTTSN 60
                Best Local Similarity
                                                                 3 GPGTTSN 9
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CZECH II;
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SEQUENCE
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Q9GLY9
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Q8CG89
                                 Matches
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                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Para-aminobenzoate synthase, glutamine amidotransferase component II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393 (2003).

EMBL; BX248586; CAD83250.1; -.
Glutamine amidotransferase; Lyase; Transferase; Complete proteome.
SEQUENCE 193 AA; 22153 MW; 6284B168601B7356 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5%; Score 39; DB 15; Length 193; 54.5%; Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Herring B.L., Dwyer D.E.;
"Australian HIV-1 env subtypes.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 AA; 21213 MW; 0079F7E335BAD27F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY081970; AAL99288.1; -... GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:005198; F:structural molecule activity; IEA. InterPro; IPR000777; GP120.
                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1...
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                       193 AA
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                Mismatches
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                                                                                                                                                                                                                                                       Envelope glycoprotein (Fragment)
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                7; Conservative
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176 DGGPNSTSNEI 186
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                                                 3 GPGTTSNRLD 12
                                                                                14 GPGTSSHRSD 23
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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PABA OR BFL568.
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Q7VRN6
                Matches
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MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Sato S., Kato T., Sasamoto S.,
Watanabe A., Ideaawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                          0. Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Megorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Megorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 16; Length 301;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                         Length 300;
                                                                                                                                                                                                                   Score 39; DB 6; Length 300
Pred. No. 1.2e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                           Hypothetical protein.
SEQUENCE 300 AA, 33123 MW; AEB590E59908795F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AA; 33514 MW; FD668FEFD296838F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Created)
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(TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000073, A/b_hydrolase. InterPro, IPR002410, Peptidase, S33.
InterPro, IPR005945, Pept_S33_TRI_F1.
InterPro, IPR0005945, Ser_estrs.
SMART; SMO0064; FYVE; 1.
SMART; SMO0184; RING; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50178; ZF_FYVE; 1.
                                                                                                                                                                                                                         56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.23
Matches 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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SEQUENCE 301 AA;
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01-MAY-2000 (TrEN
CG13727 protein.
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298MF5
AC 098MF5;
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DE PLOIDE
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Q9VVF5
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RC STRAIN=Berkeley;

RM MEDLINE=20196006; PubMed=10731132;

RR Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Endng O., Chen L.X.,
Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballaw R.M., Basu A.M. Baxendal J., Baraktaroglu L., Basaley E.M.,
Beson K.Y., Bencs P.V., Barman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Baraktaroglu L., Besaley E.M.,
Beson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Butler H.W., Cadele E., Center A., Clandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.M.,
Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.M.,
Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn D.,
RA Burtis N.C., Evangelista C.C., Ferraz C., Ferriac S., Dunkov B.C., Dunn D.,
RA Burtis N.L., Harvey D., Heiman T.J., Hernandez J.R., Reckhum K.A.,
RA Hostin D., Houston K.A., Heiman T.J., Hernandez J.R., Reckhum K.A.,
RA Hostin D., Houston K.A., Heiman T.J., Wal M.-H., Indeym C.,
Alalahi M., Kalush F., Karpen G.H., Re Z., Kenniston J.A., Kecthum K.A.,
Alalahi M., Kalush F., Karpen G.H., Re Z., Kenniston J.A., Kecthum K.A.,
Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Nablson D.L.,
Melson D.R., Nelson K.A., Li J., Li Z., Kupp D., Lai Z.,
Reniston K., Sauderi C., Stapleton M., Stupski M.P., Sarleh J.M.,
Spirskas R., Tector C., Turner R., Venter E., Wang X., Shen R., Tector C., Stapleton M., Strong S., Shen R.,
Shue B.C., Siden-Kamos I., Singson M., Strong G., Zhen D.,
Rabier E., Spradling A.C., Stapleton M., Strong G., Zhen G., Zhen G., Zhen G., Zhen K., Shen K., Holled M., R.F., Zhong F.M., Woldsep E., Wolled R., Changer E., Worles E.W., Wolled M., Shue S., Chang G., Shen K., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S
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                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.
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302 AA; 31787 MW; 5D373F9C24329B31 CRC64;
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Drosophila melanogaster (Fruit fly)
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79.162 Million cell updates/sec
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Q8WPU6
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Maximum Match 100%
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Q96k21
Q7tqj8
Q95se1
Q834l7
Q84wq1
Q86wc2
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Planctomycetaceae; Pirellula.
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01-CCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Aminotransferage Nife-putative Nifs homolog (EC 4.4.1.-).
Name-nifs; OrderedLocusNames=RB7424;
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Pfam; PF00266; Aminotran.5; 1.
Aminotransferase; Complete proteome; Lyase; Transferase.
SEQUENCE 419 AA; 43485 WW; B91867B8F2C62D79 CRC64;
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Pred. No. 44;
3; Mismatches 1
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GO; GO:0008483; F:transaminase activity; IEA
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001652; P:metabolism; IEA.
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081ZW8
096K21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;

MEDLINE=SPAIN655; PubMed=9455477;

MEDLINE=SPAIN655; PubMed=9455477;

A Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

The rediction of the coding sequences of unidentified human genes. VIII.

The rediction of the coding sequences of unidentified human genes. VIII.

The rediction of the coding sequences of unidentified human genes. VIII.

The rediction of the involved in the organization of the cytomatrix at the nerve terminals active zone (CAZ) which regulates neurotransmitter release cytomatrix at the nerve terminals active zone (CAZ) which regulates neurotransmitter release from a subset of brain glutamatergic synapses. Involved in the formation of the retinal photoreceptor ribbon synapses (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with ERC2/CAST1, RIMS1 and UNC11A. Part of a complex consisting of ERC2, RIMS1 and BSN (By similarity). SUBCELLULAR LOCATION: Cytoplasmic; localized to the active zone of presynaptic density (By similarity).

TISSUE SPECIFICITY: Exclusively expressed in brain. PTM: Myristyolated. The N-terminal myristyolation is not sufficient for presynaptic localization (By similarity).
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PubMed=10329005; DOI=10.1006/geno.1999.5788;
Winter C., tom Dieck S., Boeckers T., Bockmann J., Kaempf U.,
Sanmarti-Vila L., Langnaese K., Altrock W., Stumm M., Soyke A.,
Wieacker P., Garner C.C., Gundelfinger B.D.;
"The presynaptic cytomatrix protein Bassoon: sequence and chromosomal localization of the human BSN gene.";
                                                                                                                                      "Cloning and mapping of ZNF231, a novel brain-specific gene encoding neuronal double zinc finger protein whose expression is enhanced in eneurodegenerative disorder, multiple system atrophy."; genomics 54:50-58(1998).
                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDILINE=99026125; PubMed=9806829; DOI=10.1006/geno.1998.5516;
Habhida H., Goto J., Zhao N., Takahashi N.; Hirai M., Kanazawa I.,
Sakaki Y.;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; Y18448; CAA77176.1; -.
EMBL; Y18449; CAA77176.1; JOINED.
EMBL; Y18450; CAA77176.1; JOINED.
EMBL; Y18450; CAA77176.1; JOINED.
EMBL; Y18451; CAA77176.1; JOINED.
EMBL; AB00052; T00062.
GENEW, HGNC:1117; BSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2356-3925 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Genomics 57:389-397(1999).
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                       NCBI_TaxID=9606;
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Peldblyum T., Ulrich R.L., Ronning C.M., Brinked L.M., Daudherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Zhou L., Fraser C.M.,
"Structural flexibility in the Burkholderia mallei genome.",
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
C4-type (Potential).
C4-type (Potential).
C4-type (Potential).
3 x 7 AA tandem repeats of K-A-S-P-[LQ].
[APS]-[KST].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=rnhA; ORFNames=BMA0763;
Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 3925;
Pred. No. 5.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%; Score 43; DB 2; Length 148; 63.6%; Pred. No. 20; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                3924 F -> L (in Ref. 1).
AA; 416365 MW; 38A910B22BCACC3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AA; 16254 MW; C90D92F92CB1B60C CRC64;
                                                                                                                                                                                                        (Potential)
                                                                                                                                                                                                                      (Potential)
                                                                                                                                                                                     (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Ribonuclease HI (EC 3.1.26.4).
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 AA
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Poly-Arg.
Poly-Arg.
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NCBI_TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                      63.8%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.8
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.3
Best Local Similarity 63.6
Matches 7; Conservative
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1207
1293
2475
2980
2605
2631
3782
3924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 GPGSTSRRLD 80
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2350
2938
2599
2626
3774
3924
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EMBL; AE005998; AAK25327.1; -. PIR; C87666; C87666.
HSSP; P00647; 1G15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16674 MW;
                                                                                                                                                                                                                                                                                 HAMAP; MF 00042; -; 1.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; RnaseH; 1.
PROSITE; PS50879; RNASE_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Complete proteome;
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SEQUENCE
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                                                                                                                                                                                       STRAIN=E89543;

X PubMed=1537794;

PubMed=1537794;

A Akins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,

A Akins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,

Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,

Browk K., Brown K.A., Brown N.R., Challs G.L., Cherevach I.,

Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,

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Burkholderia pseudomalle."

Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: This enzyme is an endounclease that degrades the RNA of
RNA-DNA hybrids specifically (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 1989 / CB15;
MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
Nietman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
BERTW K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity). -!- SUBUNIT: Monomer (By similarity). -!- SUBUNIT: Monomer (By similarity). -!- SUBLELLULAR LOCATION: Cytoplasmic (Potential). -!- SIMILARITY: Belongs to the RNase H family. -!- SIMILARITY: Contains 1 RNase H domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
                    Ribonuclease HI (EC 3 1.26.4).
Name=rnhA; Synonyms=dask, herA, rnh, sdrA; ORFNames=BPSL1342;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2; Length 148; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AA; 16254 MW; C90D92F92CB1B60C CRC64;
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Libonuclease HI (EC 3.1.26.4) (RNase HI).
Name=rnhA; OrderedLocusNames=CC3365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                Burkholderiaceae; Burkholderia.
NCBI_TaxID=272560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX571965; CAH35340.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||||:||::
39 GEPGTTNNRME 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGPGTTSNRLD 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphomonoester.
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SEQUENCE
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Q9A341;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota,
Neoptera, Endopterayota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 1; Length 149;
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Magnesium (By similarity).
Magnesium (By similarity).
Magnesium (By similarity).
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Name=Arc105; Synonyms=BcDNA.GH03922; ORFNames=CG4184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Length 749;

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PEQUENCE FROM N.A.

REQUENCE FROM N.A.

MEDIJNE-2246065; PubMed=12537568;

A Ratel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacled J.M., Park S., Ffeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT Weinsting a whole-genome shotgun: Release 3 of the Drosophila

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Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
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Mang Z.Y., Wassaran D.A., Weinstock G.M., Weissenbach J.,
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Raminker J.S., Perise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter B., Blazel R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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EMBL, AF145620; AAD38595.1; -.
Flydase; FBGM0027592; ATC105.
SEQUENCE 749 AA; 80526 MW; 42375AEB7C13A1DF CRC64;
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Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone A930030J18 product:CA+/CALMODULIN-DEPENDENT PROTEIN KINASE
KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Score 43; DB 2; I
Pred. No. 1.3e+02;
1; Mismatches 3;
                                                                                                                                             313 AA.
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                                                                                                                                                                                                             ABC transporter permease protein.
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  62.3%;
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259 QGGPGNSSNTLN 270
Query Match 62.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                    2 GGPGTTSNRLDA 13
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                  STRAIN=USDA110;
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01-MAR-2003
                                                                                                                                                                       01-JUN-2003
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GO; GO:0045859; P:regulation of protein kinase activity; ISS
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RA Adachi J. Aizawa K., Akhmura T., Arakawa T., Bono H., Carninci P., RALANGA S., Furuno M., Hanagaki T., Hara A., Hashizume W., Phkuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T., A. Hayashida M., Royawa I., Royima Y., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Sakai K., Sakazume N., Sano H., Salto R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa D., Takabashi F., Takaku-Akahira S., Takada Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2001) to the Ser/Thr protein kinase family. RNSP: O14965; 1016.

MGD: MG1: Camkk2.
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GO:0005622; C:intracellular; ISS.
GO:0005509; F:calcium ion binding; ISS.
GO:0004685; F:calcium and calmodulin-dependent protein k. . .; ISS.
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C STRAIN=C57BL/6J; TISSUE=Retina;

MEDLINE=C57BL/6J; TISSUE=Retina;

MEDLINE=C57BL/6J; TISSUE=Retina;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Shibata K., Itoh M., Aizawa K., Kiteunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Retina;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                             RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005516; F:calmodulin binding; ISS.
GO:0004713; F:calmodulin binding; ISS.
GO:0004777; P:autophosphorylation; ISS.
GO:0019722; P:calcium-mediated signaling; ISS.
GO:0010165; P:mAPKKK cascade; ISS.
GO:000165; P:mApKKK cascade; ISS.
                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Retina;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001)
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STEALEMENT FUB. N. TISSUE=Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lischil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Character M.J., Maray M.J., Sadarlus D.E., Schnerch A., Schein J.E.,

A Dones S.J., Marra M.J.,

R Generation and initial analysis of more than 15,000 full-length human
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GO; GO:0005622; C:intracellular; ISS.
GO; GO:0005509; F:calcium ion binding; ISS.
GO; GO:0004685; F:calcium- and calmodulin-dependent protein k. . .; ISS.
GO; GO:0005516; F:calmodulin binding; ISS.
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InterPro; IPR011009; Kinase like.
InterPro; IPR001019; Prot Kinase.
InterPro; IPR00219; Prot Kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
SMART; SM00220; S TKC; IPR0TEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 55501 MM; 8C596D6839649F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Calcium/calmodulin-dependent protein kinase kinase 2, beta.
                                                                                                                                                                                                                                                                                                              60.9%; Score 42; DB 2; Length 503; 58.3%; Pred. No. 1.2e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AA.
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STRAIN-Mix FVB/N; TISSUE-Mammary tumor;
Strausberg R.;
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Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-restis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                             R GO; GO:0045941; P:positive regulation of transcription; ISS.
GO; GO:0045859; P:regulation of protein kinase activity; ISS.
GO; GO:0045859; P:regulation of protein kinase activity; ISS.
R InterPro; IPR00109; Kinase like.
R InterPro; IPR002190; Ser thr pkinase.
R InterPro; IPR002290; Ser thr pkinase.
R Pfam; PF00069; Pkinase; 1.
R Propom; PF00069; Pkinase; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
O SEQUENCE 541 AA; 59616 MW; FEB2385A4D793FF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CS7BL/60; TISSUE-Testis;
MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis CDNA, RIKEN full-length
enriched library, clone:6030423020 product:CA+/CALMODULIN-DEPENDENT
PROTEIN KINASE KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                      Length 541;
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSOrtium;
                                                                                                                                                                                                                                                                                2; Indels
GO:0004713; F:protein-tyrosine kinase activity; ISS. 60:0046777; P:autophosphorylation; ISS. GO:0019722; P:calcium-mediated signaling; ISS. GO:000165; P:MAPKKK cascade; ISS.
                                                                                                                                                                                                                                                   Score 42; DB 2; I
Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                             3; Mismatches
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58.3%;
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                  105 QGGPASSSNSLD 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Camkk2;
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M MOD; MOI:2444812; Camkk2.

R MOD; MOI:2444812; Camkk2.

R GO; GO:0005622; C:intracellular; ISS.

R GO; GO:0005622; C:intracellular; ISS.

R GO; GO:0005516; F:calcium and calmodulin-dependent protein k. . .; ISS.

R GO; GO:0004685; F:calcium and calmodulin-dependent protein k. . .; ISS.

R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

R GO; GO:0004777; P:autophosphorylation; ISS.

R GO; GO:00019722; P:calcium-mediated signaling; ISS.

R GO; GO:000165; P:MAPKKK cascade; ISS.

R GO; GO:000165; P:regulation of protein kinase activity; ISS.

R GO; GO:0045859; P:regulation of protein kinase activity; ISS.

R InterPro; IPR001009; Kinase—like.

R InterPro; IPR001009; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR008211; Ser_thr_pkinase.

R InterPro; IPR008211; Ser_thr_pkinase.
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Tukuda S., Furuno M., Hanaqaki T., Hara A., Hashizume W.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kono H., Konuda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kono H., Kodada M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,
Saito H., Saitoh H., Sakai C., Sakai M., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EmbL/Genbank/DDBJ databases.

SHEJ, AK031399; BAC27387.1; -.
STRINE-C7BL/6J; TISSUE=Testis;

STRINE-C7BL/6J; TISSUE=Testis;

STRINE-C7BL/6J; TISSUE=Testis;

STRINE-C7BL/6J; TISSUE=Testis;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunco H., Sakquchi S., Ikagami T., Kashiwagi K., A Pujiwake S., Inoue K., Togawa Y., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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PROSITE; PRO1201; PROTEIN KINASE ATP; 1.

PROSITE; PS001107; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS001019; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Parine/threonine-protein kinase; Transferase.

SEQUENCE 579 AA; 63477 MW; A79C6F3EICEGDDCA CRC64;
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Pred. No. 1.4e+02;
3; Mismatches 2; Indels
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Last annotation update)
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58.3%;
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Best Local Similarity 58...
7; Conservative
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Q8C078;
01-MAR-2003 (
01-MAR-2003 (
01-MAR-2004 (
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588 AA.
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SMART; SM00220; S TKC; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00118; PROTEIN KINASE DOM; 1.
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InterPro; IPR01009; Kinase like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR08271; Ser_thr_pkinase.
Fam., PF00069; Pkinase; I.
Prodom; PD00001; Prot kinase; I.
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nes 7; Conservative
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Q8CH42;
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C STRAIN=C57BL/G1 TISSUB=Medulla oblongata;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watehiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/G17 IISSUE=Medulla oblongata;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330570N16 product:CA+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TISSUE=Wedulla oblongata;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
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MGD; MGI:2444812; Camkk2.
GO; GO:0005622; C:intracellular; ISS.
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                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=10090;
                                                                   Name=Camkk2;
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                                          . .; ISS.
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RGO; GO:0005509; F:calcium ion binding; ISS.
RGO; GO:0005516; F:calcium—and calmodulin-dependent protein k. . .;
RGO; GO:0005516; F:calmodulin binding; ISS.
RGO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
RGO; GO:00046777; P:autophosphorylation; ISS.
RGO; GO:000165; P:markex cascade; ISS.
RGO; GO:000165; P:markex cascade; ISS.
RGO; GO:0045891; P:positive regulation of transcription; ISS.
RGO; GO:0045891; P:positive regulation of transcription; ISS.
RGO; GO:0045891; P:positive regulation of transcription; ISS.
RINTERPO; IPR00109; Kinase like.
RINTERPO; IPR00109; Kinase like.
RINTERPO; IPR00219; Prot kinase.
RINTERPO; IPR00219; Prot kinase.
RINTERPO; PR006271; Ser_thr_pkinase.
RPFam; PF00069; PRinase; I.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase.
SEQUENCE 588 AA, 64598 MW, 95B13E1C28FC614F CRC64;
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Bukarnota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AF453383; AAN75696.1; -.
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Burkholderiaceae, Burkholderia.
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MEDLINE=21270059; PubMed=11376489; DOI=10.1002/dvdy.1136;
Lee J.S., Ray R., Chien C.B.;
"Cloning and expression of three zebrafish roundabout homologs suggest roles in axon guidance and cell migration.";
Dev. Dyn. 221:216-230(2001).
                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Avidin family protein.
ORFNames=BPSI0311;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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GG; GG:00042802; F:protein self binding; ISS.
GG; GG:00042802; F:protein self binding; ISS.
GG; GG:0007126; P:homophilic cell adhesion; ISS.
R GG; GG:00050772; P:positive regulation of axonogenesis; ISS.
GG; GG:001657; P:ureteric bud development; ISS.
R Pfam; PF00041; fn3; 3.
SWART; SW00060; FN3; 3.
R PROSITE; PSS0083; FN3; 3.
R PROSITE; PSS0083; FN3; 3.
R PROSITE; PSS0083; IG_LIKE; 5.
R PROSITE; PSS00835; IG_LIKE; 5.
SEQUENCE 1513 AA; 165181 MW; D1743BACCCC089F0 CRC64;
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                                         Length 588
                                       Score 42; DB 2; Length 588
Pred. No. 1.5e+02;
3; Mismatches 2; Indels
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SEQUENCE FROM N.A.
Lee J.-S., Ray R., Chien C.-B.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF337035, AAK58427.1; --
HSSP; Q9HCK4; IUEM.
  64753 MW; 8026EE485C3BA06A CRC64;
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                                         60.9%;
58.3%;
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                 Ouery Match
Best Local Similarity 58.3
Tr Conservative
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Nierman W.C., Joshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T., Ulrich R.L., Romning C.M., Brinkac L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Structural flexibility in the Burkholderia mallei genome."; "Structural flexibility in the Burkholderia mallei genome."; Embl. CP000010; Aud48617.1; - EBBL, CP00010; Aud48617.1; - SEQUENCE 166 AA, 17938 MW; 52D48F78CD5812B9 CRC64;
                                                                                                             Pubmed=1537794,
A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cromin A., Crosset B., Davis P., Deshazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivilal S., Stewens K., Tumapa S., Vesaratchavest M.,
Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
I Burkholderia pseudomallei.",
IF Durkholderia pseudomallei.",
IR Burkholderia Basicity of S., 101:14240-14245(2004).
BMBL; BX571965; CAH34300.1; -.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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6; Conservative
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109 QGGPGASSDRIN 120
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NCBI_TaxID=272560;
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The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-anglogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour diagnosis and prognosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to tumour deposits in humans
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 249 AA;
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Gaps

RESULT 2 AAR93164 ID AAR93164 standard; protein; 104 AA.

An anti-alpha6beta4 integrin light chain linked to a heavy chain.

(first entry)

09-JUL-2001 AAB68087;

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AAB68087 standard; protein; 249 AA.

RESULT 1

Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

Key Region

Region

Region

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The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 lambda light chain fused downstream of a signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born

    .238
    /label= light_chain
    /note= "human lambda light chain constant region and the variable region from anti-rhesus D antibody D7C2"

                                                  Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
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                                                                                                                                                                                               Anti-rhesus D recombinant antibody D7C2 light chain.
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Pred. No. 0.089;
Wismatches
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                                                                                                                                                                                    Location/Qualifiers
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born
                                                                                                                         Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
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                                                                                    Anti-rhesus D monoclonal antibody D7C2 light chain V region.
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                                                                                                                                                                                                                                                                                                                 49. .55
/label= CDR2
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/label= CDR3
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(PROT-) PROTEINE PERFORMANCE.
                                                                                                                                                                                                                                                                            /label= CDR1
                                                29-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Margaritte C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 QGDSLRTYYAS 33
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N-PSDB; AAT26869.
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                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR2724182-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edelman L,
               AAR93164;
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babies.

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Gaps

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Query Match

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AAR93165 RESULT

· 53

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

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This polypeptide sequence comprises the VL domain of human scrv antibody to 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see AAM15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty ceferenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. ceremonis, scleroderma, vascular disorders, cataract, glaucoma, or esp. cor (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, amorophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low diseases (precombinant antigen-binding domains. These are highly specific, have low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; catract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jackson RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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st PR, Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaughan TJ, Williams AU, Janeon KS, Wilton AJ, Tempest PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 2;
Pred. No. 0.059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 1b(ii); 184pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease
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                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                     GB2305921-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45519
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tunnour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 5; Length 253;
Pred. No. 0.15;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 2228-2229; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                          16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
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90.9%;
                                                                                                                                                                                                             15-JUN-2001; 2001WO-US019110
                                                                                                                                                                                                                                                                                                          25-MAY-2001; 2001US-0293499P.
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                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 253 AA;
                                                                                                                                              WO200202641-A1
                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                           16-JUN-2000;
                                                                                                                                                                            10-JAN-2002
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Matches
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%XCCCCCCCCCCCCCCX8X414X4X4X444X44X4XX6X8XX6XX8XX6X4X6X
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immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMP) super family and induces B cell to proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used 'in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent the antibodies and fragments of the antibodies described in the method of
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                 immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; artiAIDS; vaccine; amnunodes; immune; attoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthitis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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tumour necrosis factor; B cell proliferation; B cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 5,
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH, Vaughan T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 2883-2885; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                       17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                    15-JUN-2001; 2001WO-US019110
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156 QGDSLRTYYAN 166
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                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114799/15.
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                                                                                                                                             WO200202641-A1
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                                                                                                                                                                                                                                                        16-JUN-2000;
                                                                                                           Homo sapiens.
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                                                                                                                                                                               10-JAN-2002
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiaency (CVID) and acquired immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 5; Length 243; Pred. No. 0.33; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 2905-2906; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BLyS binding scFv SEQ ID 2103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                       17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                     15-JUN-2001; 2001WO-US019110.
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157 QGDSLRTYYAN 167
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                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-114799/15.
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hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 243 AA;
                                                                                                                            WO200202641-A1
                                                                                            Homo sapiens.
                                                                                                                                                                 10-JAN-2002,
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Matches
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                           Interior describes have a minimum specifically bind. Continuous continuous continuous continuous describeration and differentiation. The antibodies of the invention have projectatic, immunosuppressive, immunostimulant, immunomodulatory, continuous prosectic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS in bloogical samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, theumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA3900-ABPA1228 represent the antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                    immunospecifically bind to
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 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
           systemic lupus erythematosus, rheumatoid arthritis, CVID, AIDS, common variable immunodeficiency, acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 5; Length 247;
Pred. No. 0.33;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Barash SC, Choi GH, Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                    invention describes novel antibodies that
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2906-2907; 3148pp; English.
                                                                                                                                                                                                                                          CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                   16-JUN-2000; 2000US-0212210P.
17-CCT-2000; 2000US-0240B1EP.
16-MAR-2001; 2001US-02748P.
21-MAR-2001; 2001US-0293499P.
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81.8%;
                                                                                                                            15-JUN-2001; 2001WO-US019110
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                           WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
                                                   Homo sapiens.
                                                                                                    10-JAN-2002
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodilatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ALDS)). ABB43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; mimunosuppressive; immunostimulati, immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for the
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi GH,
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17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
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81.8%;
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Best Local Similarity 81.6
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
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                                                                                                                                                                                             WO200202641-A1.
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                                                                                                                      Homo sapiens.
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16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P. 25-MAY-2001; 2001US-0293499P.

2000US-0240816P

7-0CT-2000;

15-JUN-2001; 2001WO-US019110. 16-JUN-2000; 2000US-0212210P.

WO200202641-A1 Homo sapiens.

10-JAN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (GVID) and acquired immunodeficiency syndrome (AIDS)). ABP43290-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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common variable immunodeficiency; acquired immunodeficiency syndrome
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Pred. No. 0.34;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Barash SC, Choi GH, Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2789-2790; 3148pp; English.
                                                                                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                            17-CCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                     15-JUN-2001; 2001WO-US019110.
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                                                                                                                                                                                                                                                                                                          SCI INC
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Best Local Similarity
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                                                                           WO200202641-A1
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                                       Homo sapiens
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XX AC ABP4
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                             89.5%; Score 51; DB 5; Length 250; 81.8%; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                     Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-platelet glycoprotein Ib human HIb-1 VL CDR1.
                                                                                                                                     Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                        Claim 1; Page 2774-2775; 3148pp; English.
                                                                                                                      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY95195 standard; peptide; 11 AA.
                                                                                                                                     Choi GH,
                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    ||||||||||
164 QGDSLRTYYAN 174
                                                                                                                                                                                                                                                                                                                                                                                           1 QGDSLKTYYAS 11
                                                                                                                                    Ruben SM, Barash SC,
                                                                                                                                                  WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                               Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY95195;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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Homo sapiens

(MILL/) MILLER J L.

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The present sequence is that of complementarity determining region 1 (CDR1) of the light chain variable region (VL) of human single chain antibody (scrv) HID-1 (see AAY95198), which is directed against platelet 34. COPATOR (SCRV) HID-1. The HID series of scrv was isolated from a human synthetic VH and VL scrv library on the basis of their binding to platelet GPID. Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coli, the HID scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet chain, including CDR fragments, are also claimed fragments of the scrv VH or VL chain, including CDR fragments, are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variable light chain; single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic; CDR1; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-platelet glycoprotein Ib human HIb-3 VL CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 3;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY95216 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                         Claim 19; Fig 5; 89pp; English.
                                                               99WO-US025495
                                                                                               98US-0106275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US025495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0106275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 .QGDSLRSYYAS 11
                                                                                                                                                                                          WPI; 2000-365744/31.
                                                                                                                               n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 AA;
                                                                                                                               (MILL/) MILLER
WO200026667-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200026667-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-1999;
                                                                                               30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1998;
                                                               29-OCT-1999;
                               11-MAY-2000
                                                                                                                                                                                                                                                             aggregation
                                                                                                                                                             Miller JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY95216;
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corrections of the light chair variable region (VL) of human single chain antibody (scrv) HID-3 (see AAY95219), which is directed against platelet glycoprotein ID (GPLD). The HID series of serv was isolated from a human synthetic VH and VL scrv library on the basis of their binding to platelet GPLD. Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coli, the HID scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Whethods of inhibiting aggregation of platelets, of binding human platelet (PPL) alpha and of selecting a VH or VL region of an antibody that.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragments of the scrv VH or VL
                                                                                                                Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; light chain, variable region, CDR1; human; gp96; cytostatic; complementarity determining region; antibacterial; virucide; fungicide; protozoacide; tumour; autologous immunization; anti-idiotypic.
                                                                                                                                                                                                               The present sequence is that of complementarity determining region 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; DB 3; Length 11; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gp96 antibody variable light chain CDR1' peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibits platelet aggregation are claimed. Fragm chain, including CDR fragments, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Welschof M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG80192 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Opelz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                   Claim 19; Fig 7; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2000; 2000DE-01019967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2000; 2000DE-01019967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FENN-) FENNING BIOMED GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.0
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Rammensee H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QGDSLRSYYAS 11
                                                                             WPI; 2000-365744/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-018649/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 AA;
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                                                                                                                                                     aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terness P,
                                             Miller JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schild H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG80192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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This invention describes a novel recombinant antibody (Ab) that binds native gp96. The product of the invention has cytostatic, antibacterial, virucide, fungicide and protozoacide activity. Complexes of gp96 with the peptides of the invention induce a immune response (cytotoxic T calls) specific for the associated peptides. Ab are used for purification or small amounts of tumour or infected complexes (C) with peptides (I), from small amounts of tumour or vicetular (C) are useful: (i) in human or veterinary medicine for autologous immunization, for treating tumour or veterinary medicine for autologous immunization, for treating tumour or veterinary (by viruses, bacteria, mycoplasma, fungi and parasites (procozoa)); and (ii) for raising anti-idiotypic antibodies. Ab make possible isolation of very pure gp96 in native form, even from small tumour samples, in a one-step chromatographic process that does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                         This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package; human.
                                                                                                                                                                                                                                                                                                                 require concanavalin A (as used in known processes and which may contaminate the final product by bleeding from the column). This sequenc represents the variable light chain complementarity determining region (CDRI') fragment of the antibody raised against human gp96 described in
        recombinant antibody specific for native gp96, useful for isolating s as complex with endogenous peptides, used for autologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoogenboom HRJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain VL3.5 from BSA binding scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB!
Pred. No. 0.018
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson KS,
Marks JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR22572 standard; protein; 101 AA.
                                                                              Claim 3; Page 13; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90GB-00022845.
90GB-00024503.
91GB-00004744.
91GB-00010549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
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                                        immunotherapy of e.g. tumor.
                                                                                                                                                                                                                                                                                                                                                                                         the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J, Pope AR, J
, Holliger KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEDI-) MED RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-056862/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccafferty J. Jackson RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9201047-A
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12-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR22572;
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AAR22572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Cells from an unimmunised donor. Heavy chains from RNA from white blood cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies were amplified separately. Four separate libraries were generated (IgG-K, IgG-lambda, IgM-Rand IgM-lambda). The purified scrv fragments were libraries were generated (IgG-K, IgG-lambda, IgM-Rand IgM-lambda). The purified scrv fragments were libraries were flowered into the phagemid pHENI for expression on the surface of fd ligated into the phagemid pHENI for expression on the surface of fd affinity selection for binding to phox.BSA by selection on tubes followed by analysis by ELISA. Of 96 clones analysed, 43 showed binding to both by analysis by ELISA. Of 96 clones analysed, 43 showed binding to both clones sequenced had the same sequence, the VH derived from a human VH3 family gene (AAR22571) and the VL from a human V lambda 3 family gene (shown here). The other was derived from a human VH family gene chuders. This sequence revealed a VH derived from a human VH family gene bunder). This sequence revealed a VH derived from a human VH family gene (AAR22570). See
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith RG, Mccafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complimentarity determining region 1"
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    .92
    'note= "complementarity determining region 3"

                                                                                                                                                                                                                                                                                also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain; RT3; human; catalytic antibody; bacteriophage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "complementarity determining region
                                                                                                                                                                                                                                                                                                                                         Score 50; DB 2; Length 101; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human derived light chain RT3 phage antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...16
note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .82
te= "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93. .103
/note= "framework region
                             Table 11; Page 152; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR80091 standard; protein; 103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US003420.
                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8
Section 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .103
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/note= "u
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                                                                                                                                                                                                                                                                                                                                                                                                    1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                    23 OGDSLRSYYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
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                                                                                                                                                                                                                                                                                                               Sequence 101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09527045-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1994;
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જારા કરેક. જારે જાર લાજી રહેતુ

Williams RO;

Titmas RC,

AAT04638 encodes AAR80091 human derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo Length 103; 0; Indels Score 50; DB 2; Pred. No. 0.2; 2; Mismatches 87.7**%**; 81.8**%**; Query Match
Best Local Similarity 81.8
Matches 9; Conservative 1 QGDSLKTYYAS 11 Sequence 103 AA;

||||||::|||| 17 QGDSLRSYYAS 27 엄

AAW95489 standard; protein; 103 AA. (first entry) 29-MAR-1999 AAW95489; 

Human-derived RT3 phage antibody light chain genetic sequence.

Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; RT3

Homo sapiens

US5855885-A

05-JAN-1999

94US-00273146.

93US-00007684. 22-JAN-1993;

CHISWELL D.
DARSLEY M J.
TITMAS R C.
MARTIN M T.
KENTEN J H. MCCAFFERTY J. (TITM/) MCCA/) CHIS/)

SMITH R. FITZGERALD K. WILLIAMS R O. (KENT/) (SMIT/) (FITZ/) (WILL/)

MJ, Williams RO, Smith R, Mccafferty J, Titmas RC; Fitzgerald K, Darsley M Kenten JH, Chiswell D,

Martin MT;

WPI; 1999-105036/09. N-PSDB; AAX00888

Kenten JH,

Production of catalytic antibodies displayed on bacteriophages -comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic

Example, Fig 20F; 117pp, English.

The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH cand VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies; which can be used for in vivo activation of a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage antibody library *555555555555555555555

Sequence 103 AA;

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Gaps ; 0

Gaps ; 0 Score 50; DB 2; Length 103; Pred. No. 0.2; 0; Indels 2; Mismatches 87.7%; 81.8%; 9; Conservative Query Match Best Local Similarity Matches

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ò d AAG93606

AAG93606 standard; protein; 104 AA (first entry) 14-SEP-2001 AAG93606;

Human anti-Rh(D) chain J04 protein sequence.

Human, anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant; red blood cell; Rh phenotype; diagnosis; therapeutic. Homo sapiens 03-JUL-2001.

96US-0028550P. 97US-00884045. (UYPE-) UNIV PENNSYLVANIA. 11-OCT-1996; 10-APR-1998; 

99US-00240274.

29-JAN-1999;

Siegel DL;

WPI; 2001-388931/41. N-PSDB; AAH68663 New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in diagnostics requiring therapeutic medicine.

Claim 1; Col 45; 162pp; English.

The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in hAQ91558 to AAQ93669. (I) has immunostimulant activity, and can be used as an immune system stimulant.

Gaps

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The present invention describes a method for detecting the presence of fibronectin isoform B (B-FN) in body fluid of an individual. The method involves passing the fluid over a solid support (SS) to which gelatin that binds FN is attached, such that if FN is present, it is retained on SS by binding gelatin, and determining the presence of B-FN on SS by determining the ability of a specific binding member for extra domain B (ED-B) of B-FN to be retained on SS. The method is useful for the quantitative determination of B-FN in a body fluid taken or collected from an individual. Other methods from the present involution can be used: for quantitating the amount of an insoluble marker protein in a sample of tissue or tumour. An elevated level of B-FN in a body fluid sample of tissue or tumour. An elevated level of B-FN in a body fluid cuch as plasma, cerebral-spinal fluid or cystic fluid obtained from an individual is indicative of the presence of a tumour in the individual. The methods are useful in diagnostic and prognostic situations. The
                             are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68015 to AAH68726 represent the nucleotide sequence which encode AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh (D) heavy chain CDR3 amino acid sequences which are given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting fibronectin isoform B in body fluid of an individual, by binding fibronectin to gelatin on solid support, and determining ability of specific binding member for Extra Domain B to be retained on support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibronectin isoform B; B-FN; extra domain B; ED-B; antibody; VL domain; angiogenesis; neoplasia; tumour; detection.
   The antibodies
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                                                                                                                                                                                                                                                                                                                                              Score 50; DB 4; Length 104;
Pred. No. 0.2;
2; Mismatches 0; Indels
can be used in diagnostic and therapeutic medicine.
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81.8%;
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         clinic, thereby providing valuable information without additional compromise to the patients or complications for the clinicians. The present sequence represents the VL domain of a B-FN ED-B specific antibody molecule, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
methods can be readily applied to small biopsy samples obtained in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Human; RH(D) binding protein; blood typing; blood product; antibody; magnetically activated cell sorting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents the amino acid sequence of a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Rh(D) binding protein. The
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81.8%; Pred. No. 0.2;
ive 2; Mismatches 0; Indels
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                                                                                                                 Score 50; DB 5;
Pred. No. 0.2;
2; Mismatches
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                                                                                                                                              5
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97US-00884045.
98US-0081380P.
99US-00240274.
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                                                                                                                  87.7%;
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QGDSLRSYYAS
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N-PSDB; ACD45327.
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Best Local Similarity
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                                                                                          Sequence 104 AA;
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27-JUN-1997;
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29-JAN-1999;
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Variable light chain; single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
Anti-platelet glycoprotein Ib human HIb-3 VL.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL/) MILLER J L.
                                                                                                                                                                                                                                                                                                                      WO200026667-A1
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                                                                                Homo sapiens.
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 AAV02501-AAV02635, and AAV02641-AAV02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain. light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
caplement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
cadipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
catectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                  Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 4; Length 106;
Pred. No. 0.2;
2; Mismatches 0; Indels
                                                                                                       Anti-adipocyte monoclonal antibody light chain, FAT 20.
                                                                                                                                                                                                                                                                                                        (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                       AAU02531 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                                    Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1, Page 112; 182pp; English.
                                                                                                                                                                                                                                                     11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                               99US-0158812P
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81.8%;
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Matches 9, Conservative
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N-PSDB; AAS03431.
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                                                                                                                                                                                                WO200127279-A1.
                                                                                                                                                                         Homo sapiens.
                                                                            29-AUG-2001
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                                                   AAU02531;
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.96 ce= "complementarity determining region 3"

/note= "framework region 4"

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99WO-US025495 98US-0106275P.

"complementarity determining region 1"

l. .22
/note= "framework region 1"

Location/Qualifiers

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49. .55 /note= "complementarity determining region

"framework region 2"

/note= "c,

.87 .e= "framework region 3"

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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scrv) HID-3 (see AAY95219), which is directed against platelet glycoprotein ID (GPID). The HID series of scrv was isolated from a human synthetic VH and VL scrv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID phagemid selection against transfected CHO cells expressing the GPID component of the GPID/IX/V complex on their surface, followed by a thround of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scrv from washed platelets by 10 which attempts were made to displace scrv from washed platelets by 12 control of secreted as free scrv by Escherichia coli, the HID scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes: They provide a new class of antithromboit aggregation of platelet dependent thromboit in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Wethods of inhibiting any any of villatelets, of binding human platelet chibits platelet aggregation are claimed inhibits platelet aggregation are claimed
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Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
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                                                                                                                                                                                               Claim 18; Fig 7; 89pp; English.
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                                                                                                  aggregation.
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AAY95215 standard; protein; 107 AA.

1 QGDSLKTYYAS 11

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23

29-AUG-2000 (first entry)

AAY95215 RESULT 22
AAY95215
ID AAY95
XX
AC AAV95
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DT 29-AU

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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scPv) HID-1 (see AAY95198), which is directed against platelet glycoprotein ID (GDL). The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID calpa component of the GPID/IX/V complex on their surface, followed by a thround of selection against washed human platelets and 2 final rounds thround of selection against washed human platelets by Tlooding with murine monoclonal antibody or mimotope peptide (see AV95229). Whether displayed as surface proteins on a phagemid or secreted as free scPv by Escherichia coli, the HID scPv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scPv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombot in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet
                                                                                                                                                                                                  Variable light chain; single chain antibody; scFv; human; HIb-1; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                        .55
:e= "complementarity determining region
                                                                                                                                                                      Anti-platelet glycoprotein Ib human HIb-1 VL.
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/note= "framework region 1"
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                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                          AAY95194 standard; peptide; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Fig 5; 89pp; English.
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23 OGDSLRSYYAS 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200026667-A1
                                                                                                                                                                                                                                                                   Homo sapiens
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                                              RESULT 23
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"complementarity determining region 1"

"framework region 2"

"complementarity determining region 3"

"framework region 3"

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                                                                                                                                                                                                                                                                                                                                                                                                Antibody; light chain; VL; amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; Albeimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.
                                                                                                                Gaps
GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed
                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of variable light chain fragment of clone D5
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                                                                               DB 3; Length 107;
                                                                                                                 0; Indels
                                                                                Score 50; DB 3
Pred. No. 0.21;
                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                AAG62969 standard; protein; 107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward G,
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                                                                               87.7%;
81.8%;
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                                                                                                                 9; Conservative
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QGDSLRSYYAS 33
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                                                                               Query Match
Best Local Similarity
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                                                 Sequence 107 AA;
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antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzbeimer's disease, prion disease, AlDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the

brain or central nervous system

Sequence 107 AA;

Ouery Match

87.7%; Score 50; DB 4; Length 107;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet
                  Gaps
                                                                                                                                                                                                                                                     Variable light chain; single chain antibody; scFv; human; HIb-3;
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ce= "complementarity determining region 3"
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                                                                                                                                                                                                                                                                  glycoprotein Ib alpha, platelet, aggregation, antiaggregant, antithrombotic, thrombus, therapy, diagnostic.
                  Indels
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  Pred. No. 0.21;
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/note= "framework region 4"
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                 Mismatches
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 81.8%;
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/note= "-
34.
                  Conservative
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                                           1 QGDSLKTYYAS 11
                                                                      21 OGDSLRSYYAS 31
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N-PSDB; AAA27663.
Best Local Similarity
Matches 9; Conserv
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                                                                                                              RESULT 25
AAY95185
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                 are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed
The scFv are composed of native human protein sequences and
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6725, Ap 12, Appl

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US-08-893-852A-3 US-08-821-818-3 US-09-052-753B-3 US-09-328-352-6725 US-09-899-896-12 US-09-134-001C-5625 Sequence Sequence Sequence Sequence Sequence Sequence

> US-09-489-039A-13931 US-09-543-681A-4818

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19243, A
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-793-450-6

US-08-665-202-35

US-09-315-574-49

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US-09-2240-274-49

US-09-226-22-34

US-09-26-22-34

US-09-26-57-3

US-09-260-527-3

US-09-260-527-3

US-09-20-10

US-09-20-10

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Maximum Match 100%
Listing first 150 summaries
                                                                                  US-10-088-639A-2_COPY_23_33
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1 QGDSLKTYYAS 11
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Perfect score:
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7560, Ap 24, Appl 3, Appli

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US-08-930-996A-8 US-09-543-681A-75 US-09-881-710-24 PCT-US91-02942-8 US-09-648-067A-15 US-07-934-373C-21

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PCT-US92-08756A-5

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US-09-107-532A-4682 US-09-562-737-30 US-09-134-000C-4702 US-08-309-512-5

Sequence

5906, Ap 6, Appli 15, Appl

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Sequence 6, Application US/08793450

Batent No. 6312690

GENERAL INFORMATION:

APPLICANT: EDELMAN, LENA

APPLICANT: MACGOREK, MICHEL

APPLICANT: KACZOREK, MICHEL

APPLICANT: MANDAINI, HASSAN

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION:

NUMBER OF ESQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STATE: VA

COUNTY: ARLINGTON

STATE: VA

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 4; Length 104;
Pred. No. 0.0047;
1; Mismatches 0; Indels
                                                  COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: US-MAR-1997
CLASSIFICATION NUMBER: US/08/793,450
FILING DATE: US-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INPORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.7%;
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Best Local Similarity 90.5
Matches 10; Conservative
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; MOLECULE TYPE: protein
US-08-793-450-2
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5626, Ap
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Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 333, Appl
Sequence 333, App
Sequence 5401, Ap
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4, Appli
5, Appli
1, Appli
2, Appli
2, Appli
9637, Ap
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Sequence 2, Appli
Sequence 19, Appl
Sequence 21, Appl
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Sequence 6948, Ap
Sequence 47, Appl
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29092, A
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Sequence 29092
Sequence 4, Ag
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US-08-793-450-2

Sequence 2, Application US/08793450

Patent No. 6312690

GENERAL INFORMATION:
APPLICANT: BDELMAN, LENA
APPLICANT: KACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
CITY: ARLINGTON
CITY: ARLINGTON
STATE: VA
US-09-252-991A-19428
US-09-717-432-2
US-09-912-484-2
US-08-999-723-2
US-09-434-427-2
US-09-548-372D-2
US-09-548-372D-2
US-09-548-372D-2
US-09-551-853D-2
US-09-215-450-19
PCT-US95-03236-21
US-08-258-639A-4
US-08-258-639A-4
US-08-900-951-4
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US-09-514-302-4
US-09-561-709B-5
US-09-561-709B-5
US-09-514-302-2
US-09-308-375-2
US-09-403-099A-1
US-09-075-769B-280
US-09-075-769B-280
US-09-075-769B-280
US-09-075-769B-280
US-09-075-769B-280
US-08-08-38-160-7
US-08-38-160-7
US-08-38-160-7
US-08-38-160-7
US-08-478-373-67
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US-08-478-373-67
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US-09-634-238-336
US-09-543-681A-6948
US-08-983-607-47
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US-09-107-532A-5401
US-09-134-000C-6797
US-08-244-646-17
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-08-897-438-67
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1938
2285
281
432
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APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Twor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSER: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UNN-1995
FILING DATE: 14-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
PRIOR APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UNN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     Sequence 35, Application US/09315574 Patent No. 6512097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-273-146-71
; Sequence 71, Application US/08273146
; Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
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81.8%;
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APPLICANT: Smith, Rodger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
  1 QGDSLKTYYAS 11
                                       22 ÓGDSLRSÝÝAŠ 32
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                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: Cal'e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                 GENERAL INFORMATION:
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TELEFAX: (
                                                                                                                     US-09-315-574-35
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Batent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    Gaps
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.7%; Score 50; DB 2;
81.8%; Pred. No. 0.025;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
  660-118-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2020
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                        94.7%;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                       1 QGDSLKTYYAS 11
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STREET: Two
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-665-202-35
                                                                                                                                                        TOPOLOGY:
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US-08-652-816A-16
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1 Sequence 49, Application US/09240274

2 Sequence 49, Application US/09240274

3 Patcent No. 62554515

5 GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

7 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

7 TITLE OF INVENTION: NUMBER: 09/09/240,274

7 CURRENT PILING DATE: 1999-01-29

7 CURRENT FILING DATE: 1999-01-29

7 EARLIER APPLICATION NUMBER: 60/081,380

8 EARLIER APPLICATION NUMBER: 60/081,380

8 EARLIER APPLICATION NUMBER: 60/028,550

8 EARLIER APPLICATION NUMBER: 60/028,550

8 EARLIER APPLICATION NUMBER: 60/028,550

9 SEALLER APPLICATION NUMBER: 60/028,550

1 SARLIER APPLICATION NUMBER: 60/028,550

1 SEALLER APPLICATION NUMBER: 60/028,550

1 SEALLER PILING DATE: 1996-10-11

1 SEQIENT: 104
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     APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 2; Length 103; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 43-4-50
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: anti-Rh(D) chain J04 < US-09-240-274-49
                                                                                                                                                                                                                                                     E: IGEN, Inc.
1530 East Jefferson St.
Darsley, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 103 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-273-146-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QGDSLKTYYAS 11
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17 QGDSLRSYYAS 27
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                STREET: 1530 Eas
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                  STATE:
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Gaps
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APPLICANT: Osbourn, JK
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: methods.
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCE: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-LOSS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
FRIOR APPLICATION DATA:
PILING DATE: 02-DEC-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 23-MAR-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92064.9
FILING DATE: 23-MAY-1996
FILING DATE: 23-MAY-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
FRIOR DATE: 02-DEC-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 02-DEC-1995
FRIOR DATE: 02-DEC-1995
FRIOR APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.7%; Score 50; DB 2; Length 109;
                     DB 3; Length 104; 0.027;
                                                                      0; Indels
                                                                    2; Mismatches
                     Score 50;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,107
FR: 28111/33308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               Sequence 16, Application US/08652816A Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: David W. Clough
REGIESTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION: INFORMATION:
                     87.7%;
81.8%;
Ouery Match
Best Local Similarity
Bare
Good 9; Conservative
                                                                                                                     1 OGDSLKTYYAS 11
                                                                                                                                                              21 QGDSLRSYYAS 31
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JOS-US-20-26.73

J. Sequence 3, Application US/09260527A

Patent No. 622859

GENERAL INFORMATION:

APPLICANT: Mikkelsen, J.D.

APPLICANT: Mikkelsen, J.D.

APPLICANT: Milats, W.G.

TITLE OF INVENTION: ANTIBODY

FILE REFERENCE: DYOUI9.001AUS

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 2.78

TYPE: PRT

ORGANISM: UNKNOWN

FEATURE:

CHER INFORMATION: Anti-homogalacturonan specific antibodies selected

CHER INFORMATION: from a naive phage display library known as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 4; Length 109;
Pred. No. 0.029;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/65,202
FILING DATE: 13-JUN-1995
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                 ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C. STREET: Four Embarcadero Center, Suite 1100 CITY: San Prancisco STATE: California
       Tumor Antigens
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230.
TELECOMMUNICATION INPORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 109 amino acids
amino acid
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                           COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 OGDSLRSYYAS 32
                         NUMBER OF SEQUENCES: 1.
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-315-574-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-260-527-3
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                                                                                                                                                                                                          Sequence 34, Application US/08665202
Sequence 34, Application US/08665202
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARE: California
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.7%; Score 50; DB 2; Length 109; 81.8%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION 342
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING APPLICATION NUMBER: US 60/000,250
ATTORNEY/AGENT INFORMATION:
                         ö
    Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hunter, Tom
REGISTRATION UNBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPANS: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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                                                                    1 QGDSLKTYYAS 11
                                                                                                23 QGDSLRSYYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-665-202-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-315-574-34
                                                                                                                                                                                RESULT 8
US-08-665-202-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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DB 4; Length 309;
0.086;
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Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/079,029
                                                                                                                                                                                                                                                                                                                     Score 50; DB Pred. No. 0.08 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Camilia W. APPLICANT: Ashkenazi, Avi J. APPLICANT: Ashkenazi, Avi J. APPLICANT: Churtharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
                                                                                       P1101R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09079029 Patent No. 6342369
                   ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REPRENCE/DOCKET NUMBER: P1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                            TOPOLOGY: Linc 9
                                                                                                                                                                                                                                                                                                                     87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 312 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||::||||
200 QGDSLRSYYAS 210
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-079-029-10
                                                                                                                                                                                                                                                                           US-09-079-029-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a OTHER INFORMATION: phage display library known as the Synthetic scFv OTHER INFORMATION: Library (#1) from the Centre for Protein OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                    Score 50; DB 3; Length 278; Pred. No. 0.077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%; Score 50; DB 3; Length 280;
81.8%; Pred. No. 0.078;
                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER TRADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
FILLING DATE: US/09/079,029
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knox, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Millats, W.G.
TITLE OF INVENTION: ANTIBODY
FILE REFERENCE: DYOUL9.001AUS
CURRENT APPLICATION NUMBER: US/09/260,527A
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: AND J.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09260527A Patent No. 6228599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                  Query Match
Best Local Similarity 81.8*;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                               175 OGDSLRSYYAS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 GGDSLRSYYAS 187
                                                                                                                                                                       1 QGDSLKTYYAS 11
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ORGANISM: UNKNOWN
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US-09-079-029-9
                                         US-09-260-527-3
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GENERAL INFORMATION:
APPLICANT: FRENKEN, LEON GERARDUS
APPLICANT: HOWELL, STEVEN
APPLICANT: LEDEBORY, ADRIANGS MAR
APPLICANT: VAN DER LOGT, CORNELIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.78;
77.88;
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SEQ ID NO 20
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 QGDGLRSYYAS 31
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Lama peruana
US-09-530-139-20
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54 DSARTYYAS 62
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Matches 8; Conserv
GENERAL INFORMATION:
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                                               Sequence 50, Application US/09240274

Sequence 50, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:

TITLE OF INVENTION: Bh D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SOFTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/240, 274

CURRENT APPLICATION NUMBER: 06/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER PILING DATE: 1998-04-10

EARLIER PILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 50

LENGTH: 106
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TITLE OF INVENTION: Rh(D) BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-44202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-01-11
SORTHARE PILING DATE: 1996-01-11
SORTHARE PILING DATE: 1996-10-11
SORTHARE: PATENTY
SORTHARE: APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-01-11
SORTHARE: PATENTY
SORTHARE: APPLICATION NUMBER: 60/028,550
EARLIER PILING DATE: 1996-01-11
SORTHARE: PATENTY
SORTHARE: DATE: 1996-10-11
LENGTH: 106
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Pred. No. 0.067;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain JOS
US-09-240-274-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THER INFORMATION: anti-Rh(D) chain J01
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US-09-240-274-48
; Sequence 48, Application US/09240274
; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 72.7.
Best Local Similarity 72.7.
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21 QGDGLRSYYAS 31
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ORGANISM: Homo sapiens
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             RESULT 14
US-09-240-274-50
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APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PAPLICATION VUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PAPLICATION VUMBER: 10/028,550
EARLIER FILING DATE: 1996-10-11
SEQ ID NO 48
LENGTHA: 106
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APPLICANT: LEDEBORR, ADRIANUS MARINUS
APPLICANT: LEDEBORR, ADRIANUS MARINUS
TITLE CANT: VAN DER LOGT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION WUMBER: US/09/530,139
CURRENT FILING DATE: 2000-04-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: anti-Rh(D) chain J02
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LEDEBOER, ADRIANUS MARINUS
VAN DER LOGT, CORNELIS PAUL
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US-09-530-139-20
; Sequence 20, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-530_139-38
; Sequence 38, Application US/09530139
; Patent No. 6670453
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Score 35; DB 4
Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                 4; Mismatches
                    CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
                                NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 117
LENGTH: 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5678
                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%;
66.7%;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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46 RGDNLETYWQS 56
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Best Local Similarity
Matches 6; Conserv
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      FILE REFERENCE:
                                                                                                                                                                             FEATURE:
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US-09-530-139-36
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APPLICANT: LEDEBORK, ADRIANUS
APPLICANT: VAN DER LOCT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REPERENCE: 60113/268075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
CURRENT APPLICATION NUMBER: PCT/EP98/06991
PRIOR APPLICATION NUMBER: PCT/EP98/06991
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
SEQ ID NO 36
LENGTH: 238
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Pred. No. 13;
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TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
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Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
                                                                                                                                                                                                                                                                                                                                                                      DB 4;
12;
              FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
PRIOR APPLICATION NUMBER: PCY/EP98/06991
PRIOR FILING DATE: 1908-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver: 2.1
SSOFTWARE: Patentin Ver: 2.1
SSOFTWARE: 224
                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Pred. No.
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; Sequence 36, Application US/09530139
; Patent No. 6670453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FRENKEN, LEON GERARDUS
                                                                                                                                                                                                                                                                                                                                                                    66.78;
77.88;
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77.8%;
                                                                                                                                                                                                                                                 ORGANISM: Unknown Organism
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Best Local Similarity 77.8.
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ORGANISM: Unknown Organism
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DSLKTYYAS 11
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|DSARTYYAS 58
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Sequence 19243, Application US/09252991A

Factor No. 6551795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

ABRUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19243

LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5678, Application US/09134000C

Patent No. 647156

GENERAL INFORMATION:

APPLICANT: Lynn boucette-Stamm et al

APPLICANT: Lynn boucette-Stamm et al

TITLE OF INVENTION: EXTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EXTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 5678

LENGTH: 86
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: Sequence US-09-562-737-117
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                                                                                                                                    Score 36; DB 4; Length 185;
Pred. No. 23;
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16;
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59.6%; Score 34; DB 2; Length 119; 60.0%; Pred. No. 35; ive 2; Mismatches 2; Indels
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Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: Garter, Faul J.
APPLICANT: Garter, Faul J.
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
CARENT Garter, Paul J.
CHILLE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT APPLICATION NUMBER: US/08/918,148A
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 24, 2004, 02:19:55 Job time : 21.6792 secs
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ilarity 60.0%;
Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79
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US-08-652-816A-10
Sequence 10, Application US/08652816A
Sequence 10, Application US/08652816A
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Sequence 10, Application US/08652816A
Sequence 10, Application:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
SPECIFICANT: MCCAFferty, JG
TITLE OF INVENTION: methods:
TITLE OF INVENTION: methods:
CORRESPONDENCES: 53
CORRESPONDENCES: 53
STREET: 6300 Sears Tower, 233 South Wacker Drive
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS PRIOR APPLICATION NUMBER: US/08/652,816A FILING DATE: 23-MAY-1996 FILING DATE: 02-DEC-1991 PRIOR APPLICATION NUMBER: GB 9206318.9 FILING DATE: 24-MAR-1992 PRIOR APPLICATION NUMBER: GB 9206318.9 FILING DATE: 23-SEP-1992 PRIOR APPLICATION NUMBER: GB 9206312.6 FILING DATE: 23-SEP-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9206372.6 FILING DATE: 07-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9206372.6 FILING DATE: 07-DEC-1995 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA:
                                                             Score 35; DB 4; Length 200;
Pred. No. 39;
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FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DAYIG W. Clough
REGISTRATION NUMBER: 36,107
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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         US-09-252-991A-19243
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Sequence 4299, Application US/09328352

Sequence 4299, Application US/09328352

Battent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
SEQ ID NOS: 8252
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Pred. No. 75;
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US-10-10-20-9568-7
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US-10-293-418-2084
US-09-880-748-2102
US-10-293-418-2102
US-09-880-748-2103
US-09-880-748-2103
US-10-293-418-2008
US-10-293-418-2008
US-10-293-418-2008
US-09-880-748-2008
US-09-880-748-2008
US-09-880-748-1090
US-10-293-418-2002
US-10-293-418-2002
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US-10-291-418-130

US-10-291-418-130

Sequence 1530, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: 00/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-01-2

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-00-16

PRIOR FILING DATE: 2000-00-16

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PRIOR FILING DATE: 2000-00-16

PRIOR FILING DATE: 2000-00-16
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-10-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2000-10-17
PRIOR PLILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PALENTIN Ver. 2.0
LENGTH : 253
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Pred. No. 0.096;
1; Mismatches 0; Indels
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90.9%;
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Best Local Similarity 90.5
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CORGANISM: Homo sapiens
US-10-293-418-1530
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; ORGANISM: Homo sapiens
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US-09-880-748-1444
US-09-880-748-1062
US-09-880-748-2021
US-09-880-748-2021
US-09-880-748-2046
US-10-293-418-1424
US-110-293-418-1424
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US-10-293-418-2107
US-09-880-748-1694
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US-09-880-748-1192
US-09-880-748-1308
US-09-880-748-1308
US-09-880-748-1426
US-09-880-748-1618
US-09-880-748-1618
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US-10-293-418-1308
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Gaps

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Gaps ö Score 53; DB 12; Length 253; Pred. No. 0.096; 1; Mismatches 0; Indels 93.08; Ouery Match 93.0%; Best Local Similarity 90.9%; Matches 10; Conservative 166 QGDSLKSYYAS 176 1 OGDSLKTYYAS 11 ò 셤

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US-09-880-748-1530 RESULT 1

ALIGNMENTS

Sequence 1530, Application US/09880748 Publication No. US2003055937A1 GENERAL INFORMATION: APPLICANT: Ruben et al.

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Sequence 2102, Application US/09880748
Publication No. US20030059937A1
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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QGDSLKTYYAS 11
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CRGANISM: Homo sapiens
US-09-880-748-2102
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FUNDICATION OF US/2003022996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

ITILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.23P2

CURRENT APPLICATION NUMBER: 00/331,469

FRIOR APPLICATION NUMBER: 60/331,469

FRIOR APPLICATION NUMBER: 60/340,817

FRIOR FILING DATE: 2001-11-16

FRIOR APPLICATION NUMBER: 00/40,817

FRIOR FILING DATE: 2001-12-19

FRIOR FILING DATE: 2001-02-15

FRIOR FILING DATE: 2001-02-15

FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-16

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR FILING DATE: 2001-03-16

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR FILING DATE: 2001-03-16

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FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-16
Sequence 2084, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF533

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-66-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

SOFTWARE: PATCHTON NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

SOFTWARE: PATCHTION VUMBER: 06/293,499

FRIOR FILING DATE: 2001-05-25

SOFTWARE: PATCHTION VUMBER: 06/293,499

FRIOR FILING DATE: 2001-05-25

SEQ ID NO 2084
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Pred. No. 0.22;
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81.8%; Pred. No. (
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81.8%;
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Best Local Similarity 81.6
Matches 9; Conservative
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156 QGDSLRTYYAN 166
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US-09-880-748-2084
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CORGANISM: Homo sapiens
US-10-293-418-2084
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Best Local Similarity
Matches 9; Conserv
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Gaps
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Sequence 2102, Application US/10293418

Publication No. US2003022396A1

GENERAL INFORMATION:

APPLICANT: Nuben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR PILING DATE: 2001-11-27

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-01-16

PRIOR PILING DATE: 2000-01-16

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-17

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PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-17
FULLICATION NO. US.703.000.939.741

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF5.3

CURRENT PILING DATE: 2001-06-15

PRIOR PPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/27,379

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET. 2.00

SEQ ID NOS: 3239
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Pred. No. 0.22;
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PRIOR APPLICATION NUMBER: 60/212,210 PRIOR FILING DATE: 2000-06-16 NUMBER OF SEQ ID NOS: 3247 SEQ ID NO 2103 LENGTH: 247
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81.8%;
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                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-293-418-2103
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US-09-880-748-2088
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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Publication No. US20030059937A1

SEQUENCE INFORMATION:
APPLICAMT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

SOFTWARE: PARCHING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PARCHIN Ver. 2.0

SEQ ID NO 2103
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Sequence 2103, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/31,469

PRIOR APPLICATION NUMBER: 60/31,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-16
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                                                                 Score 51; DB 12; Length 243;
Pred, No. 0.22;
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Pred. No. 0.22;
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81.8%;
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81.8%;
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Best Local Similarity 81.b
3; Conservative
                                                                                     Best Local Similarity, 81.8
Matches 9; Conservative
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157 QGDSLRTYYAN 167
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    ; ORGANISM: Homo sapiens
US-10-293-418-2102
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; ORGANISM: Homo sapiens
US-09-880-748-2103
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US-09-880-748-2103
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Gaps
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PUBLICATION NO. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR PELING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

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US-10-293-418-2088

Sequence 2080, Application US/10293418

Publication No. US20030221996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERBUCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 05/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-25
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Pred. No. 0.22;
2; Mismatches 0; Indels
Score 51; DB 12; Length 247;
Pred. No. 0.22;
                                                                                  2; Mismatches
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GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

LENGTH: 250
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81.8%; Pred. No. 0.22;
iive 2; Mismatches 0; Indels
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Pred. No. 0.22;
2; Mismatches 0; Indels
                           PRIOR FILING DATE: 2001.12-19
PRIOR PILING DATE: 2001.12-19
PRIOR PELING DATE: 2001-06-15
PRIOR PELING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-06-16
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PRIOR PILING DATE: 2000-06-16
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Publication No. US20030059937A1
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
            APPLICATION NUMBER: 60/340,817
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Matches 9; Conservative
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Matches 9; Conservative
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163 QGDSLRTYYAN 173
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ORGANISM: Homo sapiens
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US-09-880-748-1990
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US-09-880-748-1990
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US-10-293-418-1990
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Publication No. US2030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PES23

CURRENT APPLICATION NUMBER: US/09/880,748

FRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

NUMBER OF SEQ ID NOS: 3239
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Sequence 2002, Application US/10293418

Forbitation No. US2003223996A1

FORBERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF5.23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 60/2.11-27

FRIOR PILLING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
PRIOR PRIOR PLING DATE: 2000-10-17
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2088
                                                                                                                                                                                                                                                                                                                                                                 89.5%;
81.8%;
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Best Local Similarity 81.8
Best Local 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 QGDSLRTYYAN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Homo sapiens US-09-880-748-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-880-748-2002
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LENGTH: 249
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2002-12-03
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Pope, Anthony
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                                                                                                                                                                                                                         9; Conservative
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; ORGANISM: Homo sapiens
US-10-803-622-168
CURRENT FILING DATE: ;
NUMBER OF SEQ ID NOS: ;
SOFTWARE: Patentin veries SEQ ID NO 106
LENGTH: 96
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                   TYPE: PRT
ORGANISM: human
                                                                                                                                           US-10-308-817-106
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    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 0.22;
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Sequence 106, Application US/10453698

Publication No. US20040038308A1

GENERAL INFORMATION:

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 82 CTP (1087-37 CTP)

CURRENT PELLORTION NUMBER: US/10/453,698

CURRENT FILING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 196

SOFTWARE: PatentIn version 3.2

SEQ ID NO 106

LENGTH: 96
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          THILE REPERRICE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-61-15
PRIOR PLING DATE: 2001-66-15
PRIOR PLING DATE: 2001-66-15
PRIOR PLING DATE: 2001-66-15
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-017
PRIOR PLING DATE: 2001-017
PRIOR PLING DATE: 2001-017
PRIOR PLING DATE: 2001-06-16
NUMBER OF SEQ ID NOS: 3247
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Pred. No. 0
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Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REPERBERCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%;
81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: human
US-10-453-698-106
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APPLICANT: Marks James
APPLICANT: Marks James
APPLICANT: Clackson, Timothy
APPLICANT: Clackson, Timothy
APPLICANT: Clackson, Timothy
APPLICANT: Clackson, Timothy
APPLICANT: Winter, Gregory
APPLICANT: Winter, Gregory
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
ITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
ITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REPERBENCE: 13835-0013
CURRENT APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-10-19
PRIOR FILING DATE: 1990-10-19
PRIOR PILING DATE: 1991-03-06
PRIOR FILING DATE: 1991-03-06
PRIOR PRILING DATE: 1991-03-06
PRIOR PRILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR PRILING DATE: 1991-03-06
PRIOR FILING DATE: 1991-03-06
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DB 15; Length 96;
                                                                                        0; Indels
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Pred. No. 0.13;
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                                                                                   2; Mismatches
Score 50;
Pred. No. (
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Sequence 168, Application US/10803622
Publication No. US20040157214A1
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Griffiths, Andrew
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Sequence 7, Application US/10029926B
Sequence 7, Application US/10029926B
Publication No. US20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY, et al.
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029, 926B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258, 948
PRIOR APPLICATION NUMBER: 60/258, 948
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7.
  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: BARLIER APPLICATION NUMBER: 60/028,550
PRIOR PILING DATE: EARLIER PILING DATE: 1996-10-11
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
SOFTWARE: PATENTING DATE: 224
SOFTWARE: PATENTING DATE: 1996-10-11
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 10; Length 104;
Pred. No. 0.14;
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Sequence 8, Application US/10300675

Sequence 8, Application US/10300675

Publication No. US20030198638A1

GENERAL INFORMATION: Tumor Specific Monoclonal Antibodies

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies

FILE REFERENCE: P-IX 5519

CURRENT FILING DATE: 2002-11-19

PRIOR PILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 111
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Pred. No. 0.15;
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US-09-848-798-49
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81.8%;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-029-926B-7
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
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Publication No. US20030040665A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SOFTING METHOD FOR PRODUCTION THEREOF
FILE REPERBNCE: 09596-4122
CURRENT APPLICATION NUMBER: US/09/848,798
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APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: MCCafferty, John
APPLICANT: Pope, Anthony
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PRIOR PELING DATE: 1990-07-10

PRIOR APPLICATION NUMBER: GB 9015198.6

PRIOR PILING DATE: 1990-10-19

PRIOR PILING DATE: 1990-10-19

PRIOR PILING DATE: 1990-10-19

PRIOR PPLICATION NUMBER: GB 902450.3

PRIOR PPLICATION NUMBER: GB 910474.9

PRIOR PPLICATION NUMBER: GB 910474.9

PRIOR PLING DATE: 1990-11-12

PRIOR PLING DATE: 1990-11-12

PRIOR PLING DATE: 1991-03-06

PRIOR PLING DATE: 1991-03-06

PRIOR APPLICATION NUMBER: GB 9110549.4

PRIOR APPLICATION NUMBER: GB 9110549.4

PRIOR APPLICATION NUMBER: US 07/971,857

PRIOR PLING DATE: 1991-07-10

PRIOR PLING DATE: 1993-01-08

PRIOR PLING DATE: 1993-01-08

PRIOR PLING DATE: 1993-01-08

PRIOR PLING DATE: 1993-01-08

PRIOR PLING DATE: 1993-01-08
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Pred. No. 0
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                                                                                                                                      Sequence 168, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Hoogenboom, Hendricus
Griffiths, Andrew
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81.8%;
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Chiswell, David
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23 QGDSLRSYYAS 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-09-848-798-49
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Score 50; DB 14; Length 111;
Pred. No. 0.15;
2; Mismatches 0; Indels
Sequence 20, Application US/10300675
Publication No. US20030198638A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 24, 2004, 02:25:07 Job time : 64.717 secs
                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 111
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; CTHER INFORMATION: Recombinant variant US-10-300-675-22
                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Recombinant variant US-10-300-675-20
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81.8%;
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ORGANISM: Artificial Sequence
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Local 9; Conservative
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Matches 9; Conservative
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US-10-300-675-22
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Score 50; DB 14; Length 111; Pred. No. 0.15; 2; Mismatches 0; Indels
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Pred. No. 0.15;
2; Mismatches 0; Indels
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Pred. No. 0.15;
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-1X 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR PILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 111
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-1X 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR PELLING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 111
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, OTHER INFORMATION: Recombinant variant US-10-300-675-18
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                                                                                                                                                                                                       Sequence 16, Application US/10300675
Publication No. US20030198638A1
GENERAL INFORMATION:
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Publication No. US20030198638A1
GENERAL INFORMATION:
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81.8%;
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ORGANISM: Artificial Sequence
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US-10-300-675-18
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Score 50; DB 14; Length 111;
Pred. No. 0.15;
2; Mismatches 0; Indels
Sequence 22, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
    APPLICANT:
    APPLICANT:
    TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
    TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
    TURENT APPLICATION NUMBER: US/10/300,675
    CURRENT APPLICATION NUMBER: US/10/300,675
    CURRENT FILING DATE: 2002-11-19
    PRIOR APPLICATION NUMBER: US 09/989,901
    PRIOR PILING DATE: 2001-11-19
    NUMBER OF SEQ ID NOS: 59
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 22
    LENGTH: 111
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RESULT 24 US-10-300-675-20

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C;Accession: S38495
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S. submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pł A;Reference number: S38488
A;Reference number: S38495
                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36060
R;Williams, S.C.
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Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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                                             Indels
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Pred. No. 0.0039;
                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1993
A;Reference number: $36046
A;Accession: $36060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <WIL>
                                                                                                                                                                                                                                                                    Ig lambda chain - human (fragment)
                    90.98;
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81.8%;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
                                             10; Conservative
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A;Molecule type: DNA
A;Residues: 1-106 <MAR>
                                             Matches
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R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38488
A;Accession: S38496
                                                                                                                  gene 2 protein - p
gene 2 protein - p
hypothetical prote
hypothetical prote
glutamate-tRNA lig
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homeotic protein L
probable methylcro
hypothetical prote
ATP-dependent RNA
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scol protein homol
hypothetical prote
Ul snRNP 70K prote
probable shikimate
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hypothetical prote
probable outer-mem
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Dwarfl protein - A
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C;Species: Homo sapiens (man)
C;Date: 06-Jan_1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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A57072
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T14913
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B71612
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A60089
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629
635
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766
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1445
3871
3973
367
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Gaps

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C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S. submitted to the RMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pł A;Reference number: S38488

Ig lambda chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

**S38498** 

A.Molecule type: DNA A.Residues: 1-109 <MAR> A.Crose-references: EMBL: 223031; NID:g414039; PIDN:CAA80566.1; PID:g414040 C.Superfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin F;15-89/Domain: immunoglobulin homology <IMM>

A;Status: preliminary

Length 109;

DB 2;

Score 53;

93.08;

Match

Query

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Gaps

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C;Accession: S36272
R;Griffiths, A.D.; Malmgvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J., EM5 J. S., Malmgvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J., EMBO, J. 12, 734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Tetle: Human anti-self antibodies with high specificity from phage display libraries.
A;Tetle: Human anti-self antibodies and sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-110 cGRI>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacese: 24-Jul-1998 #sequence revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70444; S70426
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fet A;Reference number: S70442; MUID:93024508; PMID:1383695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Homo sapiens (man)
CiDate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
CiDate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
CiAccession: S13726
RiFrippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
RiFrippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
A;Frippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
A;Fries: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A;Reference number: S13726; MUID:91088295; PMID:2124677
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                                                        Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
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A;Residues: 1-115 <FRI>
A;Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405
C;Genetics:
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81.8%; Pred. No. 0.016;
ive 2; Mismatches C
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Pred. No. 0.015;
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C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>
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Similarity 81.8%;
9; Conservative
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Matches 9; Conserv
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Best Local Similarity
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A;Status: preliminary
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession. 847184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: 847181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V region (clone alpha-BSA3) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Joun-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19663
B;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-89/Domain: immunoglobulin homology <IMM>
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A;Cross-references: BMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin W region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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81.8%; Pred. No. 0.015;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Length 108;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                Score 50; DB 2;
Pred. No. 0.015;
2; Mismatches
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                                                                                                                                                                                                                                                                      87.7%;
81.8%;
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Best Local Similarity 81.8.
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                                                                                                                                                                                                                                                                                                                                                                                                                            22 QGDSLRSYYAS 32
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23 QGDSLRSYYAS 33
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847184
Ig lambda chain - human
C;Species: Homo sapiens (
                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA; Residues: 1-108 <MCI>
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A; Accession: S38498
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1.4654.746

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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18396 R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.I Cell 82, 77-87, 1995 A;Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and a A;Reference number: Z18925; MUID:95330812; PMID:7541722 A;Accession: T18396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A.F.Title: By-Dessing immunization. Human antibodies from V-gene libraries displayed on pht A.F.Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fragme
                                                                                                                                                                                                                                                                                                                           R;Voss, T.S.; Felger, I.; Weiss, N.; Beck, H.P.
submitted to the EMBL Data Library, February 1998
A;Description: Identification of a conserved 5' flanking region of Plasmodium falciparum
                                                                                                                                                                                                                 variant-specific surface protein - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
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A;Cross-references: EMBL:AF050740; NID:g2944094; PID:g2944095; PIDN:AAC05220.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Species: Homo sapiens (man)
.Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
.Accession: S19672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA.
A;Residues: 1-110 <MAR>
A;Cross-references: EMBL:X61644, NID:g37856, PIDN:CAA43825.1; PID:g1335384
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 5.4;
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Pred. No. 0.95;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig lambda chain V region (clone alpha-TEL14) - human
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A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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Similarity 72.7%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8 Matches 7; Conservative
                                 7
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42 OGDTIRSYYAS 52
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QGDSLRSSYAS 33
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160 EGDSIKTYY 168
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                        Accession: T14602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) - C(lambda) gene segments of the human immunoglobulin lam A;Reference number: Si6439; MUID:91257162; PMID:1904362
A;Accession: S25748
A;Status: preliminary; translation not shown
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R;Combriato, G.; Klobeck, H.G.
R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25741
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                                                                                                                                                                                                                                                                      F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F:34-108/Domain: immunoglobulin homology <IMM>
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Bate: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin; 148-216/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 63.6%; Pred. No. 0.33;
Matches 7; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 2;
Pred. No. 0.018;
2; Mismatches
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Pred. No. 0.054;
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R;Tonnelle, C. submitted to the EMBL Data Library, May 1990 A;Reference number: S70426 A;Accession: S70426 A;Molecule type: mRNA A;Residues: 1-90 <TON> A;Cross-references: EMBL:X53070
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81.8%;
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Best Local Similarity 81.8*;
Matches 9; Conservative
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Best Local Similarity
84...
9; Conservative
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825748
Ig lambda chain - human
C;Species: Homo sapiens ((
C;Date: 22-Nov-1993 #sequ
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C;Species: Homo ganion
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hypothetical protein jhp0718 - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A;Variety: strain J99
C.Species: 12-Reb-1999 #sequence_revision 12-Reb-1999 #text_change 08-Oct-1999
C.Sacession: F71896
C.Accession: F71896
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A.Description: The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and lambda clone JA.Reference number: S50434
A.Reference number: S50434
A.Reference number: S50434
A.Reference number: S50434
A.Residues: L-624 <DIS-A.Residues: RMBL:U18795; NID:g603241; PID:g603256; MIPS:YEL062w
R.Rousselet, G.; Simon, M.; Ripoche, P.; Buhler, J.M.
R.Reference number: S69008; MUID:95172238; PMID:7867803
                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE001439; NID:g4155275; PIDN:AAD06301.1; PID:g415528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitrogen permease regulator NPR2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YEL062*
N;Alternate names: protein YEL062*
C;Speciaes: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 23-Mar-2001
C;Accession: S44938; S50527; $69008
R;Rousselet, G.; Simon, M.; Ripoche, P.; Buhler, J.M.
Submitted to the EMBL Data Library, May 1994
A;Pescription: A second nitrogen permease regulator in Saccharomyces cerevisiae.
A;Reference number: S44938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X79105; NID:g485969; PIDN:CAA55721.1; PID:g485970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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23;
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;Molecule type: DNA
;Residues: 1-624 «ROU»
;Cross-references: EMBL:X79105; NID:g485969; PID:g485970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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Pred. No. 23;
2; Mismatches
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Pred. No. 15;
1; Mismatches
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C,Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: GB:AE001503; (A, Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
77.88;
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ilarity 63.6%;
Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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74 ODESLKTYY 82
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-429 <ARN>
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Date: 15-Oct-1999 #text_change 09-Jun-2000
C.Accesion: T18378
C.Accesion: T18378
A.Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Reference number: 218925; MUID:95330812; PMID:7541722
A.Reference number: 218925; MUID:95330812; PMID:7541722
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A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
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A;Residues: 1-429 <TOM>
A;Cross-references: GB:AE000590; GB:AE000511; NID:g2313907; PIDN:AAD07834.1; PID:g231391
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B64617
Cybcheltcal protein HP0781 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: E64617
R;Tomb, J.F; White, O; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleis
A;Residues: 1-1729 <BAR>
A;Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1 C;Genetics: EMP1
A;Gene: EMP1
A;Note: var-2
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Pred. No. 15;
1; Mismatches 1; Indels
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Pred. No. 42;
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                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                    68.48;
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Best Local Similarity 77.8-
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Best Local Similarity 66.7
Matches 6; Conservative
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151 EGDSIKTHY 159
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74 QDESLKTYY 82
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Best Local Similarity
Matches 6; Conserv
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A;Gene: EMP1
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456 QGQTLKTWYES 466

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RESULT 17

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A;Residues: 1-452 (**M**)
A;Cross-treferences: GB:K03020; NID:g189936; PIDN:AAA60082.1; PID:g189937
B;Cotton, R.G.H.; McAdam, W.; Jennings, I.; Morgan, F.J.
Biochem, J. 255, 193-196, 1988
A;Title: A monoclonal antibody to aromatic amino acid hydroxylases. Identification of the A;Reference number: S02687; MUID:89061656; PMID:2461704
                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 131.144 <COT>
R; Konecki, D.S.; Wang, Y.; Trefz, F.K.; Lichter-Konecki, U.; Woo, S.L.
Biochemistry 31, 8363-8368, 1992
A; Title: Structural characterization of the 5' regions of the human phenylalanine hydrox,
A; Reference number: 152416; MUID: 92399453; PMID: 1326329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 381-389, 'G', 391-405 <ABA>
A; Cross-references: GB:S61296; NID:9300410; PIDN:AAD13926.1; PID:g4261626
A; Experimental source: lymphocytes, mutant form
R; Kowlessur, D.; Citron, B.A.; Kaufman, S.
Arch. Biochem. Biophys. 333, 85-95, 1996
A; Title: Recombinant human phenylalanine hydroxylase: novel regulatory and structural pro
A; Reference number: S74142; MUID:96400381; PMID:8806757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-20 < KON>
A; Cross-references GB: S44225; NID: 9255493
R; Abadie, V; Jaruzelska, J; Lyonnet, S.; Millasseau, P.; Berthelon, M.; Rey, F.; Munnic
Hum. Mol. Genet. 2, 31-34, 1993
A; Title: Illegitimate transcription of the phenylalanine hydroxylase gene in lymphocytes
A; Reference number: IS4346; MUID: 93258345; PMID: 8098245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 2-21 <KOW>
R,Eigel, A.; Dworniczak, B.; Kalaydjieva, L.; Horst, J.
Hum. Genet. 87, 739-741, 1991
A,Title: A frameshift mutation in exon 2 of the phenylalanine hydroxylase gene linked to
A,Reference number: I54257; MUID:92039642; PMID:1682235
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Cross-references: GB:862592; NID:9238240; PIDN:AAB20205.1; PID:9238241;
Note: mutant sequence found in patients with phenylketonuria
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Note: a defect in this gene can cause phenylketonuria
Complex: homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
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Cross-references: GDB:119470; OMIM:261600
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Best Local Similarity 70.0
Local 7, Conservative
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                                                                                                                                                Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N;Alternate names: amyloid-fibril protein GIL
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: 802083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
A;Title: The primary structure of the variable region of an immunoglobulin IV light-chain A;Reference number: 802083; MUID:89134210; PMID:3146881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenylalanine 4-monooxygenase (EC 1.14.16.1) - human
NyAlternate names: phenylalanine 4-hydroxylase
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text_change 21-Jul-2000
C;Accession: A00508; S02687; Ī52416; I54346; S74142; I54257
C;Accession: A00508; S02687; Dibella, A.G.; Robson, K.J.H.; Woo, S.L.C.
Biochemistry 24, 556-561, 1985
A;Title: Nucleotide sequence of a full-length complementary DNA clone and amino acid sequence number: A00508; MUID:85199778; PMID:2986678
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A,Residues: 1-70;71-72;73-75;76-131;132-146 <FYK>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
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63.6%; Pred. No. 7.9;
iive 2; Mismatches
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Matches 7; Conservative
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22 QGDSLRNFVAS 32
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A;Molecule type: DNA
A;Residues: 1-270 <PAR>
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61.4%;
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60.0%;
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                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
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les 6; Conserv
     A, Molecule type: DNA
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Best Local S:
Matches 6
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CiSpecies: Pseudomonas aeruginosa
CiDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: B83497
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Ristover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Adman, S.; Yuan, W.V.
Nature 406, 959-964, 2000
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83497
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C,Keywords: core protein; glycoprotein
F;310,343,356,443,694,914/Binding site: carbohydrate (Asn) (covalent) #status predicted
                       C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-Feb-2003
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-Feb-2003
R;Shqcession: D84942
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
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/Jacession: A4280
/Bate: J.J.; Hirshon, C
irology 192, 154-160, 1993
/Title: Sequence analysis of group B rotavirus gene 1 and definition of a 1
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N;Alternate names: core protein VP1
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Pred. No. 50;
1; Mismatches
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A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
Alternate names: methionyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                       A;Gene: metG; BU109
C;Superfamily: methionyl-tRNA synthetase
C;Keywords: ligase
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 7; Conservative
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1039 GNTLKTYLAS 1048
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A, Residues: 1-1159 <EID>
A, Cross-references: GB:M97203
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DSLRYYYAS 361
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A, iccosa-references GB:AED04449; GB:AED04091; NID:g9947110; PIDN:AAG04580.1; GSPDB:GN001.
A) iccosa-references GB:AED04449; GB:AED04091; NID:g9947110; PIDN:AAG04580.1; GSPDB:GN001.
A) iccosa-references GB:AED04449; GB:AED04091; NID:g9947110; PIDN:AAG04580.1; GSPDB:GN001.
A) iccosa-references GB:AED04449; GB:AED04091; NID:g9947110; PIDN:AAG04580.1; GSPDB:GN001.
A) iccosa-references GB:AED04449; Bred. No. 27; BB 2; Length 197; Best Local Binilarity GB:AED0449; Bred. No. 27; Best Local Binilarity GB:AED0449; Bred. No. 27; Bred. No. 27; Best Local Binilarity GB:AED0449; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Bred. No. 27; Br
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(otqsu) Anala egaq sidT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 28, 2005, 17:57:45 ; Search time 82.8438 Seconds (without alignments) 51.354 Million cell updates/sec Run on:

US-10-088-639A-2_COPY_23_33 57 1 QGDSLKTYYAS 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2003s:*

6: geneseqp2003s:*

7: geneseqp2030s:* geneseqp2004s:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		do			SUMMAKIES	
Result No.	Score	Query Match	Length DB	DB	ID.	Description
	57	100.0	249	4	AAB68087	Aab68087 An anti-a
7	54	94.7	11	8	ADS82613	Ads82613 Anti-IL-2
ю	54	94.7	11	æ	ADS82595	Ads82595 Anti-IL-2
4	54	94.7	104	7	AAR93164	Aar93164 Anti-rhes
'n	54	94.7	109	œ	ADS82590	Ads82590 Anti-IL-2
9	54	94.7	110	ω	ADS82608	Ads82608 Anti-IL-2
7	54	94.7	238	~1	AAR93165	Aar93165 Anti-rhes
æ	54	94.7	242	ω	ADI58098	Adi58098 Reg IV-sp
6	54	94.7	242	ω	ADS82591	
0	. 54	94.7	245	ω	ADS82609	Ads82609 Anti-IL-2
٦.	53	93.0	110	7	AAW15538	
7	23	93.0	253	ß	ABP45519	Abp45519 Human BLy
w.	53	93.0	253	7	ADG96346	
4	51	89.5	242	ഗ	ABP46073	
'n	51	89.5	242	7	ADG96900	
9	51	89.5	243	Ŋ	ABP46091	
7	51	89.5	243	7	ADG96918	Adg96918 Single ch
89	51	89.5	247	'n	ABP46092	
6	51	89.5	247	7	ADG96919	Adg96919 Single ch
ö	51	89.5	248	S	ABP46077	
<b>ದ</b>	51	89.5		7	ADG96904	4
2	51	89.5	249	Ŋ	ABP45991	
Ü	51	89.5	249	7	ADG96818	Adg96818 Single ch
4.	51	89.5	250	ß	ABP45979	Abp45979 Human BLy
Š	51	89.5	250	7	ADG96806	Adg96806 Single ch

Aay95195 Anti-plat Aay96195 Anti-plat Aay96192 Human gp9 Ado68078 Sy cell d Adj80346 Vlambda g Aar2021 Light cha Aar2021 Human der Aaw95489 Human der Aaw95489 Fibronect Abb05054 Fibronect Abc27413 Anti-Rh(D Aav95215 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat Aay95194 Anti-plat	Aay95179 Anti-plat Aay44616 Human ant Aag62937 Amino aci
AAY95195 AAY95216 AAG80192 ADG80192 ADG80146 AAR22572 AAR22572 AAR22572 AAR23606 AAG93606 AAG93606 AAG9313 AAY95313 AAY95313 AAY953194 AAG62969 ADG62969 ADG62969 AAG62969 AAY95185	AAY95179 AAY44616 AAG62937
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000000000000000000000000000000000000000	50 50
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 6 4 8

## ALIGNMENTS

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    .33
    /note= "Complementarity determining region (CDR) 1 of the
light chain"

                                                                                                                                                                                                                                                                                           177. 193
/note= "Complementarity determining region (CDR) 1 of heavy chain"
226. 238
/note= "Complementarity determining region (CDR) 1 of heavy chain"
                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                         note= "Complementarity determining region (CDR) 1 of
                                                                                                                                                                                                  N
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                                                                                      Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                                                                  /note= "Complementarity determining region (CDR)
light chain"
188. 98
1917 chain"
1918 chain"
                                                                       An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                      Location/Qualifiers
                 AAB68087 standard; protein; 249 AA
                                                                                                                                                                                                                                                      /note= "linker"
158. .162
                                                                                                                                                                                                                                                                                heavy chain"
                                                     (first entry)
                                                                                                                                     Macaca fascicularis.
                                                     09-JUL-2001
                                                                                                                            Synthetic
                                   AAB68087;
                                                                                                                                                                                                                                               Peptide
                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                           Region
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RESULT 1
         AAB68087
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the

26-OCT-2000; 2000WO-SE002082.

WO200130854-A2

03-MAY-2001.

99SE-00003895

28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB.

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N-PSDB; ADS82622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004083249-A2
                                                                                                                                                                                                                                                       Sequence 11 AA;
                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS82595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Witek
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                   ADS82595
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                   The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on a subpopulation of horman gastrointestinal epithelial tumour cells and in target structure especially comprises alpha6beta4 integrin. The target structure especially comprises alpha6beta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, for comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis as carried out by determining the localization of antibody to
                                                                                Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic; Antiinflammatory; Gastrointestinal; Antibooriatic; Gene therapy; antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21; IL-21; autoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection; psoriasis; hyperproliferative disorder; 18A5; complementarity determining region; CDR; light chain; L1 CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams AJ;
          Tordsson MJ, Kearney PP;
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 57; DB 4; Length 249; 100.0%; Pred. No. 0.034; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-IL-21R antibody 18A5 L1 CDR, SEQ ID 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valge-Archer V,
          Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                Claim 1; Page 55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS82613 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2003; 2003US-0454336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                       tumour deposits in humans
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitters MJ,
                                                                                                                                                                                                                                                                                                                                                                                                    1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                           23 ÓGDSLKTYYAS 33
                                             WPI; 2001-308619/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-691025/67
                                                                                                                                                                                                                                                                                                                            Sequence 249 AA;
                                                          N-PSDB; AAF84797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004083249-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-2004,
          Brodin TN,
Nilson BHK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young DA,
Witek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS82613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
ADS82613
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The present invention relates to human antibodies, or their antigen-binding fragments, that selectively bind to a human interleukin-21 receptor (IL-21R). The antibodies of the invention are referred to as WUF, WUF-germline, WUI, 1864, 1885, 1985, CP5G2 and R18. The antibodies selectively bind the extracellular domain of human IL-21R, or inhibit the binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an antibody or fragment of the invention are useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, transplant rejection or psorianis) or hyperproliferative disorders. The present sequence is an anti-IL-21R antibody light chain complementarity determining region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunosuppressive, Cytostatic, Antirheumatic, Antiarthritic, Antiinflammatory, Gastrointestinal; Antipsoriatic, Gene therapy; antibody, interleukin-21 receptor; interleukin-21; receptor; IL-21; interleukin-21; autoimmune disorder; rheumatoid archritis; inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young DA, Whitters MJ, Valge-Archer V, Collins M, Williams AJ; Witek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 8; Length 11;
Pred. No. 0.0043;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis, hyperproliferative disorder, 18G4, complementarity determining region, CDR, light chain, L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-IL-21R antibody 18G4 L1 CDR, SEQ ID 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMHP ) WYETH. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                 Claim 5; SEO ID NO 71; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS82595 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2004; 2004WO-US007444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2003; 2003US-0454336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-691025/67.
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Example 1; Page 30; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMHP ) WYETH
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                                                                                                                                                                                                                                                                                                                                                                              16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οA,
                                                                                                                                                                                                                                                                                                                                                    ADS82590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young
Witek
                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                             ADS82590
     8X555555555X8
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                      The present invention relates to human antibodies, or their antigen-
binding fragments, that selectively bind to a human interleukin-21
receptor (IL-2IR). The antibodies of the invention are referred to as
WUF, MUF-germline, MU1, 1864, 1875, 1975, CP5G2 and R18. The antibodies
selectively bind the extracellular domain of human IL-2IR, or inhibit the
binding of IL-2I to an IL-2IR. Pharmaceutical compositions comprising an
antibody or fragment of the invention are useful for diagnoshing,
preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
inflammatory bowel disease, Crohn's disease, transplant rejection or
psoriasis) or hyperproliferative disorders. The present sequence is an
anti-IL-2IR antibody light chain complementarity determining region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-rhesus D monoclonal antibody D7C2 light chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region'
                                                                                                                                                                                                                         Score 54; DB 8; Length 11;
Pred. No. 0.0043;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaabihi H;
                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaczorek M,
Claim 5; SEQ ID NO 53; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          AAR93164 standard; protein; 104 AA.
                                                                                                                                                                                                                           94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49. .55
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94FR-00010566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94FR-00010566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINE PERFORMANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edelman L, Margaritte C,
                                                                                                                                                                                                                                        Best Local Similarity 90.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .93
                                                                                                                                                                                                                                                                                1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                QGDSLRTYYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-162018/17.
N-PSDB; AAT26869.
                                                                                                                                                                                                   Sequence 11 AA;
                                                                                                                                                                         the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSP ) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1996
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The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by born rissect cells which have been transformed by a baculovizal vector comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding fragments, that selectively bind to a human interleukin-21 receptor (IL-21R). The antibodies of the invention are referred to as MUF, MUF-germline, MUI1, 18G4, 18A5, 19F5, CPSG2 and R18. The antibodies selectively bind the extracellular domain of human IL-21R, or inhibit the binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an antibody or fragment of the invention are useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive, Cytostatic, Antirheumatic; Antiarthritic; Antiinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy; antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21; altoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to human antibodies, or their antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             psoriasis; hyperproliferative disorder; 18G4; variable region;
                                                                                                                                                                                                                                               Score 54; DB 2; Length 104; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-IL-21R antibody 18G4 VL domain, SEQ ID 48.
                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 48; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS82590 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2004; 2004WO-US007444.
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                                                                                                                                                                                                                                               94.7%;
90.9%;
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                  1 QGDSLKTYYAS
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N-PSDB; ADS82599.
                                                                                                                                                                                                      Sequence 104 AA;
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Gaps

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Indels

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Pred. No. 0.051; L; Mismatches

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10; Conservative

Best Local Similarity Matches 10; Conserv

11

1 QGDSLKTYYAS

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inflammatory bowel disease, Crohn's disease, transplant rejection or psoriasis) or hyperproliferative disorders. The present sequence is an anti-IL-21R antibody light chain variable domain (VL) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy; antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21; autoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA, Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis; hyperproliferative disorder; 18A5; variable region; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
                                                                                                         Length 109;
                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Anti-IL-21R antibody 18A5 VL domain, SEQ ID 66.
                                                                                                         Score 54; DB 8;
Pred. No. 0.05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 66; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMHP ) WYETH.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                       ADS82608 standard; protein; 110 AA
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90.9%;
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Best Local Similarity 90.9
Marches 10; Conservative
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                                                                         Sequence 109 AA;
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Witek J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies.
                                                                                                                                                                                                                                                                                                                                        20. .238
/label= light_chain
/note= "human lambda light chain constant region and the
variable region from anti-rhesus D antibody D7C2"
                                                                                                                                                                                     Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/label= signal_peptide
/note= "encoded by synthetic linker"
                                                                                                                                                           Anti-rhesus D recombinant antibody D7C2 light chain.
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Pred. No. 0.12;
1; Mismatches
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                              AAR93165 standard; protein; 238 AA
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90.9%;
                                                                                                                                   (first entry)
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QGDSLRTYYAS
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N-PSDB; AAT26888.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-SEP-1994;
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                                                                                                                                                                                                                                                            Synthetic.
                                                                                                         AAR93165;
            23
                                                                                                                                                                                                                                                                                                  Peptide
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Sequence 110 AA;

Query Match

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QGDSLRTYYAS 52

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regeneration IV (Reg IV) protein. The invention specifically comprises the amino acid and coding sequences of single chain antibody fragments (scFv's) that bind Reg IV protein. The antibody of the invention is useful for treating, preventing and ameliorating: inflammatory bowel disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g. non-insulin dependent diabetes or insulin dependent diabetes), and cancer of the gastrointestinal tract. The antibody of the invention is also useful for detecting the expression of a Reg IV protein. The present amino acid sequence represents an scFv of the invention.
                                                                                                                                                                                                                                                                                                                             antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv; inflammatory bowel disorder; ulcerative colitis; Crohn's disease; diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody, useful for treating, preventing or ameliorating inflammatory bowel disorder, cancer of the gastrointestinal tract or diabetes (non-insulin dependent diabetes).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises an antibody that specifically binds a
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                                                                                                                                                                                                                                                                     Reg IV-specific single chain antibody fragment (scFv) #57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Pred. No. 0.12;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 58; 324pp; English.
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                                                              ADI58098 standard; protein; 242 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2002; 2002US-0392382P
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                                                                                                                                                                                                      22-APR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                    ADI58098;
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Gaps

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The present invention relates to human antibodies, or their antigen-binding fragments, that selectively bind to a human interleukin-21 receptor (IL-21R). The antibodies of the invention are referred to as WUF, WUF-germline, MUI, 1864, 1875, 1975, CP5G2 and R18. The antibodies selectively bind the extracellular domain of human IL-21R, or inhibit the binding of IL-21R on IL-21R. Pharmaceutical compositions comprising an antibody or fragment of the invention are useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis, infammatory bowel disease, Crohn's disease, transplant rejection or psoriasis) or hyperproliferative disorders. The present sequence is an anti-IL-21R antibody scrv domain of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
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           Immunosuppressive, Cytostatic, Antirheumatic; Antiarthritic; Antiinflammatory; Gastrointestinal; Antiposriatic; Gene therapy; antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21; IL-21; autoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohu's disease; transplant rejection; psoriasis; hyperproliferative disorder; 1864; scFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 49; 143pp; English.
                                                                                                                                                 Location/Qualifiers
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/label=_H2_CDR
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/label= H1_CDR
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/label= L1
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/label= H:
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les 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                               WO2004083249-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 242 AA;
                                                                                                                      Homo sapiens
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158 QGDSLRTYYAS 168

antibody 18A5 scFv, SEQ ID 67.

(first entry)

Location/Qualifiers

label= H1_CDR label H2_CDR 223. .234 /label= L3_CDR

H3_CDR

99. .107 /label= H

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The present invention relates to human antibodies, or their antigen-
binding fragments, that selectively bind to a human interleukin-21
receptor (IL-21R). The antibodies of the invention are referred to as
MUF, MUF-germline, MUI1, 1864, 1845, 19F5, CP562 and R18. The antibodies
selectively bind the extracellular domain of human IL-21R, or inhibit the
binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
antibody or fragment of the invention are useful for diagnosing,
preventing or treating autoimmune disorders (e.g. rheumacoid arthritis,
inflammatory bowel disease, Crohn's disease, transplant rejection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                          Immunosuppressive, Cytostatic, Antirheumatic; Antiarthritic;
Antiinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy;
antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21;
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                                                                                                                                                             IL-21R; autoimmune disorder; rheumatoid arthritis;
inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                               psoriasis; hyperproliferative disorder; 18A5; scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis) or hyperproliferative disorders. The parti-IL-21R antibody scFv domain of the invention
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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N-PSDB; ADS82618.
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                                                                                                                                                                                                                                Homo sapiens
                                             16-DEC-2004
                                                                               Anti-IL-21R
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Witek J;
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Collins M, Williams AJ;

Valge-Archer V,

Whitters MJ,

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This polypeptide sequence comprises the VL domain of human scFv antibody 1046, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see AAM15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty cestenosis, acleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), continue and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VW and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low diseasch in the constants (pref. less than 5 mM) and low IC50s for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
                                                                                                                                                                                                                        antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; catrard; glaucoma; scarring; glomerulonephritis; osseoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jackson RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaughan TJ, Williams AJ, Green JA, Jack.
18on KS, Wilton AJ, Tempest PR, Pope AR;
                                                                                                                                                                                                       Transforming growth factor beta-1; TGF-beta-1; human;
                                                                                                                                                              Anti-TGF beta-1 scFv antibody 10A6 VL domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 1b(ii); 184pp; English.
                                      AAW15538 standard; protein; 110 AA.
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                                                                                                                     (first entry)
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                                                                                                                     27-NOV-1997
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19-JAN-1996;
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                                                                               AAW15538;
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RESULT 11
                     AAW15538
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Gaps

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93.0%; Score 53; DB 2; Length 110; 90.9%; Pred. No. 0.078; ive 1; Mismatches 0; Indels

Conservative

Local Similarity les 10; Conserv

Query Match Matches

Sequence 110 AA;

1 QGDSLKTYYAS 11

Query Match

Best Loca Matches

23

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RESULT 12

ABP45519 standard; protein; 253 AA.

ABP45519;

(first entry) 19-AUG-2002 Human BLyS binding scFv SEQ ID 1530.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunedisorsessystemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrôme.

Homo sapiens

WO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US019110

16-JUN-2000; 2000US-0212210P.

17-OCT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0273739P. 25-MAY-2001; 2001US-0293499P.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY SCI INC (HUMA-) HUMAN GENOME

Choi GH, Vaughan T, Hilbert Barash SC, Ruben SM,

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WPI; 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2228-2229; 3148pp; English

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and the invention ABP45519
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Sequence 253 AA;

Gaps ö Score 53; DB 5; Length 253; Pred. No. 0.19; 0; Indels 1; Mismatches 93.0%; 90.9%; Ouery Match Best Local Similarity 90.9 Marches 10; Conservative

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166 QGDSLKSYYAS 176

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RESULT 13 ADG96346 ID ADG

ADG96346 standard; protein; 253 AA.

ADG96346;

(first entry) 11-MAR-2004 Single chain antibody that immunospecifically binds BLyS SeqID 1530.

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

WO2003055979-A2

10-JUL-2003

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Hilbert D; Vaughan TJ, Choi GH, Barash SC, Ruben SM,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1530; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 19434 and encodes a protein that is a member of the tumour chromosome lagat and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrws) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods correctly and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders only astheria gravis and multiple sclerosis, inflammatory disorders e-g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various continining and antisheumatic, antialrenthritic, neuroprocective, antianthreumatory, antisathmatic, antialrenthritic, neuroprocective, antianthrial and orthory antisathmatic, antialery of the polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTS: The sequence data for this patent did not form part of inventions. in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences the printed specification, but was obtained 

Sequence 253 AA;

Gaps ö 93.0%; Score 53; DB 7; Length 253; 90.9%; Pred. No. 0.19; ive 1; Mismatches 0; Indels 93.0

Query Match

Best Local Similarity 90.9

Matches 10; Conservative

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1 QGDSLKTYYAS 11

OGDSLKTYYAS 11

Single chain antibody that immunospecifically binds BLyS SeqID 2084.

(first entry)

11-MAR-2004

ADG96900;

ADG96900 standard; protein; 242 AA.

RESULT 15 ADG96900

B cell proliferation, differentiation; scFv, myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic. antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;

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BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunomodulatory; antirheumatic; antilDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding scFv SEQ ID 2084.
                                                                                                                                                                          ABP46073 standard; protein; 242 AA.
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17-0CT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027548P.
21-MAR-2001; 2001US-0277379P.
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                                                                                                                                                                                                                                                                                                                  (first entry)
   166 QGDSLKSYYAS 176
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                                                                                                                                                                                                                                           ABP46073;
                                                                                                   RESULT 1

ABP 46073

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ABP 19-

ABP 110-

ABP ADI 110-

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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 2084; 394pp; English.

Vaughan TJ, Hilbert

Choi GH,

Barash SC,

Ruben SM,

WPI; 2003-505530/47.

14-NOV-2002; 2002WO-US036496. 16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P. (HUMA-) HUMAN GENOME SCI INC.

WO2003055979-A2.

.0-JUL-2003.

Unidentified

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1943 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrve) derived, prefersably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The from the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leaving in a sectionma and multiple collections or continued and multiple leaving in the continued and proliferative disorders including leaving in the continued and multiple collections are not continued and multiple collections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiarthritic, neuroprotective, antiarthritic, neuroprotective, antiarthritic, neuroprotective, polypeptide sequence is a single chain antiabody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.5%; Score 51; DB 7; Length 242; 81.8%; Pred. No. 0.43; 0; Indels ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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les 9; Conserv
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Matches
This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell to proliferation and differentiation. The antibodies of the invention have cytostatic, immunospensive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and ciseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ADDS)). ABR43990-ABR4722B represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 0.43;
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Gaps

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156 QCDSLRTYYAN 166

1

1 QGDSLKTYYAS

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89.5%; 81.8%;

Conservative

Local Similarity nes 9; Conserv

Query Match Matches

|||||:||||: 156 QGDSLRTYYAN 166 OGDSLKTYYAS 11

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Search completed: April 28, 2005, 18:17:18 Job time : 89.8438 secs

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643, App 12, Appl 40126, A

Sequence Sequence Sequence Sequence

ALIGNMENTS

4299, Ap 9, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

-252-991A-19243 -513-999C-4175

Appli Appli Appli Appli Appli

Sequence Sequence Sequence

Sequence

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Sequence 2, Application US/08793450

Sequence 2, Application US/08793450

Sequence 2, Application US/08793450

Setent No. 631260

BAPELICANT: EDELMAN, LENA

APPLICANT: MARGARITTE, CHRISTEL

APPLICANT: CHAAPHIH, HASSAN

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

STRESPONDENCE ADDRESS: 25

CORRESPONDENCE ADDRESS: 35

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 3; Length 104;
Pred. No. 0.0065;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR.1997
CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:

NAME: OBLOW, NORMAN F.

REGISTRATION NUMBER: 660-118-0 PCT
TELEPHONE: 703-413-3000
                                      US-08-652-816A-10
US-09-471-276-837
US-09-18-148-79
US-09-328-352-4299
US-07-637-890-6
US-07-637-399-6
US-07-637-399-6
US-08-893-852A-3
US-08-893-852A-3
US-08-821-818-3
US-09-952-7538-3
US-09-922-7538-3
                                                                                                                                                                                                                                                      US-09-270-767-40126
                                                                                                                                                                                                                       US-09-538-092-643
US-09-899-896-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 104 amino acids
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Best Local Similarity 90.9
Matches 10; Conservative
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MOLECULE TYPE: protein
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USA
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Sequence 35, Appl
Sequence 16, Appl
Sequence 71, Appl
Sequence 49, Appl
Sequence 4, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 174, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 174, Appl
Sequence 174, Appl
Sequence 1249, Appl
Sequence 1249, Appl
Sequence 1249, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appl:
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                                                                                                                   (without alignments)
36.750 Million cell updates/sec
                                                                                                  April 28, 2005, 18:06:50 ; Search time 22.3438 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-65-202-35
US-09-726-219A-168
US-09-726-219A-168
US-09-240-74-49
US-09-240-74-49
US-09-203-74-49
US-09-203-74-49
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US-09-200-527-1
US-09-200-527-1
US-09-200-203-10
US-09-200-203-10
US-09-240-274-47
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US-09-471-276-1249
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                                                                                                                                                                                                                                                                  513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
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57

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                Perfect score:
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                                                                         OM protein
                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                               Sequence:
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                                                                                                      Run on:
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Gaps

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E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 amino acids
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 QGDSLRSYYAS 32
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                                     San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                  USA
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-315-574-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
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Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABEIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 3; Length 238;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA: F8 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      Sequence 6, Application US/08793450 Patent No. 6312690 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                 QGDSLKTYYAS 11
                                                      23 OGDSLRTYYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARLINGTON
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                                                                                                                     RESULT 2
US-08-793-450-6
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Sequence 35, Application US/09315574
; Sequence 35, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; CONTRY: USA
; CONTRY: USA
; CONFUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER PROMBINE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER PROMBINE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION UNMER: US/09/315,574
FILING DATE: 20-MAY-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION UNBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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Gaps

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APPLICANT: Chiswell, David
APPLICANT: Pitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                     Score 50; DB 4; Length 101; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.7%; Score 50; DB 2; Length 103;
81.8%; Pred. No. 0.037;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RYAN, JOHN W.
REGISTRATION NUMBER: 33,771
                                                                                                                                                                                                                                                                2; Mismatches
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ 1D NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ 1D NO 168
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: IGEN, Inc.
1530 East Jefferson St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/08273146 Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Rodger
McCafferty, John
Chiswell, David
Daraley, Michael J.
Fitzgerald, Kevin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
                                                                                                                                                                                                                  87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 103 amino acids
amino acid
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                           1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-09-726-219A-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville
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PPLICANT: Bonert, Timothy
:TLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 4;
Pred. No. 0.035;
                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 35:
INFORMATION FOR SEQ ID NO: 35:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PELLON DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR FILING DATE: 1990-11-12
PRIOR PLICATION NUMBER: GB 9024503.6
PRIOR PLILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 910549.4
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR FILING DATE: 1991-07-10
           FILING DATE: 14-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 60/000,250
FILING DATE: 15-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UNN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1991-05-15
APPLICATION NUMBER: PCT/GB91/01134
    US 60/000, 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-726-219A-168
Sequence 168, Application US/09726219A
; Patent No. 6806079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Research Council
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoogenboom, Hendricus
Griffiths, Andrew
Jackson, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marks, James
Clackson, Timothy
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holliger, Kasper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 QGDSLRSYYAS 32
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: RORDING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: U5/09/240,274
CURRENT APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,50
EARLIER APPLICATION NUMBER: 60/081,50
EARLIER PILING DATE: 1996-10-1
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PALENTIN Ver: 2.0
SEQ ID NO 49
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Pred. No. 0.039;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 3; Length 104;
Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-va-/xu-430-4

Sequence 4, Application US/09720493

Patent No. 6827925

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited

APPLICANT: Tempest, Philip R

APPLICANT: Tempest, Philip R

APPLICANT: Holtet, Thor L

APPLICANT: Holtet, Thor L

APPLICANT: Milliams, Andrew J

APPLICANT: Milliams, Andrew J

APPLICANT: Milliams, Andrew J

CURRENT FILING IN Improvements relating to antibodies

FILE REFERENCE: AHB/CP5775333

CURRENT APPLICATION NUMBER: US/09/720,493

CURRENT APPLICATION NUMBER: B9814383.7

PRIOR APPLICATION NUMBER: GB 9814383.7

PRIOR PELING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DAT
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                                                                                                                                                                                              . Sequence 49, Application US/09240274
; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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17 QGDSLRSYYAS 27
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                         US-09-240-274-49
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US-09-720-493-4
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Gaps
                                                                              APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, July
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago States of America
COMPUTER: Illinois
COMPUTER: Illinois
COMPUTER: Illinois
COMPUTER: Proppy disc.
COMPUTER: Proppy disc.
COMPUTER: Applicant PC-Doog/MS-Dos
STATE: 111001
COMPUTER: PROPPY DATA:
COMPUTER: SYSTEM: PC-Doog/MS-Dos
SOFTWARE: 13-MS-1996
COMPUTER: 23-MS-1992
CURRENT APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 24-MR-1992
PRIOR APPLICATION NUMBER: GB 926318.9
FILING DATE: 24-MR-1992
PRIOR APPLICATION NUMBER: GB 926312.6
FILING DATE: 3-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926312.6
FILING DATE: 3-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926312.6
FILING DATE: 3-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926312.6
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926312.6
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 926312.6
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: GB 926304.9
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: GB 926304.9
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: GB 926304.9
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: BAING AND CHOUGH
PRILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: 24.107
RESERRANCE/DOCKET NUMBER: 23.107
RESERRANCE/DOCKET NUMBER: 23.107
RESERRANCE/DOCKET NUMBER: 23.107
RESERRANCE/DOCKET NUMBER: 23.107
RESERRANCE/DOCKET NUMBER: 23.107
REPRESENCE/DOCKET NUMBER: 23.107
REPRESENCE/DOCKET NUMBER: 23.107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 2
Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
Sequence 16, Application US/08652816A Patent No. 5872215 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-665-202-34
; Sequence 34, Application US/08665202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.7%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 OGDSLKTYYAS 11
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1||||::|||| 23 QGDSLRSYYAS 33

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Sequence 8, Application US/09203768A
Sequence 8, Application US/09203768A
Sequence 8, Application US/09203768A
Sequence 8, Application:
APPLICANT: Huse, William D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Thunc Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
FILE REFERENCE: P-IX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50, DB 4; Length 109;
Pred. No. 0.04;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 4; Length 111; Pred. No. 0.04; 0; Indels
                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
                                                                                                                                               PELIGATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UUN-1995
PRIOR APPLICATION NUMBER: US 60/665,202
PRIOR APPLICATION NUMBER: US 08/665,202
APPLICATION NUMBER: US 08/665,202
ATTORNEY/AGENT INFORMATION:
NAME: HUNCAT, TOM
RECISTRAINON NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-260-527-3
; Sequence 3, Application US/09260527A
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.7%;
81.8%;
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81.8%;
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Best Local Similarity 81.0
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Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .... 1 QGDSLKTYYAS 11
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                           FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-203-768A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-315-574-34
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SEQ ID NO 8
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-203-768A-8
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US-09-315-574-34

US-09-315-574-34

Sequence 34, Application US/09315574

Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: MARKS, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
         GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FLING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FLING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FLING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNGE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFISENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 38,498
REFERENCE/OCKET NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 02307E-061410
TELECOMMUNICATION NUMBER: 02307E-061410
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STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                         SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
Salifornia
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
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ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 109 amino acids
amino acid
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Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-08-665-202-34
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
OTHER INFORMATION: from a naive phage display library known as the
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a OTHER INFORMATION: phage display library known as the Synthetic scPv OTHER INFORMATION: Library (#1) from the Centre for Protein OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
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81.8%; Pred. No. 0.11;
tive 2; Mismatches 0; Indels
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Patent No. 6228599
GENERAL INFORMATION:
APPLICANT: Knox, J.P.
APPLICANT: Minkelsen, J.D.
TITLE OF INVENTION: NATIBODY
TITLE REFERENCE: DYOULS. 001AUS
CURRENT FILIOR DATE: 1999-02-26
NUMBER OF EQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 278
TYPE: PRI
ORGANISM: UNKNOWN
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CURRENT APPLICATION NUMBER: US/09/260,527A
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09260527A Patent No. 6228599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Knox, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Willats, W. G.
TITLE OF INVENTION: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.0
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Best Local Similarity 81.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 280
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US-09-260-527-1
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US-09-079-029-9
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Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 28, 2005, 18:28:04 Job time: 23.3438 secs
                                                                                                                                                                                                                                                                            SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
UNDBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                P1101R2
                                                                                                                                                                                                                                                                                                                      APPLICALLON
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 91101
TELEFONNICATION INFORMATION:
TELEFAX: 650/225-5416
TELEFAX: 650/922-5416
TELEFAX: 650/922-5416
TELEFAX: 650/922-5416
TELEFAX: 650/922-9881
; INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                             ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.7%;
81.8%;
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Best Local Similarity 81.0
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197 QGDSLRSYYAS 207
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168, App 168, App 13, App 13, App 192, App 316, App 316, App 41, Appli 65, Appli 65, Appli 65, Appli 65, Appli

Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

US-09-880-748-1990
US-10-293-418-1990
US-10-303-418-1990
US-10-303-418-1990
US-10-803-623-168
US-09-848-798-49
US-10-803-623-168
US-10-803-623-168
US-10-10-105-192
US-10-10-105-192
US-10-10-105-192
US-10-10-105-192
US-10-10-105-193
US-10-10-105-193
US-10-10-105-193
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> US-10-910-124-8 US-10-888-959-8 US-09-988-115A-59 US-10-310-719-36

Sequence 168, A Sequence 19, Ap Sequence 13, Ap Sequence 13, Ap

Sequence 1 Sequence 1 Sequence 1

Sequence

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata1/lpubpaa/US106_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US106_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US10_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US11_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US11_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US10_PUBCOMB.ppp:*
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Sequence 18, Application US/10625307A .
Sequence 18, Application US/10625307A .
Publication No. US20050049403A1
GENERALIT NFORMATION:
APPLICANT: Thompson, Julia E.
APPLICANT: Vaughan, Tristan J.
APPLICANT: Green, Jonathan A.
APPLICANT: Jackson, Ronald H.
APPLICANT: Jackson, Roulse
APPLICANT: Wilton, Alison J.
APPLICANT: Wilton, Alison J.
APPLICANT: Wilton, Alison J.
APPLICANT: Pope, Anthony R.
TITLE OF INVENTION: Specific Binding Members for Human Transforming Growth Factor Bets;
TITLE OF INVENTION: Materials and Methods
FILE REFERENCE: 213899-00031
CURRENT APPLICANT: UNDER: US,10/625,307A

CURRENT FILING DATE: 2003-07-23  PRIOR APPLICATION NUMBER: 09/054.847	PRIOR FILING DATE: 1998-04-03	; PRIOR APPLICATION NUMBER: 08/571,755 ; PRIOR FILING DATE: 1995-12-13	NUMBER OF SEQ ID NOS: 125	; SOFTWARE: Patentin version 3.1	SEQ ID NO 18	; LENGTH: 110	; TYPE; PRT	; ORGANISM: Human	US-10-625-307A-18		Query Match 93.0%; Score 53; DB 17;	Best Local Similarity 90.9%; Pred. No. 0.054;	Matches 10; Conservative 1; Mismatches 0;	
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	Description	Semience 18. Appl	Sequence 1530, Ap	Sequence 1530, Ap	Sequence 2084, Ap	Sequence 2084, Ap	Sequence 2102, Ap	Seguence 2102, Ap	Sequence 2103, Ap	Sequence 2103, Ap	Sequence 2088, Ap	Sequence 2088, Ap	Sequence 2002, Ap	Sequence 2002, Ap
	di .	7 US-10-625-307A-18	0 US-09-880-748-1530	5 US-10-293-418-1530	0 US-09-880-748-2084	5 US-10-293-418-2084	0 US-09-880-748-2102	5 US-10-293-418-2102	.0 US-09-880-748-2103	.5 US-10-293-418-2103	.0 US-09-880-748-2088	5 US-10-293-418-2088	0 US-09-880-748-2002	5 US-10-293-418-2002

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Length 110; Indels

Gaps

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Sequence 2084, Application US/10293418
Fublication No. US20030223996A1
GENERAL INFORMATION: Antibodies that Immunospecifically Bind BLyS
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
TITLE REFERENCE: PPS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
FILE REFERENCE: PPS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
FRIOR PILING DATE: 2002-11-27
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PELING DATE: 2001-06-15
PRIOR PELING DATE: 2001-06-15
PRIOR PELING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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; Sequence 2084, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILB REPERENCE: PFS23
                                           Score 53; DB 15; Length 253;
Pred. No. 0.13;
1; Mismatches 0; Indels
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Pred. No. 0.28;
2; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-6.15

PRIOR PILING DATE: 2000-17

PRIOR PILING DATE: 2000-10.17

PRIOR PILING DATE: 2001-0.3

PRIOR FILING DATE: 2001-0.3-16

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHING VET: 2.0
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                                                     93.0%;
90.9%;
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Best Local Similarity 90.5
Matches 10; Conservative
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166 QGDSLKSYYAS 176
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; ORGANISM: Homo sapiens
US-09-880-748-2084
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Matches 9; Conserv
US-10-293-418-1530
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Fublication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

FRIOR APPLICATION NUMBER: 60/212,210

FRIOR APPLICATION NUMBER: 60/212,210

FRIOR APPLICATION NUMBER: 60/210,816

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR APPLICATION NUMBER: 60/276,248

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR APPLICATION NUMBER: 60/277,379

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFULD NOS: 3239
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| Sequence 1530, Application US/10293418
| Publication No. US2030322396A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al.
| ITILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| FILE REFERENCE: PF523P2
| CURRENT FILING DATE: 2002-11-27
| PRIOR APPLICATION NUMBER: 60/331,469
| PRIOR PLILING DATE: 2001-11-16
| PRIOR PLILING DATE: 2001-12-19
| PRIOR PLILING DATE: 2001-06-15
| PRIOR PLILING DATE: 2001-06-15
| PRIOR PLILING DATE: 2001-06-15
| PRIOR PLILING DATE: 2001-03-21
| PRIOR PLILING DATE: 2001-03-21
| PRIOR PLILING DATE: 2001-03-16
| PRIOR PLILING DATE: 2001-03-16
| PRIOR PLILING DATE: 2001-03-16
| PRIOR PLILING DATE: 2001-03-16
| PRIOR PLILING DATE: 2001-03-16
| PRIOR PLILING DATE: 2000-06-16
| PRIOR PLILING DATE: 2000-06-16
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Pred. No. 0.13;
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Best Local Similarity 90.5
Best Local 10; Conservative
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SEQ ID NO 1530
                             23 QGDSLKSYYAS 33
  1 OGDSLKTYYAS 11
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; ORGANISM: Homo sapiens
US-09-880-748-1530
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ORGANISM: Homo sapiens
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US-09-880-748-1530
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Sequence 2103, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 2103

LENGTH: 247
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPRENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
FRIOR APPLICATION NUMBER: 60/31,469
FRIOR FILING DATE: 2001-11-16
FRIOR APPLICATION NUMBER: 60/31,469
FRIOR APPLICATION NUMBER: 60/31,469
                                                                                                                                                                                                                                                                                                                                                             89.5%; Score 51; DB 15; Length 243; 81.8%; Pred. No. 0.28; ive 2; Mismatches 0; Indels
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Pred. No. 0.29;
2; Mismatches 0; Indels
                  | PRIOR APPLICATION NUMBER: 60/276, 248 |
| PRIOR FILING DATE: 2001-03-16 |
| PRIOR PELING DATE: 2000-116 |
| PRIOR FILING DATE: 2000-117 |
| PRIOR APPLICATION NUMBER: 60/212, 210 |
| PRIOR PILING DATE: 2000-06-16 |
| NUMBER: 0F SEQ ID NOS: 3247 |
| SEQ ID NO 2102 |
| LENGTH: 243
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  FILING DATE: 2001-03-21
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Matches 9; Conservative
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                                                                                                                                                                                                                                                         TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2102
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CORGANISM: Homo sapiens
US-09-880-748-2103
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Best Local Similarity
Matches 9; Conserv
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Sequence 2102, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

LENGTH. 2012
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Sequence 2102, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR PLICATION NUMBER: 60/331,469

PRIOR PLICATION NUMBER: 60/340,817

PRIOR PLILING DATE: 2001-12-19

PRIOR PLILING DATE: 2001-06-15

PRIOR PPLICATION NUMBER: 09/880,748

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2005-05-25

PRIOR PPLICATION NUMBER: 60/233,499

PRIOR PLILING DATE: 2005-05-25

PRIOR PPLICATION NUMBER: 60/277,379
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                                                                                                                                                                                                        Score 51; DB 15; Length 242;
Pred. No. 0.28;
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Pred. No. 0.28;
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81.8%;
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81.8%;
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2084
LENGTH: 242
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Best Local Similarity 81.6
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Best Local Similarity 81.6
Matches 9; Conservative
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157 QGDSLRTYYAN 167
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                                                                                                    TYPE: PRT GAGANISM: Homo sapiens US-10-293-418-2084
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; ORGANISM: Homo sapiens
US-09-880-748-2102
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Pred. No. 0.29;
2; Mismatches 0; Indels
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Pred. No. 0.29;
2; Mismatches
          FILE REFERENCE: PF523B2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2000-01-6
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
LENGTH: 248
LENGTH: 248
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; Publication No. US20030059937A1
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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US-10-293-418-2088
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US-09-880-748-2002
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US-09-880-748-2002
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Publication No. US2003059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 00/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 22-9

SOFTWARE: PatentIn Ver. 2.0
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 0.29;
2; Mismatches 0; Indels
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Pred. No. (
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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162 QGDSLRTYYAN 172
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CORGANISM: Homo sapiens
US-10-293-418-2103
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ORGANISM: Homo sapiens
US-09-880-748-2088
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US-09-880-748-2088
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US-10-293-418-2088
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RESULT 15
US-10-293-418-1990
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFREENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16
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Pred. No. 0.29;
2; Mismatches 0; Indels
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Sequence 2002, Application US/10293418
Publication No. US20030223996A1
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Best Local Similarity 81.8%;
Matches 9; Conservative ;
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SEQ ID NO 1990
LENGTH: 250
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163 QGDSLRTYYAN 173
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CORGANISM: Homo sapiens
US-10-293-418-2002
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CORGANISM: Homo sapiens
US-09-880-748-1990
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Gaps
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GENERAL INFUGATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT PILING DATE: 2001-11-27

FRIOR APPLICATION NUMBER: 60/331,469

FRIOR FILING DATE: 2001-11-27

FRIOR PILING DATE: 2001-12-19

FRIOR FILING DATE: 2001-12-19

FRIOR FILING DATE: 2001-05-15

FRIOR FILING DATE: 2001-05-25

FRIOR APPLICATION NUMBER: 60/293,499

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-16

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FRIOR FILING DATE: 2000-10-17

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Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 28, 2005, 19:02:12 Job time : 69.2344 secs
                                                                                                                                                                                                                                                        ; Sequence 1990, Application US/10293418; Publication No. US20030223996A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8
Local Similarity 91.8
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 QGDSLRTYYAN 174
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1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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5.1.6
Compugen Ltd.
version :
GenCore (c) 1993
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55 ; Search time 15.125 Seconds (without alignments) 69.976 Million cell updates/sec Run on:

US-10-088-639A-2_COPY_23_33 57

1 QGDSLKTYYAS 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOUTHER	
Result No.	Score	Query Match	Query Match Length	08	ΩI	Description
	53	93.0	109	. 7	S38496	Iq lambda chain -
7	20		96	~	836060	Ig lambda chain -
m	20	87.7	106	7	S38495	Ig lambda chain -
4	20	87.7	108	~	S38498	סו
Ŋ	20	87.7	108	~	S47184	g lambda
9	20	87.7	109	'n	S19663	Ig lambda chain V
7	20	87.7	110	~	836272	g lambda
80	20	87.7	115	~	S13726	g lambda
σ	20	87.7	127	~	S70444	g lambda
10	49	86.0	233	~	S25748	Ig lambda chain -
11	45	78.9	233	7	S25741	Ig lambda chain -
12	44	77.2	2135	~	T14602	variant-specific s
13	41	71.9	110	~	S19672	Ig lambda chain V
14	39	68.4	1729	~	T18396	erythrocyte membra
15	39	68.4	292	~	T18378	variant-specific s
16	38	66.7		~	E64617	hypothetical prote
17	38	66.7	429	~	F71896	
18	38	66.7	624	~	S44938	€
19	37	64.9	146	~	S02083	Ig lambda chain V-
50	36	63.2	270	7	AG0916	probable hydrolase
21	36	63.2	452	-	WHHUF	phenylalanine 4-mo
22	36	63.2	547	C3	D84942	methionine-tRNA li
23	36	63.2	1159	Н	A44280	inner layer protei
24	35	61.4	197	~	B83497	hypothetical prote
25	35	61.4	56	~	H84378	
56	35	61.4	313	~	H72724	probable microsoma
27	35	61.4	36	~	T24058	hypothetical prote
28	35	61.4	408	~	AC2188	netical pr
29	35	61.4	561	N	JE0158	ㄷ

Ig lambda chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

RESULT 2

C,Accession: S3660
R,Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Reference number: S36046
A;Reference number: S36060
A;Returus: preliminary
A;Molecule type: DNA
A;Residues: 1-96 < WIL>
A;Cross-references: EMBL: 222202; NID: G312325; PIDN: CAA80211.1; PID: G312326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology < IMM>

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Gaps

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Score 50; DB 2; Length 96; Pred. No. 0.014; 2; Mismatches 0; Indels

Query Match 87.7%; Best Local Similarity 81.8%; Matches 9; Conservative 2

1 QGDSLKTYYAS 11

N-acetyl-beta-D-gl	autotransporter pr	variant-specific s	Ig lambda chain V-	allophycocyanin be	hypothetical prote	hypothetical prote	hypotherical prote	vdlc protein - Hel	xylose isomerase (	probable phosphopy	phosphopyruvate hy	gene 8 protein - p	sodium/pantothenat	hypotherical prote	hypothetical prote
872211	AF3204	T14029	L3HUSH	B44462	D71978	E64527	G70438	T09452	E86813	T03267	T02221	WMBP8Z	F97807	A84260	T36084
~	N	~	Н	7	~	~	8	~	7	~	~	-	~	7	~
580	898	2228	108	161	189	189	218	284	439	446	446	448	464	529	561
4.	4.	4.	9.	9.	9.	9.	9	9.	9.	9.	9.	9.	9.	9.	9.
61	61	61	59	59.6	59	59	59	29	29	53	59	59	53	59	29
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35	35	35	34	34	34	ň	Ö	e	e	e	'n	e	m	m	ń

## ALIGNMENTS

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C;Accession: $38496
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S submitted to the BMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pł A;Beference number: $38488
A;Accession: $38496
A;Status: preliminary
A;Accession: S18496
A;Status: preliminary
A;Residues: 1-109 <AMR>
A;Residues: 1-109 <AMR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                          C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 0.004;
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S38496
Ig lambda chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 93.0%;
Local Similarity 90.9%;
hes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 10
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OGDSLRSYYAS 33

23

В

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R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A; Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha A; Reference number: S19663; MUID: 92085276; PMID: 1748994
A; Accession: S19663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: 836272
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: 836256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig lambda chain V region (clone alpha-BSA3) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
A;Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-89/Domain: immunoglobulin homology <a href="https://dx.doi.org/10.1007/10.1007/">https://dx.doi.org/10.1007/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-109 <MAR>
A;Residues: 1-109 <MAR>
A;Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                Gaps
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A, Cross-references: BMBL-Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
A, Cross-references: BMBL-Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C; Superfamily: immunoglobulin v region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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81.8%; Pred. No. 0.016;
Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                        Score 50; DB 2; Length 108;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.7%; Score 50; DB 2; Length 109; illarity 81.8%; Pred. No. 0.016; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;15-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                             87.7%;
81.8%;
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Ig lambda chain V region - human
C;Species: Homo sapiens (man)
                                                                                                                                                                                   Ouery Match
Best Local Similarity 81.0
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23 QGDSLRSYYAS
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nes 9; Conserv
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S19663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S36272
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Matches
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347184

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: S47184

R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

8;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

8;McIntosh, R.S.; Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien

A;Reference number: $47181
                                                                                                                                                                                                                                                                                                                                                    C; Accession: S38495
R; Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, & Submitted to the EMBL Data Library, June 1993
A; Description: Human antibody fragments specific for human blood group antigens from a facession: S38498
A; Reference number: S38498
A; Accession: S38495
A; Accession: Sylviniary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, Submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38498
A;Status: preliminary
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                                                                                                                                                                                                          Jambda chain - human (fragment)
Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: EMBL:223029; NID:9414037; PIDN:CAA80564.1; PID:9414038 C. Suberfamily: immunoplobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 15-89/Domain: immunoglobulin homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglobulin</a> homology <a href="https://downsin.immunoglobulin">https://downsin.immunoglob
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Length 106;

0; Indels

Score 50; DB 2; Pred. No. 0.015; 2; Mismatches

87.78; 81.8%;

Best Local Similarity 81.8 Matches 9; Conservative

Query Match

Residues: 1-106 <MAR>

à g . .

Length 108

87.7%; Score 50; DB 2; 81.8%; Pred. No. 0.016; live 2; Mismatches

Query Match Best Local Similarity 81.8 Matches 9; Conservative

A; Molecule type: DNA A; Residues: 1-108 < MAR>

1 QGDSLKTYYAS 11

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22 ÓGDSLRSÝÝAS 32

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-108 <MCI>

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A,Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A,Reference number: S16439; MUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $25/41
R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) c(lambda) gene segments of the human immunoglobulin lamt A;Reference number: $16439; MUID:91257162; PMID:1904362
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A;Description: Identification of a conserved 5' flanking region of Plasmodium falciparum A;Reference number: Z18158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variant-specific surface protein - malaria parasite (Plasmodium falciparum) (fragments)
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                                                                                                                        A; Residues: 1-233 <COM>
A; Residues: 1-233 <COM>
A; Cross-references: EMBL:XS7813; NID:g33725; PIDN:CAA40850.1; PID:g33726
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-233 <CON>
A; Residues: 1-233 <CON>
A; Cross-references: EMBL:XS7805; NID:933707; PIDN:CAA40943.1; PID:933708
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Pred. No. 0.34;
4; Mismatches 0; Indels
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Pred. No. 0.055;
1; Mismatches
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Pred. No. 5.4;
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                                          A, Accession: $25748
A, Status: preliminary; translation not shown
A, Molecule type: mRNA
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A, Status: preliminary; translation not shown
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81.8%;
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77.8%;
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Best Local Similarity 77.8'
Conservative 7;
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Best Local Similarity 63.6
Matches 7; Conservative
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160 EGDSIKTYY 168
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Best Local Similarity
Matches 9; Conserva
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A; Residues: 1-2135 <VOS>
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                                                Ririppiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P. Morleic Acida Res. 18, 7134, 1990
Nyleic Acida Res. 18, 7134, 1990
A; Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup A; Reference number: S13726; MUID:91088295; PMID:2124677
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 24-Jul-1998 Heactuence revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S70444; S70426
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of A;Reference number: S70442; MUID:93024508; PMID:1383695
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S25748
Ig lambda chain - human
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
  C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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A; Experimental source: cell line E29.1, clone VL 29-1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 115;
                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>
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;1-20/Domain: signal sequence #eratus predicted <SIG>
;21-127/Product: Ig lambda chain V region (fragment) #status
;34-108/Domain: immunoglobulin homology <1NM>
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Pred. No. 0.018;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2;
Pred. No. 0.017;
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fresidues: 1-127 cCUI>
frosidues: 1-127 cCUI>
frosimental source: clone E29.1
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81.8%;
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Best Local Similarity 81.0-
Best Local 9; Conservative
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A; Accession: S70426
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-115 <FRI>
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A; Residues: 1-90 <TON>
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A; Status: preliminary
                                Accession: S13726
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151 EGDSIKTHY 159
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A.Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
A,Accession: S19672
A;Molecule type: mRNA
A;Residues: 1-110 cMAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fragm
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Modecule type: mRNA
A;Residues: 1-1729 «BRR»
A;Cross-references: UNIPROT:Q25734; EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134
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NyAlternate names: erythrocyte membrane binding protein 1 (EMP1)

(Species: Plasmodium falciparum

C,Baccession: 178378

R,Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.

Cell 82, 77-87, 1995

A;Title: Cloning the P falciparum gene encoding PfEMP1, a malarial variant antigen and A;Reference number: Z18925; MUID:95330812; PMID:7541722
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A;Cross-references: UNIPROT:Q25733; EMBL:U27338; NID:g914918; PID:g914919; PIDN:AAB60251
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                                                Species: Homo sapiens (man)
Bate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
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A;Molecule type: DNA
A;Residues: 1-2924 <BAR>
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C;Genetics:
A;Gene: EMP1
A;Introns: 2476/3
A;Introns: 2476/3
Query Match
Best Local Similarity 66.7%; Pred. No. 74; Delta 0; Indels 0;
Matches 6; Conservative 3; Mismatches 0; Indels 0;
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                                                                     01:42:46; Search time 9.13208 Seconds (without alignments) 62.721 Million cell updates/sec
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         GenCore version 5.1.6
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PH4H_HUWAN
SYM_BUCAP
SYM_BUCAP
SYM_BUCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and characterization of three Drosophila melanogaster glucuronyltransferases responsible for the synthesis of the conserved glycosaminoglycan-protein linkage region of proteoglycans: two novel homologs exhibit broad specificity toward oligosaccharides from proteoglycans, glycosproteins, and glycosphingolipids.";
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Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheron A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
Momillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, COFACTOR, AND DEVELOPMENTAL STAGE. MEDLINE=22513909; Pubmed=12511570; Kim B.-T., Tsuchida K., Lincecum J., Kitagawa K., Bernfield M., Sugahara K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 270; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                              protein; Hydrolase; Complete proteome.

147 147 BY SIMILARITY.

204 204 BY SIMILARITY.

2136 BY SIMILARITY.

70 AA; 29062 MW; 1C2374B6047DA872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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MEDLINE=20196011; PubMed=10731137;
                                                                                                                                                                              EMBL; AF233324; AAF33425.1; -. EMBL; AE008885; AAL22811.1; -. StyGene; SG?772; yegA. InterPro; IPR002925; DLH. Pfam; PF01738; DLH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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MEDLINE-21534948; PubMed=11677609; MEDLINE-21534948; PubMed=11677609; MCTCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: 4-carboxymethylenebut-2-en-4-olide + H(2)0 = 4
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28-FEB-2003 (Rel. 41, Last annotation update)
Putative carboxymethylenebutenolidase (BC 3.1.1.45) (Dienelactone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Profeobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%; Score 36; DB 1; Length 270; 60.0%; Pred. No. 9.3;
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ACT_SITE
ACT_SITE
CONFLICT
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DEVELOPMENTAL STAGE: Expressed at low levels from early embryos to

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Admarabettally,

RATAINSEDERTALLEY,

RAGENER AD., Celniker S. E., Holf R. A., Borns C.A., Gocayne J.D.,

RAGEME M.D., Celniker S. E., Holf R. A., Borshins R. A., Galle R. F.,

RAGEORG R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N.,

RAGEORG R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N.,

RAGEORG R.A., Lewis S. E., Richards S., Ashburner M., Henderson S.N.,

RAGEORG R.A., Brands T. R., Yandell M.D., Zhang O., Chen L. X.,

RADII J.F., Agbayani A., An H. -J., Andrews-Frankoch C., Baldwin D.,

RADII J.F., Agbayani A., Barardale J., Bayraktaroglu L., Beasley E.M.,

RADII J.F., Agbayani A., Bulok J., Bayraktaroglu L., Beasley E.M.,

RADEORO R., Boucher M., Bauck J., Broketein P., Brottier P.,

RADORON R., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,

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RADORO R., Doup L.E., Downes M., Dugan R., Raris M.,

RADORO R., Boone F., Gorrell J. H., Gu Z., Guan P., Harris M.,

RADORO R., Boucher A., Bowland T.J., Wel M.-H., IDegaer K.,

Aloake R., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,

RADORO R., Jougo L.E., Downes M., Dugan R., Houck J.,

Houston K.J., Evangelista C.C., Ferraz C., Ferraics J., Roll W., McLeotham N.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kupl D., Lai Z.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Liang Y., Lin X.,

RADORO R., Molth R., Molth R., Molteod M.P., McChecot M. P., McChecot M. P., McChecot M. P., McChecot M. Salush R.,

Raderacolo R., Nelson R.A., Mixon K., Musskern D.R., Pacleb J.M.,

Raderacolo R., Remington K., Stunders R.D.C., Scheeler F., Shen H.,

Raderacolo R., Wassagman D.A., Weinstock G.M., Weissenbach J.,

Raderacolo R., Wassagman D.A., Weinstock G.M., Weissenbach J.,

Radilam S.M., Woodage T., Shan M., Zhang S., Zhu X., Smith H.,

Radibas R., Jenger B.W., Shonin G.M., Venter E., Wang X.,

Radibas R., Jenger P., Saveri J.S., Zhan M., Zhong S., Zhu X., Smith H.,

Radibas R., Jenger B., Shonin G.M., Venter E., Shan R.,

Radibas R., Jenger C., Siden-Kiamos J., Shan
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SEQUENCE FROM N.A.

STRAIN=Berkeley; TISSUE=Head;

MEDIINE=22466066; PubMed=12537569;

A Stapleton M., Carlson M., Encotein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., A prosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

-I- FUNCTION: Involved in the biosynthesis of L2/HNK-1 carbohydrate epitope on bort glycolipids and glycoproteins. Shows strict specificity for Gal betal-331 betal-4XJ, exhibiting negligible incorporation into other galactoside substrates.

-I- CATALYTIC ACTIVITY: UDP-glucuronate + 3-beta-D-galactosyl-4-beta-D-galactosyl-0-beta-D-galactosyl-4-beta-D-galactosyl-0-beta-D-galactosyl-4-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-galactosyl-0-beta-D-
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Tradecky P., Huang.Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.E.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stappeton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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-!- CÓFÁCTÓR: Manganese. -!- PATHWAY: Glycosylation. -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flydase; FBGH0066114; GlcAT-I.
InterPro; IPR005027; Glyco trans 43.
Pfam; PF03160; Glyco transf 43. I.
Pransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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amino acid sequence of human phenylalanine hydroxylase.";
Biochemistry 24:556-561(1985).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CATALYTIC BASE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
V -> L (IN REF. 1 AND 2).
69910A46534218B0 CRC64;
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                        adults; maximal expression in third instar larvae. SIMILARITY: Belongs to the glycosyltransferase family 43.
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Pred. No. 11;
1; Mismatches 2; Indels
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EMBL; AL033125; CAA21824.1; ALT_SEQ.
EMBL; AE003430; AAN09117.1; -.
EMBL; AY060634; AAL28182.1; -.
HSSP; O94766; 1FGG.
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REVIEW ON PKU VARIANTS.
MEDLINE=93244826; PubMed=1301187;
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REVIEW ON PKU VARIANTS
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MEDLINE=91169506; PubMed=1672290;
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MEDLINE=90136055; PubMed=2615649;
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                                                                                                         DATABASE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munnich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valle D.;
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                                                                                                                                                                                                                                               HSSP; P00959; IMEA.
HSAMAP; MF 000959; IMEA.
InterPro; IPR002000; tRNA-synt_1a.
InterPro; IPR001212; tRNA-synt_I.
InterPro; IPR001304; tRNA-synt_I.
PERM: IROO1313; tRNA-synt 1; 1.
PRINTS; PR01041; TRNASYNTHER;
TIGRFAMS; TIGR00399; metG; 1.
TIGRFAMS; TIGR00399; metG; 1.
Aminoacyl-tRNA synthetase; Protecome.
Metal-binding; Zinc; Complete protecome.
""HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator ENNA(fMet) aminoacylation (By similarity).

CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphate + L-methionyl-tRNA(Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-1- SUBUNIT. Monomer (By similarity).
-1- SUBCELLUTAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          symbiotic bacterium).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.,
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
LeCOT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last amoutation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
3 ZINC (BY SIMILARITY).
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ATP (BY SIMILARITY)
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Pred. No. 2
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Matches 7; Conservative
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162 1
545 AA;
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A Clark M.A. Baumann L., Baumann D.;

Clark M.A. Baumann L., Baumann D.;

"Buchnera aphidicola (Aphid endosymbiont) contains genes encoding

"Buchnera aphidicola (Aphid endosymbiont) contains genes encoding

"Buchnera aphidicola (Aphid endosymbiont) contains genes encoding

"Cur. Microbiol. 37:1356-1358(1998).

"LefukTion): 13 required not only for elongation of protein synthesis

"LefukTion in itiation of all mRNA translation through

"LefukTion for the initiation of all mRNA translation through

"CATALYTIC ACTIVITY: ATP + L-methionin + tRNA(Met) = AMP +

diphosphate + L-methiony - L-methionin + tRNA(Met) = AMP +

diphosphate + L-methiony - tRNA(Met).

"COFACTOR: Binds 1 zinc ion per subunit (By similarity).

"COFACTOR: Binds 1 zinc ion per subunit (By similarity).

"SUBCELLULAR LOCATION: Cyroplasmic.

"SUBCELLULAR LOCATION: Cyroplasmic."

"The Core of the color of the subunit of the synthetase family.
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"A 3-base pair in-frame deletion of the phenylalanine hydroxylase gene results in a kinetic variant of phenylketonuria.";
J. Biol. Chem. 266:9351-9354(1991).
                                                                                                                         VARIANTS PKU SER-48 AND GLY-221.
MEDLINE=91348662; PubMed=1679030;
Konecki D.S., Schlotter M., Trefz F.K., Lichter-Konecki U.;
Konecki D.S., bellotter M., Trefz F.K., Lichter-Konecki U.;
Hub identification of two mis-sense mutations at the PAH gene locus in a Turkish patient with phenylketonuria.";
Hum. Genet. 87:389-393(1991).
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28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Briksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
Science 296:2376-2379 (2002).
       Aulehla-Scholz C., Horst J.; "Phenylalanine hydroxylase gene: novel missense mutation in exon causing severe phenylketonuria."; Genomics 9:193-199(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93052278; PubMed=1358789; Economou-Petersen E., Henriksen K.F., Guldberg P., Guettler F.; "Molecular basis for nonphenylketonuria hyperphenylalaninemia.";
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Pred. No. 16;
1; Mismatches 2; Indels
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MEDLINE-91236693; PubMed=1709636;
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28-FEB-2003 (Rel. 41, Last seqn
28-FEB-2003 (Rel. 41, Last ann
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les 7; Conservative
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Q9ZHD7;
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Matches
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Gaps

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EMBL; M97203; -; NOT_ANNOTATED_CDS
                PIR; A44280; A44280
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PHAB SYNY3
ID PHAB SYNY3
AC Q01952;
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P01714;
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SEQUENCE
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      between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                  Pfam; PF00133; tRNA-synt_1; 1.—
PRINTS; PR01041; TRNASYNTHMET.
TIGRPAMs; TIGR00398; metG; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIATE=93297100; PubMed=8390749;
MEDIATE=93297100; PubMed=8390749;
Biden J.J., Hirahon C.;
"Sequence analysis of group B rotavirus gene 1 and definition of a rotavirus-specific sequence motif within the RNA polymerase gene.";
Virology 192:154-160(1993).
-i- FUNCTION: RNA POLYMERASE ACTIVITY IS THOUGHT TO BE ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA-directed RNA polymerase subunit VPI (EC 2.7.7.48) (Inner layer protein VPI) (Core protein VPI)
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-!- SIMILARITY: Belongs to the rotaviruses VP1 protein family.
                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 547;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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ATP (BY SIMILARITY).
ZINC (BY SIMILARITY).
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ZINC (BY SIMILARITY).
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=28877;
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InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002304; tRNA-synt met.
                                                                                                     EMBL; AP001118; BAB12828.1; -. HSSP; P00959; 1MEA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein.
complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 1159;
Pred. No. 45;
2; Mismatches 1; Indels
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InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007097; RNA_pol_reo.
InterPro; IPR00817; Rotavirus VP1.
Pfam; PF05740; Rotavirus VP1; I.
Core protein; RNA-directed RNA polymerase; Transferase.
SEQUENCE 1159 AA; 131649 MW; E355F9BF79E225A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 245:2171-2176 (1970).

-!- MISCELLANEOUS: This is a Bence-Jones protein.
-!- SIMILARITY: Contains i immunoglobulin-like domain.
-!- SIMILARITY: Contains i immunoglobulin-like domain.
-!- SIMILARITY: Contains i immunoglobulin-like domain.
-!- SIMILARITY: Contains i immunoglobulin-like domain.
-!- SIMILARITY: Contains i immunoglobulin-like domain.
-!- SIMILARITY: Contains i immunoglobulin-like.
-!- SIMILARITY: SIMILARITY: NAS.
-!- SIMILARITY: SIMILARITY: NAS.
-!- SIMILARITY: SIMILARITY: NAS.
-!- SIMILARITY: SIMILARITY: NAS.
-!- SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY: SIMILARITY:
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g lambda chain V-III region SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; IGV, 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
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70.0%;
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Best Local Similarity bo...
7; Conservative
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QGDSLRGYDAA 32
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                            STRAIN=210, NRRL B-4449, and IO-1;
Brlandson K.A., Park J.-H., Delamarre S.C., El Khal W., Kao
Bassaran P., Brydges S.D., Batt C.A.;
"The xylose and xylan loci of Lactococcus lactis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the xylose isomerase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Xylose isomerase (EC 5.3.1.5).
                                                                                                                                                                                                                                                                                                                                                    STRAIN=IL1403;
MEDLINE=21235186; PubMed=11337471;
Q9CFG7; Q9RAV8; Q9X416; Q9X422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
247
275
388
407
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                                                                                                                                                     NCBI_TaxID=1360;
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                                                                                               XYLA OR LL1509
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METAL
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 18:1252-1258(1997).
-!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex. Allophycocyanin has a maximum absorption at approximately 650 nanometers.
-!- SUBGNUT: Heterodimer of an alpha and a beta chain.
-!- PTM: Contains one covalently linked bilin chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Kocani H., Tanaka A., Asamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muzaki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.,
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
                                                                                                                                   Su X., Goodman P., Bogorad L.;
Excitation energy transfer from phycocyanin to chlorophyll in an
apch-defective mutant of Synechocystis sp. PCC 6803.";
j. Biol. Chem. 267:22944-22950(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000340; Phycobilisome; 1.
TIGRFAMs; TIGR01337; apcB; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sazuka T., Ohara O.;
"Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION (BY SIMILARITY).
PHYCOCYANOBILIN CHROMOPHORE (BY SIMILARITY).
; 63F01E5903BA1BB3 CRC64;
                    Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
                  (strain PCC 6803)
                                                                                             SEQUENCE FROM N.A.
MEDLINE=93054612; PubMed=1429645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97443974; PubMed=9298645;
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MOD RES 71 71 ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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  OR SLR1986.
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  APCB
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PRINTS; PR00688; XYLOSISNRAASE.
PROSITE; PS00172; XYLOSE ISOMERASE 1; 1.
PROSITE; PS00173; XYLOSE ISOMERASE 2; 1.
Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R -> M (IN STRAINS NRRL B-4449 AND IO-1)
D -> Y (IN STRAINS 1210).
A -> S (IN STRAINS NRRL B-4449 AND IO-1)
V -> A (IN STRAINS NRRL B-4449 AND IO-1)
T -> S (IN STRAINS NRRL B-4449 AND IO-1)
H -> Y (IN STRAINS NRRL B-4449 AND IO-1)
H -> Y (IN STRAIN IO-1).
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7744A3655B81B759 CRC64;
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                                                                                                                                                                                                                                                                                                              MAGNESIUM 1 (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY).
MAGNESIUM 2 (BY SIMILARITY).
MAGNESIUM 2 (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY).
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Pred. No. 40;
3; Mismatches
                                                                              PIR; E86813; E86813.
HSSP; P54273; LAOD.
HAMAP; MF_00455; -; 1.
InterPro; IPR001998; Xylose_isom.
EMBL; AF092040; AAD20243.1; -. EMBL; AF092041; AAD20249.1; -. EMBL; AF092042; AAD20255.1; -.
                                                             AE006381; AAK05607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.6%;
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Best Local Similarity
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VARIANT
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439 AA.

PRT;

STANDARD;

RESULT 11 XYLA_LACLA ID XYLA_LACLA

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                                                                                                                                                                                                                                                                                                                                                                   (In) Plant Gene Register PGR95-084.

    -!- COFACTOR: Magnesium is required for catalysis and for stabilizing

                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSE1).
                                                                                                                                          Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                              STRAIN=Cv. Tainong 67; TISSUB=Seed; Hsing Y.-I.C., Twac C.-W., Heich J.-S., Chen Z.-Y., Shu T.-F., Chow T.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Glycolysis.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULIAR LOCATION: Cytoplasmic.
-!- DEVELOPMENTAL STAGE: Expressed during early embryogenesis.
-!- SIMILARITY: Belongs to the enolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 446; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
MAGNISIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNISIUM (BY SIMILARITY).
FECD81319246D477 CRC64;
                                                                                                                                                                                                                                                                                                                                                  rice early embryogenesis-specific enolase cDNA.";
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HEAD BPPZA.

ID HEAD BPPZA
AC P07531
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
    446 AA.
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Probom; PD000902; ENOLASE:
TIGREPAMS; TIGR01060; eno; 1.
PROSITE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium.
ACT_SITE 164 164 B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000941; Enclase.
Pfam; PF00113; enclase; 1.
Pfam; PF03952; enclase N; 1.
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    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GDSLKNVYKS 291
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HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene; 042971; -
                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the dimer.
    ORYSA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. B73; TISSUE=Root;
MEDLINE=99063764; PubMed=9847102;
Lal S.K., Lee C., Sachs M.M.;
"Differential regulation of enolase during anaerobiosis in maize.";
Plant Physiol. 118:1285-1293(1998).
-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-
D-glycerate hydro-lyase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
-!- PATHWAY: Glycolysis.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MAGNESIUM (BY SIMILARITY).
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Pfam; PF0352; enolase; 1.
PRINTS; PR00148; ENOLASE.
Probom; PD000902; Enolase; 1.
TIGRFAMS; TIGR01060; eno; 1.
PROSITE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium; Multigene family.
ACT_SITE 164 BY SIMILARITY.
                                                                                                                                            446 AA
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MAGNESIUM
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                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
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nes 7; Conservative
                                                                                                                                            STANDARD;
                                        109 GNSLKEFYAN 118
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GDSLKTYYAS 11
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HSSP; P56252; 1PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                         Zea mays (Maize)
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ID ENO2_MAIZE
AC P42895;
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Gaps

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3; Indels

Major head protein (Late protein Gp8)

Matches

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EMBL; X59720; CAA42393.1;
                     PIR; S19381; S19381.
GermOnline; 138887; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
MY16 MOUSE
ID MY16 MOUSE
AC P17564;
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MEDLINE=97245290; PubMed=9080049;
Lai M.H., Silverman S.J., Gaughran J.P., Kirsch D.R.;
Lai M.H., Silverman S.J., Gaughran J.P., Kirsch D.R.;
"Multiple copies of PBS2, MRP1 or LRE1 produce glucanase resistance and other cell wall effects in Saccharomyces cerevisiae.";
Yeast 13:199-213(1997).
-! FUNCTION: Not known; overexpression of both LRE1 and PBN1 confers resistance to laminarinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         MEDIINE-87031573; PubMed-3095188;
Paces V., Vlcek C., Urbanek P.;
"Nucleotide sequence of the late region of Bacillus subtilis phage
                                        Viruses, dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
phi-29-like viruses:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Fuller L.J., Kelly A., Lewis C., McKee R.A., Pearson B.M., Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 448;
Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 AA; 49754 MW; 70B6108E556BBCB2 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                              a close relative of phi 29.";
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Best Local Similarity 75.00.
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                                                                                                                                                                                                                                                         Gene 44:107-114(1986).
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                     Bacteriophage PZA
                                                                                           NCBI_TaxID=10757;
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                                                                                                                                                                                                                                                      Gaps
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Lord K.A., Hoffman-Liebermann B., Liebermann D.A.;
Lord K.A., Hoffman-Liebermann B., Liebermann D.A.;
"Sequence of MyD116 cDNA: a novel myeloid differentiation primary
response gene induced by IL6.";
Nucleic Acids Res. 18:2823-2823(1990).
-:- INDUCTION: By interleukin-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SGD; S0000556; LREI.
GO; GO:0004860; F:protein kinase inhibitor activity; IDA.
GO; GO:0001628; F:transcription regulator activity; IDA.
GO; GO:0007047; P:cell wall organization and biogenesis; IGI.
GO; GO:0009408; P:response to heat; IDA.
SEQUENCE 586 AA; 65152 MW; 7C777C5259247DC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%; Score 34; DB 1; Length 657; 60.0%; Pred. No. 62; ive 3; Mismatches 1; Indels
                                                                                                                                                                                            59.6%; Score 34; DB 1; Length 586; 66.7%; Pred. No. 54; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Myeloid differentiation primary response protein MyD116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9B217001019C38A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S10001; slow...
MGD; MGI:1100516; Myd116.
Differentiation; Antigen; Repeat.
4.5 X TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X51829; CAA36128.1; -.
                                                                                                                                                                                                                         Local Similarity 66.7
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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179 GETVKTYQAS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
398
436
451
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                                                                                                                                                                                                                                                                                                                                                                  531 DALKTFHAS 539
                                                                                                                                                                                                                                                                                                            3 DSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
323
361
361
399
437
657 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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IF38_YEAST

RESULT 17

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118 QVESLKTYFFS 728
                 1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHAB SYNY4
Q02924;
                                                                                                                  TRICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                              riturus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                      SECUENCE
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                                                                                                                  HBB1 TRI
P10785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initiation factor; Protein biosynthesis; Transport; Protein transport.

ASP/GLU-RICH (ACIDIC).

SER-RICH.
                                        01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Eukaryotic translation initiation factor 3 93 kDa subunit (eIF3 p93)
                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:90-93(1997).

-!- FUNCTION: Binds to the 40S ribosome and promotes the binding of methionyl-trnah and mRNA.

-!- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE NUCLEUS;
PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.

-!- SUBUNIT: eIF-3 is composed of up to 8 different subunits.

-!- SUBCELLULAR LOCATION: Cytoplasmic; mainly.

-!- SIMILARITY: Contains 1 PCI domain.

-!- SIMILARITY: BELONGS TO THE EIF3S8 FAMILY.
                                                                                                                                                                                                                                                        ESTOURNCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE=97313268; PubMed=9169872;
MEDLINE=97313268; PubMed=9169872;
MEDLINE=97313268; PubMed=9169872;
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moult S., Odéll C., Pearson D., Rajandream M.A.
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                 (Nuclear transport protein NIP1).
NIP1 OR YMR309C OR YM9924.01C OR YM9952.11C.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005737; G:cytoplasm; IDA.
GO; GO:0005852; C:cukaryotic translation initiation factor 3 .
GO; GO:000343; F:translation initiation factor activity; IDA.
GO; GO:0006413; P:translational initiation; IDA.
InterPro; IPR008905; eIF3c.N.
InterPro; IPR00870; PCI.
Pfam; PF05470; eIF3C.N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; 'DB 1; Length 812; Pred. No. 77;
                                                                                                                                                                                                  MEDLINE=93066237; PubMed=1332047;
Gu Z., Moerschell R.P., Sherman F., Goldfarb D.S.;
"NIPL, a gene required for nuclear transport in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 89:10355-10359(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 V -> D (IN REF. 1).

541 K -> N (IN REF. 1).

743 K -> N (IN REF. 1).

7543 K -> N (IN REF. 1).

7544 MW, EE05097C44C45A4C CRC64;
                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces
  812 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L02899; -; NOT ANNOTATED_CDS.
EMBL; Z54141; CAA90827.1; -.
EMBL; Z49212; CAA89142.1; -.
                          01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.68;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00088; PINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A46417; A46417.
GermOnline; 142988; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S0004926; NIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=4932;
IF38 YEAST
P32497;
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CONFLICT
CONFLICT
SEQUENCE
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Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
The first sequenced normal hemoglobin lacking histidine in position
146 of the beta-chains. The primary structures of the major and minor hemoglobin components of the great crested newt (Triturus cristatus, Urodela, Amphibia)...
1901. Chem. Hoppe-Seyler 369:1343-1360(1988).
1901. Chem. Hoppe-Seyler 369:1343-1360(1988).
1902. Chem. Hoppe-Seyler 169:1343-1360(1988).
1902. Chem. Hoppe-Seyler 169:1343-1360(1988).
1902. Chem. Hoppe-Seyler 169:1343-1360(1988).
1903. The Burnich Hemoglobin is A TETRAMER OF TWO ALPHA-1 CHAINS AND TWO BETR-1 CHAINS AND TWO BETR-1 CHAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization of the genes encoding allophycocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                 Triturus cristatus (Great crested newt) (Warty newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 145;
Pred. No. 19;
0; Mismatches . 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 62 IRON (HEME DISTAL LIGAND).
91 91 IRON (HEME PROXIMAL LIGAND).
145 AA; 16003 MW; BEF06F441B42BA80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Oxygen transport; Transport; Erythrocyte.
                                                                           01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin beta-1 chain (Major).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUB SPECIFICITY: Red blood cells.
-!- SIMILARITY: Belongs to the globin family.
PIR, S02025; S02025.
HSSP, P02070; IFSX.
INTERPRO; IPR002337; Beta haem.
InterPro; IPR000971; Globin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Allophycocyanin beta chain.
145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6714)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93222481; PubMed=8467079;
Dimagno L.M., Haselkorn R.;
                                                  01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00042; globin; 1.
PRINTS; PR00814; BETAHAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01033; GLOBIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=8323;
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Gaps

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2; Indels

2; Mismatches

63.68;

7; Conservative

Matches

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Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (28-FEB-2003 (10-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSGA PSEAE
Q915ŪS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 21
KSGA_PSEAE
  124FF
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168 / JH642;
MEDLLIRE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region of
                    Plant Mol. Biol. 21:835-846(1993).
-1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex. Allophycocyanin has a maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00502; Phycobilisome; 1.
Probom; PD000344; Phycobilisome; 1.
TIGRPAMS; TIGRO1337; apo8; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168 / JH642;
MEDLINE=95219086; PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
"Complete nucleotide sequence of a skin element excised by DNA rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Systematic sequencing of the 283 kb 210 degrees-232 degrees the Bacillus subtilis genome containing the skin element and
subunits and two linker proteins from Synechocystis 6714."; Plant Mol. Biol. 21:835-846(1993).
                                                                                  absorption at approximately 650 nanometers.
SUBUNIT: Heterodimer of an alpha and a beta chain.
PTM: Contains one covalently linked bilin chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 161;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 71 METHYLATION (BY SIMILARITY).
81 81 PHYCOCYANOBILIN CHROMOPHORE.
161 AA, 17242 MW; 63F0047008630A73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein yqaC precursor.
YQAC OR BSU26370.
                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR006245; ApcB.
Interpro; IPR001659; Phycobilisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology 142:3103-3111(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%;
                                                                                                                                                                                                                                                                                                                                           EMBL; L02308; AAA69683.1; -.
PIR; S33624; S33624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00318; 1B33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sporulation genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACSU
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BINDING
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P45900;
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AC BACSU
DT 10-NOV
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RA Azevedo V., Bourster N., Moszer II., Alberlin A., Morchert S., Ravedo V., Bourster N., G., Bessierse P., Bolottin A., Borchert S., Borrise R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S., Borrise R., Bourster L., Caldwell B., Capbano V., Carter N.M., Chois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britan K.D., Ernigton J., Pabret C., Ferrari E., Foulger D., Antian K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Ra Eriz C., Fujita M., Prijita Y., Fuma S., Galizzi A., Galleron N., Adiseppi G., Guy B.J., Hagaa K., Halech J., Harwood C.R., Henaut A., Antibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Railbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Railbert H., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Lardinois S., Jauber J., Makai S., Noback M., Medina N., Mellado R.P., Mizuno M., Moest D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Racecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sacott A.M., Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sacott A.M., Regiuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Takeuchi M., Tamakoshi A., Taraan T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara T., Takamara P., Takamara T., Meitzenegger T., Anthers P., Wanbutt R., Wedler H., Weitzenegger T., Anthers P., Wanbutt R., Wedler H., Weitzenegger T., The Complete genome sequence of the Gram-positive bacterium Bacillus R. Thillogue.
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Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a co-operative
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PIR, B69944; B69944.
Subrilat; BG11254; yqaC.
Hypothetical protein; Signal; Complete proteome.
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Last annotation update)
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Query Match
Best Local Similarity 62.5.,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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TISSUE=Liver;
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THTR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Specifically dimethylates two adjacent adenosines in the loop of a conserved hairpin near the 3'end of 16S rRNA in the 30S particle. Its inactivation leads to kasugamycin resistance (By
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N' N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fimilarity).
SIMILARITY: Belongs to the rRNA adenine N-6-methyltransferase
family. KsgA subfamily.
                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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PIR; H83571; H83571.
HAMAP, PR. 20667; -; 1.
InterPro; IPR00137; RRNA A dimeth.
InterPro; IPR00137; RRNA A Dimeth.
InterPro; IPR00139; RanaAD; 1.
FARM; SM00550; RADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; LADC; 
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                      Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulatory protein recX. RECX OR LL2182.
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87 QGDALKFDFAS 97
                                                              dimethyltransferase).
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                                                                                                                                                                          NCBI_TaxID=287;
                                                                                       KSGA OR PA0592
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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"Primary structure of avian hepatic rhodanese.";
J. Protein Chem. 9:369-377(1990)
-!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE DETOXIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%; Score 33; DB 1; Length 270; 63.6%; Pred. No. 38; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THTR_CHICK STANDARD; PRT; 289 AA.
P25524;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA; 31270 MW; 1968460506330C4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91113289; PubMed=2275748;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE006447; AAK06280.1; -.
PIR; F86897; F86897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAWAP; MF 01114; -; 1.
InterPro: IPR003783; RecX.
Pfam; PF02631; RecX; 1.
Complete proteome.
SEQUENCE 270 AA; 31270 MW
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Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ÓGKSLALÝÝIS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00586; 1RHS.
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                                                                                                                                                                                                 ö
                                                     HINGE.
RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   Tritirachium album.
Bukaryota, Fungi, Ascomycota, mitosporic Ascomycota, Tritirachium.
NCBI_TaxID=5558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and characterization of the gene encoding a novel, thermostable serine proteinase from the mould Tritirachium album
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P06873, 2PRK.

MEROSS, SOB. 054; -.

InterPro; IPR000209; Peptidase_SB.

InterPro; IPR009209; Protease inhib.

Pfam; PP00082; Peptidase_SB, I.

PRINTS; PR00723; SUBTILIASE_ASP; I.

PROSITE; PS00136; SUBTILIASE_ASP; I.

PROSITE; PS00138; SUBTILIASE_HIS; I.

PROSITE; PS00138; SUBTILIASE_HIS; I.

PROSITE; PS00138; SUBTILIASE_ER; I.

Hydrolase; Serine procease; Zymegen; Calcium-binding; Signal.
                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 4:1789-1792(1990).
-1- FUNCTION: Thermostable serine proteinase.
-1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
-1- SIMILARITY: Belongs to peptidase family S8.
                                                                                    SIMILARITY).
BY SHVILARITY.
SUBSTRATE (THIOSULFATE) BINDING
(BY SIMILARITY).
                                                                                                                               SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 22563 / Limber;
STRAIN=ATCC 2263 / Limber;
STRAIN=91171881; PubMed=2077361;
Samal B., Karan B., Boone T.C., Osslund T.D., Chen K.K., Stabinsky Y.;
                                                                                                                                                                         Score 33; DB 1; Length 289;
Pred. No. 40;
                                                                                                                                                                                                2; Indels
                                                                                                                                                      8BFCF671DE0B2BA4 CRC64;
                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Proteinase R precursor (BC 3.4.21.-).
                                                                                                                                                                                                 1; Mismatches
PROSITE; PS00380; RHODANESE 1; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
Transferage; Mitochondrion; Repeat.
DOMAIN 24 142 RHODANESE 1.
                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                      289 AA; 32286 MW;
                                                                                                                                                                           57.9%;
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Best Local Similarity 66.79,
6; Conservative
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284
186
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100 GDELGTFYA 108
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172
186
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P23653;
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Berkeley Fast; TISSUE=Root;
MEDLINE=91316216; PubMed=1859865;
Lal S.K., Johnson S., Conway T., Kelley P.M.;
"Characterization of a maize cDNA that complements an enclase-deficient mutant of Escherichia coli.";
Plant Mol. Biol. 16:787-795(1991).
-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: Magnesium is required for catalysis and for stabilizing
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                      SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                               (VIA CARBONYL OXYGEN) (BY
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55;
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CALCIUM 2 (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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PROTEINASE R.
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the enolase family.
                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                               CALCIUM 2 ('SIMILARITY)
                                                                                                                                                                                                                                                                                             Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the dimer (By similarity).
-!- PATHWAY: Glycolysis.
-!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                             40926 MW;
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Pfam; PF00113; enolase; 1.
Pfam; PF03952; enolase_N; 1.
                                                                                                                                                                                                                                                                                          57.9%;
85.7%;
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HSSP; P56252; 1PDZ.
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ProDom; PD000902; Enolase; 1
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PROSITE; PS00164; ENOLASE; 1
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ENOI OR PGH1.
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387 AA;
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Best Local Similarity
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                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
ENO1_MAIZE
ID _ENO1_MAIZE
AC P26301;
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                                                                                                                                                                         Gaps
                                                                                                                            Query Match 57.9%; Score 33; DB 1; Length 446; Best Local Similarity 70.0%; Pred. No. 65; Matches 7; Conservative 0; Mismatches 3; Indels
164 164 BY SIMILARITY.
251 251 MAGNESIUM (BY SIMILARITY).
302 302 MAGNESIUM (BY SIMILARITY).
329 329 MAGNESIUM (BY SIMILARITY).
446 AA, 48063 MW, 6266C48914F35198 CRC64;
    ACT_SITE
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282 GDSLKDLYKS 291 2 GDSLKTYYAS 11 g ò

Search completed: September 24, 2004, 01:55:13 Job time : 14.1321 secs

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Sequence:

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Searched:

Database

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025734 plasmodium 0816495 plasmodium 081495 plasmodium 025733 plasmodium 025733 plasmodium 025733 plasmodium 0816573 plasmodium 0816573 plasmodium 081786 plasmodium 090786 plasmodium 090786 plasmodium 090786 plasmodium 081260 plasmodium 081567 plasmodium 081567 plasmodium 081786 thermoanaer 097784 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 methanosarc 097774 plasmodium 097777 arabidopsis 079777 arabidopsis 079777 preudomonas 09777 plasmodium 09778 arabidopsis 09886 fagus sylva 09758 trichoderma 081717 preudomonas 081716 pseudomonas 081716 pseudomonas 081717 trichoderma 081777 trichoderma 081777 trichoderma 081777 trichoderma 081778 paenibacilla 07775 paenibacilla 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07795 caenorhabd 07
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QBde36 vibrio vuln
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Q97bs6 thermoplasm
Q8f688 leptospira
08jk71 heliotis vi
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Q8NKZ5
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Q80UW2
Q8R7K6
Q9V554
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Q977X1
Q877X1
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Q893C4
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Q9SCD6
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Q51716
Q8RU48
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Q8DE36
Q82XF9
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QBA7T4
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Q81CU1
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Q9ND10
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09u7k1
09bjjl
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       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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TISSUE-Hodgkin lymphoma, and Mantle cell lymphoma;

Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Hansmann M.L., Brauninger R.,
"Analysis of a clonally related mantle cell and Hodgkin lymphoma
indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
cell precursor in a germinal center.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564424; CAD92031.1; -.
Hypothetical protein (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
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81.8%; Pred. No. 0.064;
ive 2; Mismatches 0; Indels
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Pred. No. 0.29;
3; Mismatches 0; Indels
                                                                                                     Foundation and the first property of the EMBL/GenBank/DDBJ databases. Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. EMBL; L43092; AAA69746.2; -. HSSP; PO1709; AAA69746.2; -. InterPro; IPR007110; Ig-like. InterPro; IPR007356; Ig-v. Fran; PF0047; ig; 1. SWART; SW00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
Rearranged V131 segment (Rearranged V131 gene segment)
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107 Aa; 11306 MW; A2B04B371B7A5F00 CRC64;
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Best Local Similarity 81.8
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QGDSLRSFYAS 14
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Best Local Similarity
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                                                                                   TISSUE=Lymphocytes;
                                                                    SEQUENCE FROM N.A.
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                                                         Q7tv69 prochloroco Q891j3 bradyrhizob Q7xa6 cynodan dac Q982a0 rhizobium la G982a0 coxiella bu Q81m12 oryza sativ Q84m12 oryza sativ Q84m5 coxiella bu Q81m12 oryza sativ Q84cr5 pseudomonas Q7xbe4 oryza sativ Q92ha9 rtomato spot Q92ha9 rtomato spot Q92ha9 arteptomyce Q98x57 streptomyce Q88x20 clostridium P79738 trichoderma Q980z6 sulfolobus Q9280z sulfolobus Q9280z sulfolobus Q9290 drosophila Q92bi Streptomyce Q85z0 fusobacteri Q82bi Satreptomyce Q85z0 fusobacteri Q82bi Satreptomyce Q85z0 fusobacteri Q88mf4 drosophila Q92bi Syrza sativ
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Q9bj18 plasmodium
Q9bj14 plasmodium
Q9bj15 plasmodium
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Q9jx89 neisseria m
Q8jx89 neisseria m
Q8zmmi streptomyce
P71871 mycobacteri
Q7twal mycobacteri
Q8g659 bifidobacte
Q3g60 gapevine v
Q9z1x8 rattus norv
Q8lbwl arabidopsis
O24901 helicobacte
Q9zn04 helicobacte
Q8c579 mus musculu
O67537 aquifex aeo
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Q970n5 sulfolobus
Q9cjt9 pasteurella
Q7vf65 helicobacte
                                                28w643 bacteriopha
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Q8LMD5
Q9HMD2
Q9HM12
Q8CKS
Q7KBE4
Q92HA9
Q9ZKB4
Q9ZKB6
Q9ZKB6
Q9ZKB6
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Q9NSD6 ID Q9NSD6 AC Q9NSD6; DT 01-0CT-2000 ( DT 01-0CT-2000 (

107 AA

PRELIMINARY;

RESULT 1

RESULT 3 096405 ID 09 AC 09

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Vose T.S., Thompson J.K., Waterkeyn J., Felger I., Weiss N.,
Cowman A.F., Beck H.P.;
Cowman A.F., Beck H.P.;
Genomic distribution and functional characterisation of two distinct
and conserved Plasmodium falciparum var gene 5' flanking sequences.";
Mol. Biochem. Parasitol. 107:103-115(2000).
EMBL; AF050740; AAC05220.1; -.
EMBL; AF050740; AAC05220.1; -.
EMBL; PT14602; T14602.
GO; GO:0009405; P:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004289; P:PEMP.
Pfam; PF03011; PFEMP.
Pfam; PF03011; PFEMP.
NON TER 2135 2135
SEQÜENCE 2135 AA; 242712 MW; C42CEBOC32F4A36F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE=99404835; PubMed=10477185; MEDIJNE=99404835; PubMed=10477185; Mard C.P., Clottey G.T., Dorris M., Ji D.-D., Arnot D.E.; Maniyais of Plaemodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Blochem, Parasitol. 102:167-177(1999).

EMBL; AF127315; AAD527951; -.
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NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 24;
2; Mismatches 0; Indels
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Pred. No. 2.9;
3; Mismatches 0; Indels
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55 AA; 6259 MW; 4DDB2C769853F649 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=20183858; PubMed=10717306;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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160 EGDSIKTYY 168
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31 EGESIKTYY 39
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                      Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                   Score 44; DB 5; Length 161;
Pred. No. 1.5;
2; Mismatches 0; Indels
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                                                                                                                                                                      falciparum parasites.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ29510; CAD22362.1;
Hypothatical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 192
192 AA; 22196 MW; 022557CE5559DC4C CRC64;
                01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
Erythrocyte membrane protein 1 (Fragment).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Variant-specific surface protein (Fragment).
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Last annotation update)
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77.8%;
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
01-MAY-1999 (TrEMBLrel. 10,
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43 EGDSIKTYY 51
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Kirchgatter K., Mosbach R., del Portillo H.A.;
"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
from central Brazil.";
Exp. Parasitol. 95:154-157(2000).
EMBL; AF172801; AAF89791.1; -.
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"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
from central Brazil.";
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 6.4;
3; Mismatches 0; Indels
                                                                                                        Length 60;
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7010 MW; FF173327A53AC20A CRC64;
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72 AA; 8198 MW; 715D9AD0DE2D5785 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Variant surface protein (Fragment).
Plasmodium falciparum.
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Last annotation update)
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Pred. No. 5.1;
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0C-2001 (TrEMBLrel. 19, Last ann
Variant surface protein (Fragment).
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MEDLINE=20372615; PubMed=10910718;
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MEDLINE=20372615; PubMed=10910718;
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EMBL; AF172803; AAF89793.1; -.
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ilarity 66.7%;
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ilarity 66.7%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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EGDSIKTHY 44
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Q9ND13;
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SEQUENCE FROM N.A.
MEDLINE=99404835; PubMed=10477185;
WARDLINE=99404835; PubMed=10477185;
WARD C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences.";
MOI. Biochem. Parasicol. 102:167-177 (1999).
EMBL; AF127282; AAD52762.1; -...
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that
recombination rearranges constrained sequences.";
Mol. Biochem. Parasitol. 102:167-177(1999).
EMBL; API27755.1; -.
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NCBI_TaxID=5833;
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                              54 AA; 6050 MW; 94F71D9C1FAAD823 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Brythrocyte membrane protein 1 SD102H (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 4.5;
3; Mismatches
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66.7%;
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28 EGDSIKTHY 36
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28 EGDSIKTHY 36
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Matches 6; Conserv
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Amanatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
By George R.A., Lewis S. R. Yandell M.D., Zhang O., Chen L.X.,
By George R.A., Lewis S. R., Fichards S., Ashburner M., Henderson S.N.,
By Bandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peieifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Feankch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Beson K.Y., Benes P.V., Barman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., buller H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Burtis R.C., Busam D.A., Burtler H., Cadieu E., Center A., Chandra I.,
RA Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Goog F., Gorrell J.H., Gu Z., Gaun P., Harris M.,
RA Hostin D., Harvey D., Hehman T.J., Hernandez J.R., Heisehmann W.,
RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Heisehman D.,
Alali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei N.-H., Moshrefi A.,
Res D., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Alazon D., Moshrefi A., Moshrefi A., Moshrefi A.,
Resungton K.A., Nixon K., Nussern D.,
Res Rout S.M., Wod M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
Ra Balazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Alliams S.M., Woodeage T., Worley K.C., Wu D., Yang G., Zho Q., Zheng L.
Wellson D.R., Worley K.C., Wu D., Yang G., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q., Zho Q.,
                                                                                                                                                           CG10745 protein.
CG32130 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly)
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Bohydroidea, Endopterygota, Diptera; Brachycera; Muscomorpha;
Bohydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%; Score 39; DB 5; Length 516; 70.0%; Pred. No. 51; ive 0; Mismatches 3; Indels
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GO, GO:0005515; F:protein binding; IEA.
                                                                                                          Last sequence update)
Last annotation update)
516 AA.
                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
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                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                        01-MAY-2000 (TrEMBLrel. 13,
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hes 7; Conservative
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   PRELIMINARY;
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SEQUENCE 516 AA; 55
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EMBL, AF050739; AAC05219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 5; Length 179;
Pred. No. 16;
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MEDLINE=99404835; PubMed=10477185;
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PfEMP-1/var genes sugg
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                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Erythrocyte membrane protein 1 SD105E (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Variant-specific surface protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombination rearranges constrained sequences.";
Mol. Biochem. Parasitol, 102:167-177(1999).
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 19, Last ann
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144 EGDSIKTHY 152
                                         :|||:||:|
40 EGDSIKTHY 48
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ramantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Amanatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Worten J.E., Yandell M.D., Zhang Q., Chen L.X., Randon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Fefeiffer B.D., RA Adams M.D., Called G., Walson C.R., Miklos G.L.G., Randon R.C., Backer E.G., Helt G., Walson C.R., Miklos G.L.G., Randon R.C., Backer E.G., Helt G., Walson C.R., Miklos G.L.G., Randon R.M., Baul A., Barendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Baul B., Bhandari D., Bolshakov S., Ballew R.M., Baul B., Blander G., Glamkov C., Blokin D., Botchan M.R., Bouck J., Burkler H., Cadieu E., Center A., Chadra I., Ra Cerler B., Davies P., L., Dong C., Ways A.D., Deu I., Dietz S.M., A Grayley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Hostin D., Houston K.A., Hewland T.J., Wei M.-H., Ibegwam C., Jullian M., Harvey D., Hehman T.J., Hermandez J.R., Harris M.L., Harvey D., Hehman T.J., Wei M.-H., Ibegwam C., Jullian M., McIntcoh T.C., McLeod M.P., McBherson D., Merkluv G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Nelson D.L., Reinfert R., Weinferd S., Shen H., Rainfort K., Ramington K.A., Nixon K., Nusskern D.M., Palacy C., Stanfer E., Spradling A.C., Stapleton M., Strong R., Sun E., Sanith H., Walsh R., Tector C., Turner R., Venter E., Wang A., Yen R., Wang Z.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J., Walls M., Weissenbach J., Wall M., Wei Serbeler E., Spradling A.C., Stapleton M., Stung G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q
                                                                                                                                                                                                                                              CG10745 protein.
CG310745 protein.
CG321310 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NEBI_TaxID=7227;
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Pred. No. 54;
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Pfam; PF02179; BAG; 1.
SEQUENCE 542 AA; 58776 MW; 5BC0CE3558333557 CRC64;
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GO; GO:0005515; F:protein binding; IEA.
                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                542 AA
                                                                                                                                                      Created)
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
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70.0%;
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7; Conservative
                                                                                PRELIMINARY;
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RA MEDINE-20196006; Pubbed-1073132;

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RA Adams M.D., Celniker S.E., Holt R.A., Brabiners R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Batton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Abril J.E., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Abril J.E., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Beson K.Y. Baros P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Eusam D.A., Bulke C., Davenport L.B., Daviss P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Daviss P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Jewise M. A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Adlali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Merkilov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nalson D.L.,

RA Spier E., Siden-Kiamos I., Simpson M., Stupek M., Rales M., Pillans N., Ralush R., Willen B. E., Wolfers R.D.C., Scheeler F., Schen H.,

RA Merkilov G. Milshina N.V., Mobarry C., Morris J., Mosher F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Stupek M., Wang X.,

Mount S.M., Moy M., Wurphy B., Murphy L., Murny D.M., Wang X.,

Ra Spier E., Spradling A.C., Simpson M., Stupek M., Wang X.,

Mang Z.-Y., Wassarman D.A., Wainistcok G.M., Weissenband J.,

Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,

Ra Sheng X.H., Wassarman D.A., Wallson D., Wang S., Yao Q.A.,

Ra Miliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,

Ra H. Shore S.H., Wassarman D.A., Walliams S.M., Woodage T., Stangeon M., Strong R., Shun B.,

Ra Charley S.M., Wayser B.W., Rubin G.M., Wang S., Zhu X., Smith H.O.,

Ra Charley S. Salen-Kamos I., Simpson M., Strong R., Salen S., Shore S., Shore S., Sh
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A Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.Y., Busam D.A.,
Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Diegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
T "Sequencing of Drosophila melanogaster genome.";
                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
0332130 protein (GH02003p).
0332130 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Encopprintidae; Drosophila.
                                                    609 AA.
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000)
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227,
                                                                         Q9VU81; Q95TF3
                                               Q9VU81
RESULT 16
Q9VU81
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Gaps

.. 0

3; Indels

0; Mismatches

QGQQFKTYYA 260 QGDSLKTYYA 10

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GO; GO:0003891; F:delta DNA polymerase activity; IEA.
GO; GO:0003877; F:DAA binding; IEA.
GO; GO:0003877; F:DNA binding; IEA.
GO; GO:0003877; F:DAA binding; IEA.
GO; GO:0003893; F:eta DNA polymerase activity; IEA.
GO; GO:0003895; F:eta DNA polymerase activity; IEA.
GO; GO:001599; F:eta DNA polymerase activity; IEA.
GO; GO:0016850; F:damma DNA-directed DNA polymerase activity; IEA.
GO; GO:0016450; F:happa DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:theta DNA polymerase activity; IEA.
GO; GO:0016452; F:theta DNA polymerase activity; IEA.
GO; GO:0016454; F:zeta DNA polymerase activity; IEA.
GO; GO:0016454; F:zeta DNA polymerase activity; IEA.
GO; GO:0016454; F:zeta DNA polymerase activity; IEA.
GO; GO:0016456; F:theta DNA polymerase activity; IEA.
GO; GO:0016457; P:theta DNA polymerase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
STRAIN=Malayan Camp.
STRAIN=Malayan Camp.
MEDLINE=95308012; PubWed=7541722;
Baruch D.I., Pasloske B.L., Singh H.B., Bi X., Ma X.C., Feldman M., Taraschi T.F., Howard R.J.;
Taraschi T.F., Howard R.J.;
"Cloning the P. falciparum gene encoding PfEMP1, a malarial variant intigen and adherence receptor on the surface of parasitized human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00116; DNA_POLYMERASE B; 1.
DNA replication; DNA-binding; DNA-directed DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1086 AA; 123702 MW; ACE3B2DF0E7B77FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1729 AA; 195156 MW; 7BFEEC2131FFBA11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocytes.";
Cell 82:77-87(1995).
EMB1, U27339; AAA8914.1; -.
PIR, T18396; T18396.
GO; GO:0005539; F: glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.4%; Score 39; DB 12; 77.8%; Pred. No. 1.1e+02; tive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006172; DNA_pol_B.
InterPro; IPR00613; DNA_pol_B dom.
InterPro; IPR006133; DNA_pol_B exo.
Pfam; PP00136; DNA_pol_B; 2.
Pfam; PF03104; DNA_pol_B exo; 1.
PRINTS; PR00106; DNA_Pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
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ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 77.8% les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03011; PFEMP; 2.
NON TER 1729 1729
SEQUENCE 1729 AA: 1057
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Q25734;
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Matches
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                                                                      8888888888888888
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"Evolution of Ascoviruses from Iridoviruses."
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CAȚALYȚIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                         Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman E., Garlson J.W., Celniker S.E.,
Tupy J.L., Bergman E., Garlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B.; Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR059435; AAL13341.1;
EMBL; AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
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ENBLE, AX059435; AAL13341.1;
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ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; AAL13341.1;
ENBLE, AX059435; ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENBLE, ENB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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NCBI_TaxID=113368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 5; Length 609;
Pred. No. 61;
0; Mismatches 3; Indels
         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65965 MW; A035C54287E9C354 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0006915; P:apoptosis; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 22, Last annotation update)
Delta DNA polymerase (EC 2.7.7.7).
Heliotis virescens ascovirus 3c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1086 AA
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70.0%;
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Best Local Similarity 70..
Best According 70..
Conservative
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Pfam; PF02179; BAG; 1.
SMART; SM00264; BAG; 1.
SEQUENCE 609 AA; 65965
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QGDSLKTYY 9

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150 EGDSIKTHY 158
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Plasmodium falciparum.
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SEQUENCE FROM N.A.
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EMBL, AL844509; CAD52143.1; -...

GO; GO:0005339; F:glycosaminoglycan binding; IEA.

GO; GO:0005405; P:pathogenesis; IEA.

InterPro; IPR004258; PFEMP.

PFam; PF03011; PFBMP; 2.
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AL031747; CAB892091;
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0009812; P:matabolism; IEA.
InterPro; IPR004055; P:pathogenesis; IEA.
InterPro; IRR004258; PFEMP.
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 2.4e+02;
3; Mismatches 0; Indels
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2163 AA; 245805 MW; FSF7AC66BE2ABC09 CRC64;
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                                                                                                                                                                                                                                                Created)
Last sequence update)
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                                                                                                                                                                                           PRT; 2162 AA
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01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-CT-2003 (TrEMBLrel. 25, 01-OCT-2003)
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Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                       PRELIMINARY;
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PROSITE; PS00886; ILVD E
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151 EGDSIKTHY 159
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150 EGDSIKTHY 158
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es 6; Conserv
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MEDLINE=2225708; PubMed=12368867;
MEDLINE=2225708; PubMed=12368867;
MIDGAINE=2225708; PubMed=12368867;
MIDGAINE=2255708; PubMed=12368867;
MIDGAINE, Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherwach I., Chillingworth C.,
Crolin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Crolin A., Davies R., Goodhead I., Gailliam R., Hamlin N., Hance Z.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
Squares S., Craig A., Newbold C., Barrell B.G;
Squares C., Paragold C., Barrell B.G;
M., Schenen C., Elsamodium falciparum chromosomes 1, 3-9 and 13.";
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Devlin K., Baker S., Davies P., Mungal K., Berriman M., Fain A.,
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                        Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
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SEOUENCE 2207 AA; 251407 MW; 44CD679B3D2FCE24 CRC64;
                                                                              01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Erythrocyte membrane protein 1 (PfEMP1).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
PfEMPI variant 1 of strain MC.
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2207 AA
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                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004258; PFEMP.
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MEDLINE=95330812; PubMed=7541722;
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66.7%;
   PRELIMINARY;
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Best Local Similarity 66.7
Matches 6; Conservative
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendal J., Bayraktaroglu L., Beasley E.M.,
Ralew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Downes M., Dugan-Rocha S., Pleischmann W.,
R Posler C., Gabriellan A.E., Garg M. S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rak Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                 MEDLINE=99404835; PubMed=10477185; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; Malysis of Plasmodium falletiparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Blochem. Parasitol. 102:167-177 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                    54 AA; 5986 MW; 43552A60661F4D71 CRC64;
                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Erythrocyte membrane protein 1 SD102G (Fragment).
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Last annotation update)
                                        54 AA.
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
60.0%;
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Best Local Similarity 60.0
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28 EGDSIRGYYA 37.
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                                        09U7K6
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                       29U7K6
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Baruch D.I., Pagloske B.L., Singh H.B., Bi X., Ma X.C., Feldman M., Taraschi T.F., Howard R.J.;
"Cloning the P. falciparun gene encoding PfEMP1, a malarial variant antigen and adherence receptor on the surface of parasitized human
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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K -> N.

S -> T.

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                                                                                                                                     GO, GO:0005499; F:electron transporter activity; IEA.
GO; GO:0005539; F:electron transporter activity; IEA.
GO; GO:000539; F:glycosaminoglycan binding; IEA.
GO; GO:000618; P:electron transport; IEA.
InterPro; IPR000405; P:electron transport; IEA.
InterPro; IPR000455; CytC heme_BS.
InterPro; IPR004258; PFEMP.
PROSITE; PS00190; CYTOCHROME_C; 1.
VARIANT 104 104 S -> T.
VARIANT 105 105 E -> K.
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Last annotation update)
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Cell 82:77-87(1995).
EMBL; U27338; AAB60251.1; -.
PIR; T18378; T18378.
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151 EGDSIKTHY 159
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915 QGDDIKTYF 923
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SEQUENCE 9271 AA; 1
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658 65
722 72
2924 AA;
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskren D.R., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskren D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskren D.M., Pacled J.W.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
She B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Nusskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Nulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A p.J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou S., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Cience 297:2185-2195(2000).
R EMBL, AE003642; AAF533771; -.
R EMBL, AE003642; AAF533771; -.
R EMBL, AEBONO40977; CG15292.
SEQUENCE 56 AA; 5926 MW; ECFE0402469F031C CRC64;
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Best Local Similarity 63.0.
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Search completed: September 24, 2004, 02:18:24 Job time : 61.717 secs

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NCBI_TaxID=9606;
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Q6GMW4
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099u7k5
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Q9vu81
Q704x8
Q704x9
Q8jk71
Q25734
Q8iev1
Q9nfb6
Q8i495
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021984
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                               1612378 segs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
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57
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0811f1
0811f1
0800W5
       Q7pv90
025470
                                          O7WU96
FBX2 MOUSE
Q8R7K6
       Q7FV90
Q25470
Q25162
WPR2 YEAST
Q6B264
Q62ES3
Q63YA8
Q81LF1
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## ALIGNMENTS

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80.78;
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44 EGDSIKTYY 52
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
Home sapiens This EMBLrel. 26, Last annotation update)
Home sapiens This CDS feature is included to show the translation of the corresponding V region. Presently translation qualifiers on V_region features are illegal. (Fragment)
                                                                                                                                                                                                                                                              Gaps
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SEQUENCE FROM N.A.
TISSUE-Hodgkin lymphoma, and Mantle cell lymphoma;
Tinguely'M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                              0; Indels
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 143092; AAA69746.2; -.
PIR; S70444, S70444.
HSSP; P01709; 2MCG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SM00406; IGV; 1.
SMART; SM00407; IGC1; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 2.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

Hypochetical protein:

SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA; 11306 MW; A2B04B371B7A5F00 CRC64;
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2004 (TrEMBLrel. 27, Last annotation update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Rearranged V131 segment (Rearranged V131 gene segment)
                                                                                                                                                                                                   Score 54; DB 2;
Pred. No. 0.026;
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                                                                                                                                                                                                                                                                                                                                                       42 QGDSLRTYYAS 52
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21 QGDSLRSYYAS 31
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SEQUENCE FROM N.A.
MEDLINE=22030713; PubMed=12034453; DOI=10.1016/S0166-6851(02)00038-5;
Fernandez V., Chen Q., Sundstroem A., Scherf A., Hagblom P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.2%; Score 44; DB 2; Length 161; 77.8%; Pred. No. 1.7; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          Length 81;
Hansmann M.L., Brauninger A.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ564423; CAD92031.1; -.
BMBL; AJ564424; CAD92031.1; -.
HSSP; P01709; IDCL.
HRSP; P01709; IDCL.
InterPro; IPR001710; Ig-like.
InterPro; IRR001596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Q., Wahlgren M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF039281; AAD02164.1; -.
NON TER 161 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AA; 19005 MW; 164F7D8D9E1AE384 CRC64;
                                                                                                                                                                                                                                                                                                        CFF1D4666B794C9F CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2;
Pred. No. 0.33;
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Mol. Biochem: Parasitol. 121:195-203(2002).
EMBL; AJ449510; CAD22362.1; --
Hypothetical protein.
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last ann
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MEDLINE=994494815; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
MEDLINE=9940498135; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
Maral C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences.";
Mol. Biochem. Parasitol. 102:167-177(1999).
EMBL, AFI27775; AAD52755:1.
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MEDILINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
MEDILINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
MANTA C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences.";
MMOI. Biochem. Parasitol. 102:167-177(1999).
EMBL; AF127782; AAD52762.1; -.
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Pred. No. 5.4;
3; Mismatches 0; Indels
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Pred. No. 5.4;
                                                                     DB 2; Length 55
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                                                                                                        Indels
                                  4DDB2C769853F649 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Erythrocyte membrane protein 1 SD102B (Fragment).
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66.7%;
                                  6259 MW;
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Best Local Similarity 66.7
Matches 6; Conservative
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31 EGESIKTYY 39
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MEDLINE=20183858; PubMed=10717306; DOI=10.1016/S0166-6851(00)00176-6; Voss T.S., Thompson J.K., Waterkeyn J., Felger I., Weiss N., Cowman A.E., Beck H.P.; Reck H.P.; Reck H.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDINTR=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
"Analysis of Plasmodium falciparum PEMP-1/var genes suggests that
recombination rearranges constrained sequences.";
MOI. Biochem. Parasticol. 102:167-177(1999).

EMBL, AF127315; AADS2758.1; -.

EMBL, AF127318; AADS2758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and conserved Plasmodium falciparum var gene 5' flanking sequences.";
Mol. Blochem. Parasitol. 107:103-115(2000).
BMBL; AF0507040; AAC05220.1;
PIR; T14602; T14602.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro: IPR004258; PFEMP.
Pfam; PP03011; PFEMP; 2.
NON TER 2135 2135
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WL-2004 (TrEMBLrel. 27, Last annotation update)
Erythrocyte membrane protein 1 SD126F (Erythrocyte membrane protein 1
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Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=5833;
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Pred. No. 27;
                                                                     Length 192;
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1
192
22196 MW; 022557CE5559DC4C CRC64;
                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Variant-specific surface protein (Fragment).
                                                                     Score 44; DB 2;
Pred. No. 2.1;
                                                       77.2%; Scor.
77.8%; Pred. No. 4...,
2; Mismatches
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nes 7; Conservative
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nes 7; Conservative
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160 EGDSIKTYY 168
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                                                                                                                                          1 QGDSLKTYY 9
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192 1
192 AA;
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SEQUENCE
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                                                                     Query Match
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**09TVZ4** 

RESULT 7
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MEDIJINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; "Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Biochem. Parasitol. 102:167-177(1999).
                                                                                                                                                           MEDLINE-20372615; PubMed=10910718; DOI=10.1006/expr.2000.4520;
Kirchgatter K., Mosbach R., del Portillo H.A.;
"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
                                        01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Variant surface protein (Fragment).
Plasmodium faloiparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5833;
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19;
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Pred. No. 7.6;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                 74 AA; 8410 MW; 91E750363D125C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Erythrocyte membrane protein 1, SD105E (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
74 AA.
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Pred. No. 19;
2; Mismatches
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Name=var;
Plasmodium falciparum.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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PRT;
                                                                                                                                                                                                      from central Brazil.";
Exp. Parasitol. 95:154-157(2000).
EMBL; AF172803; AAF89793.1; -.
NON TER 74 74
SEQÜENCE 74 AA; 8410 NW; 91E75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.4%;
66.7%;
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                           (TrEMBLrel. 15,
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Best Local Similarity 66.,
                                                                                                                                                                                                                                                                                                                              Local Similarity 66.7 nes 6; Conservative
PRELIMINARY;
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MEDLINE=20372615; PubMed=10910718; DOI=10.1006/expr.2000.4520;

Kirchgatter K., Mosbach R., del Portillo H.A.;

"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates from central Brazil.";

Exp. Parasitol. 95:154-157(2000).

EMBL, AF172801; AAF89791.1; -.

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SEQÜENCE 72 AA; 8198 MW; 715D9AD0DE2D5785 CRC64;
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Nogueira P.A., Wunderlich G., Tada M.S., Costa Jd.N., Menezes M.J.,
Scherf A., Pereira-da-Silva L.H.;
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Jasamodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 6;
2; Mismatches 1; Indels
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Pred. No. 7.3;
3; Mismatches 0; Indels
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60 AA; 7010 MW; FF173327A53AC20A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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28 EGDSIKTHY 36
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36 EGDSIKTHY 44
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01-JUN-2003
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"Longitudinal Assessment of Plasmodium falciparum var Gene
"Iranscription in Naturally Infected Asymptomatic Children in Papua New
Guinea.";
J. Infect. Dis. 189:1942-1951(2004).
EMBL; AY462689; AAR31929.1;
InterPro; IPR009085; Hde.
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MEDLINE=20183858; PubMed=10717306; DOI=10.1016/S0166-6851(00)00176-6; Voss T.S., Thompson J.K., Waterkeyn.J., Felger I., Weiss N., Cowman A.F., Back H.P., Mack T. Deck H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back H.P., Back
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 30;
3; Mismatches 0; Indels
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Add15285 Fruitfly
Abb63795 Drosophil
Abb63195 Human nuc
Aab40011 Anti-hill
Aau16608 Human nov
Abb10678 Human nov
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Auu16186 Human nov
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note= "Complementarity determining region (CDR)

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226. .238 /note= "Complementarity determining region (CDR) 1 of heavy chain"

Kearney PP;

Tordsson MJ,

Ohlsson LG,

Karlstroem PJ,

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26-OCT-2000; 2000WO-SE002082.
                                                                                                       (ACTI-) ACTIVE BIOTECH AB
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N-PSDB; AAF84797.
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## ALIGNMENTS

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An anti-alpha6beta4 integrin light chain linked to a heavy chain.
            AAB68087 standard; protein; 249 AA
                                    09-JUL-2001
                        AAB68087;
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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

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                                                                                                                                                                                       The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal peithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial tumour cells and trarget structure especially comprises alphasbeta4 integrin. The starget structure especially comprises alphasbeta4 integrin. This is a tumour-associated antigen. The anti-body, and its fragments, are useful for treating onnditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to tumour deposits in humans
Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
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ID ABB64583 standard; protein; 182 AA.
                                                                                                                                     Claim 1; Page 55-56; 75pp; English.
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GNNYRPS 55
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13-MAR-2003.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176 and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      odourant receptor; fruitfly; mating; repulsion; flight; insect damage; disease spread; pesticide; insect management program.
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, SEQ ID NO 20541; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.2%; Score 37; DB 4; Length 182; 100.0%; Pred. No. 61; ive 0; Mismatches 0; Indels
                                                                      Orosophila melanogaster polypeptide SEQ ID NO 20541.
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                                                                                                                                                                                                                                                                                                                                           Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD15285 standard; protein; 182 AA.
                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                           26-MAR-2002 (first entry)
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Best Local Similarity luv...
G; Conservative
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                                                                                                                pharmaceutical
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                                                                                                                                                                                                        27-SEP-2001.
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               ABB64583;
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modulate these receptors cause various behavioural responses such as mating, repulsion or flight. Accordingly, the present invention describes such compounds (both natural and synthetic) that are useful for attracting insects to traps or to localised toxins, for repelling insects from individuals or populated residential areas, or for interfering with the function of olfactory system such that insects are unable to locate food and hosts. As such, these compounds can be used to control insect damage and the spread of disease, and will significantly reduce dependence on toxic pesticides having a direct and immediate impact on coordinated insect management programs. This polypetide sequence is a brosophila melanogaster odourant receptor protein, which is homologous to the African malaria mosquito proteins of the invention.
                                                                                                                                                                                                                                                                                              This invention relates to novel Anopheles gambiae odourant receptor genes and encoded proteins thereof. Specifically, it refers to the isolated genes of the African malaria mosquito that are related to the 'classical' Drosophila odourant receptor genes, and compounds that bind to and
                                                                                                                                                                                               Novel Anopheles gambiae odorant receptor polypeptides and nucleic acid encoding the polypeptides, useful as targets for identifying pest control
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                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 37; 172pp; English.
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                                04-SEP-2002; 2002WO-US028315.
                                                               04-SEP-2001; 2001US-0317401P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                               Lee KJ, Ong J, Nguyen TT,
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                                                                                              (SENT-) SENTIGEN CORP
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                                                                                                                                                              WPI; 2003-300885/29.
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 182 AA;
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WPI; 2001-656860/75.
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Best Local Similarity
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                                                                                                                                                                      interactions.
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This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding preferences that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39772-B40063 represent anti-IL-12 CDR3 related amino acid sequences are given in AAB40064-B40067-B40064-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B40067-B400
the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity defermining region, CDR; antirheumatic; antiarthritic; antiaclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 527.
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fas P, Friedrich S, Mylee
Widom A, Elvin JG, Dunca
Holtet TL, Du Fou SL;
                                                                                                                                                                              90.2%; Score 37; DB 4; Length 930; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
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Labkovsky B, Sakorafas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warne NW,
Smith S, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB40011 standard; peptide; 7 AA
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Veldman GM, Venturini A,
Derbyshire EJ, Carmen S,
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(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                        6; Conservative
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Best Local Similarity
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                                                                                                                              Sequence 930 AA;
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Kaymakcalan
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                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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Pred. No. 2.7e+02;
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100.0%; Pred. No. ...
0; Mismatches
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06-SEP-2000;
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with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12
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                                                                                                                                                                      87.8%; Score 36; DB 3; Length 7;
85.7%; Pred. No. 1.4e+06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel secreted protein, Seq ID 1561.
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12-MAR-2000; 2000US-0186350P.
11-MAR-2000; 2000US-0189844P.
11-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0190076P.
19-MAY-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0214886P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216847P.
11-JUL-2000; 2000US-0216890P.
26-JUL-2000; 2000US-021690P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                        Sequence 7 AA;
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17-NOV-2000; 2000US-0249210P.

17-NOV-2000; 2000US-0249211P.

17-NOV-2000; 2000US-0249211P.

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17-NOV-2000; 2000US-0249245P.
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N-PSDB; AAS26595.
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Barash SC, Ruben SM;

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1561; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a laso be used in allabutating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. corplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. corneal infection, narrest, and isorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage capabilities, fat content lipid, protein, carbohydrate, vitamins, minerall secreted protein of the invention. Note: The sequence represents a novel secreted protein of the invention.

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                                                                                                                                                                              Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                     Gaps
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Score 36; DB 4; Length 201;
Pred. No. 1e+02;
1; Mismatches 0; Indels
                                                                                                         ABU55677 standard; protein; 201 AA
87.8%;
                                                                                                                                                               Human novel polypeptide #764.
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2000US-0229287P.
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2000US-0237037P
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Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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124 GSNYRPS 130
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                                        1 GNNYRPS
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                                                                                                                                                                                                                                                                                                                                                New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 1e+02;
1; Mismatches 0; Indels
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          02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-023935P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-024186P.
01-NOV-2000; 2000US-0244617P.
01-NOV-2000; 2000US-0248617P.
01-NOS-2000; 2000US-0248617P.
01-NOS-2000; 2000US-0248617P.
01-NOS-2000; 2000US-0251866P.
                                                                                                                                                                        08-DEC-2000; 2000US-0251869P
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85.7%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GSNYRPS 130
                                                                                                                                                                                                                                                                                                   WPI; 2003-147444/14.
                                                                                                                                                                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNNYRPS
                                                                                                                                                                                                                                                                                                                    N-PSDB; ABX73936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      renal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG10678;
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ABG10678
XX
AC ABG1
XX
DT 13-F
XX
XX
DD NOVE
XX
XX
KW HUMA
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COO
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HOWO
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed corivity of (II) is useful in gene therapy techniques to restore normal certivity of (II) is useful in gene therapy techniques to restore normal certivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the printed and to produce other types of data and products dependent on DNA and casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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85.7%; Pred. No. 2.2e+02;
live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOP9; member of the PAS superfamily; bHLH-PAS; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 41037; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription regulator; hypoxia.
                                                                                                                                                                                                                                                                                Tang YT;
30-MAR-2001; 2001WO-US008631.
                                                                            31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
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Best Local Similarity 85.7;
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                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                 2001-639362/73
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                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
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Claim 1; Page 102-105; 187pp; Japanese.
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                                                                                                      Sequence 588 AA;
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18-APR-2000;
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07-JUN-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                    The present sequence represents MOP9, a novel member of the PAS superfamily, where PAS stands for PER/ARNT/SIM domains. MOP9 CDNA (see AAX58980 was cloned from human brain mRNA. MOP9 displays extended homology to MOP3 (see AAX06291). It pairs with CLOCK and MOP4 (see AAX06292) and binds an E-box element with flanking region specificity. The invention provides novel MOP 2-9 nucleic acids (see AAX5891-88) and proteins (see AAX66299-97). These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOP8 are alphaclass hypoxia-inducible factors. Others are involved in circadian signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                         87.8%; Score 36; DB 2; Length 585;
85.7%; Pred. No. 2.9e+02;
iive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #4.
                                                                                                              Developmental signal transduction associated proteins
                                                             Gu YZ, Hogenesch JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                       (WISC ) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                         ABG92868 standard; protein; 588 AA.
                                                                                                                                  Claim 5; Page 106; 106pp; English
98WO-US025314.
                    97US-0066863P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001; 2001WO-JP007197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2001; 2001JP-00035743
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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GSNYRPS 124
                                                                               WPI; 1999-371120/31.
N-PSDB; AAX58988.
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                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                  GNNYRPS
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                                                                                                                                                                                                                                                                      Sequence 585 AA;
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                                                           Bradfield CA,
27-NOV-1998;
                    28-NOV-1997;
                                                                                                                                                                                                                                                  transduction
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19-NOV-2002
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                                                                                                                                                                                                                                                                                                              Matches
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ID ABG9
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The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiant; vasorropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein: rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Malbaimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                       Score 36; DB 5; Length 588;
Pred. No. 2.9e+02;
1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel secreted protein, Seq ID 1139.
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                                                                                                                                                                                                                                                                                                              87.8%;
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2000US-0184664P.
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2000US-0189874P.
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2000US-0225758P.
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2000US-0226279P.
2000US-0226681P.
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2000US-0228924P.
2000US-0229343P.
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2000US-0231244P
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2000US-0236327P.
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2000US-0230437P.
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2000US-0233063P.
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2000US-0232398P.
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2000US-0241787P.
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08-NOV-2000; 2000US-0246526P
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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23-AUG-2000;
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13-0CT-2000)
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2000US-0249213P.
2000US-0249214P.
2000US-0249215P.
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2000US-0249216P.
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2000US-0249208P.
2000US-0249209P.
2000US-0249210P.
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2000US-0249212P.
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2000US-0251030P.
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     08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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05-DEC-2000;
06-DEC-2000;
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17-NOV-2000;
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Ruben SM Rosen CA, Barash SC,

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives. WPI; 2001-488783/53. N-PSDB; AAS26173.

Claim 11; SEQ ID NO 1139; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunossays e.g. radioimmunossays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune classase e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. corneal infection, arrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. corneal infection, cardiovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypetides can also be used to aid wound healing and epithelial cell proliferation, cransplantation, for supporting cell culture of primary tissues, to transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage

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(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 591 AA;
                  29-SEP-2000;
02-OCT-2000;
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19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, ocfactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                             Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; phyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; oytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                               Gaps
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                                              Length 591;
                                    Score 36; DB 4; Length >>*
Pred. No. 2.9e+02;
                                                              1; Mismatches
                                                                                                                                            ABU55255 standard; protein; 591 AA
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2000US - 021886P
2000US - 0216880P
2000US - 0217487P
2000US - 0217487P
2000US - 0217496P
2000US - 0218290P
2000US - 0220963P
2000US - 0220963P
2000US - 0220964P
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2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
                                                                                                                                                                                                 Human novel polypeptide #342.
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2000US-0225757P.
2000US-0225758P.
                                           87.8%;
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2000US-0225267P.
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2000US-0225270P.
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2000US-0231413P.
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27-SEP-2000; 2000US-0235834P-
29-SEP-2000; 2000US-023637P-
29-SEP-2000; 2000US-023637P-
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                                                                                                                                                                               (first entry)
                                                               6; Conservative
                                                                                            124 GSNYRPS 130
                                                                                1 GNNYRPS 7
                                                     Best Local Similarity
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                                                                                                                                                                              18-MAR-2003
                                                                                                                                                                                                                                                                                        Homo sapiens.
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14-AUG-2000;
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system; lumpus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gestrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left reart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and spendicitis), allergic reactions and conditions (e.g. asthma), blood appendicitis), allergic reactions and conditions (e.g. asthma), blood infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.
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85.7%; Pred. No. 2.9e+02;
ive 1; Mismatches 0;
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                                                                02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
13-OCT-2000; 2000US-023935P.
20-OCT-2000; 2000US-024966P.
20-OCT-2000; 2000US-024186F.
20-OCT-2000; 2000US-024186F.
20-OCT-2000; 2000US-024186F.
2000US-0236370P.
2000US-0236802P.
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2000US-0251868P.
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(first entry)
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The present sequence is that of human aryl hydrocarbon receptor nuclear translocator-4 (ARNT4), a novel basic helix-loop-helix (bHLH)/PAS protein translocator-4 (ARNT4), a novel basic helix-loop-helix (bHLH)/PAS protein that is an important regulator of vascular endothelial call growth factor (VEGF) gene expression, especially in the vascular system. ARNT4

converse with endothelial PAS domain protein 1 (EPAS1, see AAY79161), comprises administering to the hypoxia responsive element of the VEGF gene. A claimed method of inhibiting angiogenesis in a mammal compound which inhibits binding comprises administering to the mammal a compound which inhibits binding comprises administering to the mammal a compound which inhibits binding comprises administering to the mammal a compound which inhibits binding comprises administering to a set vivity can also be used to regulate circadian rhythms, e.g. by forming a heterodimer with Clock, or to treat circadian rhythms, e.g. by forming a heterodimer with Clock, or to treat circadian circal and isorders. Expression of ARNT4 through the methods of gene therapy using ARNT4 bNA can be used to promote new blood vessel formation, to treat peripheral vascular disease, cerebral vascular disease, hypoxic tissue damage, coronary vascular disease, or following transient isobaemic attacks, vascular graft aurgery, balloon angioplasty, circulation
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                                                                                                    Modulation of angiogenesis in mammals, useful for treating e.g. atherosclerosis, tumors, wounds, vascular disease, hypoxic tissue damage, ischemia, balloon angioplasty, frostbite, gangrene or poor circulation.
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Pred. No. 3e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                         Claim 26; Page 31-32; 57pp; English.
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29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
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2001US-0339245P,
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                          WPI; 2000-205996/18.
N-PSDB; AAZ94062.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clock gene Baml2 and expressed clock protein BMAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aryl hydrocarbon receptor nuclear translocator-4; ARNT4; human; anglogenesis; antiatteriosclerotic; antitumour; atherosclerosis; tumour; vascular disease; vulnerary; cardiant; vascuropic; cerebroprotective; gene therapy; circadian rhythm.
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sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
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85.7%; Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 94-97; 187pp; Japanese.
                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP
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                                                                                                                                                                                                                              23-AUG-2001; 2001WO-JP007197.
                                                                                                                                                                                                                                                                                 13-FEB-2001; 2001JP-00035743
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WPI; 2002-667007/71. N-PSDB; ABS68502.

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23-AUG-2001; 2001WO-JP007197
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19-NOV-2002
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, nor other benign or precancerous lesions, e.g. atclectasis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, atchiectasis. Cor diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences the lung cancer, such as antibodies. Sequences
Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                            Gaps
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87.8%; Score 36; DB 6; Length 602;
85.7%; Pred. No. 3e+02;
                          0; Indels
                          1; Mismatches
                            6; Conservative
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Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #2. ABG92866 standard; protein; 622 AA. (first entry) (revised) |:||||| 135 GSNYRPS 141

Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

ö Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders. The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, aleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG922865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise Gaps ; Length 622; 0; Indels Score 36; DB 5; Pred. No. 3e+02; Mismatches Claim 1; Page 85-88; 187pp; Japanese. ABG92879 standard; protein; 636 AA. 87.8%; 155 GSNYRPS 161 7 1 GNNYRPS Sequence 622 AA; os field) RESULT 18 ABG92879 ò 원

BMAL2 (brain-muscle-Arnt-like protein 2)-related protein #4. 19-NOV-2002 (first entry) ABG92879;

Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.

23-AUG-2001; 2001WO-JP007197., 13-FEB-2001; 2001JP-00035743. WO200264785-A1 Unidentified 22-AUG-2002. 

Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders. WPI; 2002-667007/71. Okano T; Fukada Y,

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BWAL2 amino acid.sequences of the invention Example 1; Fig 3; 187pp; Japanese.

Sequence 636 AA;

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Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                    Human, clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
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Score 36; DB 5; Length 636;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
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Pred. No. 3.1e+02;
1; Mismatches 0; Indels
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                                                                                                   ABG92865 standard; protein; 636 AA.
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87.8%;
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169 GSNYRPS 175
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169 GSNYRPS 175
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N-PSDB; ABS68501.
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19-NOV-2002
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                                                                      BLys, B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomblatory; antirheumatic; antiAIDS; vaccine; immuno; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, mimunodeficitiency (CVID) and acquired immunodeficitency (e.g. common variable immunodeficitency and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
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Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2258-2259; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMBRIDGE ANTIBODY TECHNOLOGY.
Human BLyS binding scFv SEQ ID 1555.
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16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2001; 2001WO-US019110.
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GKNYRPS 197
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ZBC gene; zinc binuclear cluster protein;

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AAG80220;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and followed are: (II) and polyclonal matisers or a monoclonal antibody raised to infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of muchogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. Sequencing of the confenting of the confenting of the detection of drugs to treat or prevent P. falciparum. Sequencing of the confenting of proteins and many parts of the subsequent identification of proteins encoded by the complexity of the parasitic lifecycle, and a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and many parts of the world, and there is a pressing need for represent nucleotide and protein sequences given in the present cepresent nucleotide and protein sequences given in the present property or property or specifically mentioned within the
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                                 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
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Plasmodium falciparum chromosome 2 related protein SEQ ID NO:146.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
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                                                                                                                                                                                                                                                                                                                                                                Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 347-350; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum, useful as ant
diagnosis of P.falciparum infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP35687 standard; protein; 919 AA
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100.0%; Pre-
0; }
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                                                                                                                                                                                                   99WO-US026796.
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                                                                                      Plasmodium falciparum
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                                                                                                                                                                                                                                                                      HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                              VENTER J C.
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                                                                                                                           WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification
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                                                                                                                                                                                                   05-NOV-1999;
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                                                                                                                                                               1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                              Hoffman S,
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                                                                                                                                                                                                                                                                                                          (GARD/) (VENT/)
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(CARU/)
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Matches

ઠ g RESULT 22 ABP35687

XXXXXXXXX

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metabolite by a fungus. This involves modulating the expression of at least one 28C (ainc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a formulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decreased water amounts of the production, which translates into decreased in the analog in downstream processing. The sequences given the production and the secondary metabolites are suppressed to the production and the secondary metabolites are suppressed to the production and the secondary metabolites are suppressed that must be handled in downstream processing. The sequences given the secondary metabolites are suppressed to the secondary metabolites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene.
antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; ergetamine; and evastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in records ABP35575-ABP35722 represent ZBC proteins. Note: The sequer
lata for this patent did not form part of the printed specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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85.7%; Pred. No. 1e+03;
iive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published pct sequences
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                                                                                                                                                                                           insecticide; antineoplastic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GNNYLPS 136
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             WO200224865-A2
                                                                                                                                                                                                                                                                                 Unidentified
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cubypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders consupplement. (I) consider expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders considers, forenaics, gene mapping, identification of mutations of and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and canno acid sequences ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from WIPO at the celectronic format directly from W
                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 52042; 103pp; English.
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                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                        Tang YT;
                                                                                            31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73
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83 GNDYRPT 89
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                                                                                                                                                                               (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel fusion protein (I) that has, at its Neterminus, one or more epitopes that bind specifically to autoantibodies (AAb) againet the islet cell antigen IA2 and, at its C-terminus, one or more epitopes that bind specifically to autibodies (Ab) directed against the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding it, vectors containing (II) and transformed calls, are useful for diagnosis and prognosis of diabetes mellitus type I stiff-man syndrome, polyglandular autoimmune syndrome or other autoimmune conditions associated with AAb against GAD65 or IA2. (I) provides a rapid and simple antibodies against both IA2 and GAD65, simultaneously. Unlike known fusions, where the GAD65 component is at the N-terminus, (I) contains, correctly folded conformational epitopes that can react with most MICA autoantibodes. This sequence represents the human autoantibody MICA-9 variable region heavy chain used in the method of the invention
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glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome; polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65; variable region; heavy chain; MICA-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion protein, useful for diagnosis of diabetes type I and other metabolic diseases, is reactive with autoantibodies against both glutamate decarboxylase and islet cell antigen.
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food supplement; medical imaging; diagnostic; genetic disorder.
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85.7%; Pred. No. 2e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rapp I,
                                                                                                                                                                                                                                                                                       29-MAR-2001; 2001EP-00107702
                                                                                                                                                                                                                                                                                                                                                10-APR-2000; 2000DE-01017782
25-MAY-2000; 2000DE-01025840
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N-PSDB; AAI68769.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II) and the second of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a colyppeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and produce applications in colyppeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 46111; 103pp; English.
                                                                                                                                           Tang YT;
                      31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                           Drmanac'RT, Liu C,
                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS79939.
                                                                                           (HYSE-) HYSEQ INC.
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; Ouery Match 80.5%; Score 33; DB 4; Length 157; Best Local Similarity 71.4%; Pred. No. 2.8e+02; Matches 5; Conservative 2; Mismatches 0; Indels Sequence 157 AA;

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US-08-442-859-4 US-08-398-489-4

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US-08-478-039-80 US-08-476-49A-80 US-09-489-039A-12288 US-08-476-349A-108 US-08-523-894-2

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US-09-107-532A-5033

12288, A 108, App 2, Appli 2592, Ap 23, Appli 23, Appli 23, Appli 6, Appli 10, Appli 10, Appli 10, Appli 59, Appli 10, Appli 59, Appli

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US-09-252-991A-26847 US-09-543-681A-7526

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127, App 24655, A 5009, Ap 4, Appli 25610, A 20, Appl 12, Appl

8455, Ap 13394, A 4186, Ap 15, Appl

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US-09-489-039A-13394 US-09-543-681A-4186

US-09-489-039A-8455

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11, Ap 5841,

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6327, Ap 22867, A 4, Appli 4, Appli 4, Appli

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(c) 1993 - 2004 Compugen Ltd.
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| Sequence 11252, Application US/09489039A |
| Sequence 11252, Application US/09489039A |
| Sequence 11252, Application US/09489 |
| Sequence 11252, Application US/09489 |
| TITLE OF INVENTION: WICLEIC ADDIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: WIMBER: US/09/489, 039A |
| CURRENT APPLICATION NUMBER: US/09/489, 039A |
| CURRENT APPLICATION NUMBER: US/09/489, 039A |
| PRIOR PAPLICATION NUMBER: US/09/489, 039A |
| PRIOR PAPLICATION NUMBER: US/09/489 |
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| CORGANISM: Klebsiella pneumoniae |
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| CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGANISM: CORGAN
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US-09-489-039A-11409
US-09-489-039A-11409, Application US/09489039A
; Sequence 11409, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
    APPLICANT: Gary Breton et. al
    APPLICANT: Gary Breton et. al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.5%; Score 33; DB 4; Length 157; Best Local Similarity 83.3%; Pred. No. 95; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                             Score 36; DB 4; Length 602;
Pred. No. 98;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                             h 87.8%;
Similarity 85.7%;
6; Conservative
       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   |:||||||
135 GSNYRPS 141
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129 GNNYQP 134
                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                            US-09-374-454-19
   Sequence 7, Appli
Sequence 7, Appli
Sequence 188, App
Sequence 138, App
Sequence 16879, A
Sequence 16879, A
Sequence 1670, App
Sequence 50, Appl
Sequence 4670, App
Sequence 26, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 8, Appli
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Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 30121, A
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 13, Appli
Sequence 19, Appli
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Sequence 6214, Appli
Sequence 31, Appli
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US-09-543-681A-4837
US-09-543-681A-4837
US-09-294-56-7
US-09-489-847-188
US-09-489-847-188
US-09-489-037-1337
US-09-489-037-1337
US-09-540-235-3318
US-09-540-235-3318
US-09-328-352-4670
US-09-328-352-4670
US-09-328-352-4670
US-09-328-352-4670
US-09-328-352-4670
US-09-328-352-4670
US-09-328-36-318
US-09-252-991A-7777
US-09-252-991A-30677
US-09-252-991A-30677
US-09-252-991A-30677
US-09-252-991A-30677
US-09-252-991A-30677
US-09-252-991A-30121
US-09-34-901-18
US-09-34-901-18
US-09-34-901-18
US-09-34-901-18
US-09-34-901-18
US-09-34-901-19
US-08-02-36-319
US-08-02-36-319
US-08-02-36-319
US-08-02-397-885-10
US-08-02-489-319
US-08-02-489-319
US-08-02-489-319
US-08-02-489-319
US-08-02-489-319
US-08-03-397-885-10
US-08-03-397-885-10
US-08-179-481-53
US-08-179-481-53
US-08-111-202-111
       \begin{smallmatrix} 1 & 2 & 2 & 3 & 2 \\ 1 & 2 & 2 & 3 & 2 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2 & 2 & 2 & 3 \\ 2
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 Length 324;
80.5%; Score 33; DB 4; Length 32, 71.4%; Pred. No. 1.8e+02; ive 2; Mismatches 0; Indels
Query Match 80.5
Best Local Similarity 71.4
Matches 5; Conservative
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153 GNDYRPT 159
                                                          1 GNNYRPS 7
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Sequence 19, Application US/09374454

Sequence 19, Application US/09374454

Patent No. 6395548

GENERAL INFORMATION:
APPLICANT: Hee, Mu-En
APPLICANT: Haieh, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05433/037001
CURRENT FILING DATE: 1999-08-13
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: US 60/096,515
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 602

RESULT 1 US-09-374-454-19

US-08-345-321-4 RESULT 4

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSE:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                85.7%; Pred. No. 1.4e+02;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTOREY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc_feature

) LOCATION: (B) LOCATION 1...233

) SEQUENCE DESCRIPTION: SEQ ID NO: 7214:

US-09-107-532A-7214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                    Sequence 7214, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08035392; Patent No. 5484732; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                      6; Conservative
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Matches 5; Conservat
              Best Local Similarity
Matches 6; Conserv
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                                                                            1 GNNYRPS 7
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US-09-107-532A-7214
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Pred. No. 1.2e+02;
Sequence 4, Application US/08345321
Fatent No. 5914109
GENERAL INFORMATION:
APPLICANT: ZOLLA-PAZNER, SUSAN
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
NUMBER OF SEQUENCES: 22
CORRESPONDENTE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: 5725 and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT. pm
SEQ ID NO 4449
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20004
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZOLLA-PAZNER1B
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APPLICATION NUMBER: US/07/872,675
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REPERRNCE/DOCKET NUMBER: 20LL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%;
85.7%;
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INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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US-09-621-976-4449
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DB 4; Length 159;

78.0%; Score 32;

Query Match

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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08035392
Patent No. 5484732
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85.7%;
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AMINO ACID
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                               Query Match 78.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear; MOLECULE TYPE: protein US-08-035-392-4
                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 GNNSRPS 385
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                                                                                                                                                                                                                                     US-08-504-511A-2
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US-08-035-392-4
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Patent No. 5561224
GENERAL INFORMATION
APPLICANT: Rosenfeld, M. G.
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Righ & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                        APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 348;
                                                                                                                                                                                                           COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; I
Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: ED-2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/504,511A
FILING DATE: 20-JUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
TOPOLOGY: 1:-
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Best Local Similarity 85.7%;
Matches 6; Conservative (
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ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: protein US-08-035-392-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   La Jolla
: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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0
                                                   0;
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 430;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels
Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 435
ATTONREY/AGNET INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,645
TELEFRANCE/POCKET NUMBER: 36,607
TELEFRANCE/FORKEY DONCES TO NO: TELEFRANCE (619) 455-5100
TELEFRANCE (619) 455-5100
TELEFRANCE CHARACTERISTICS:
TENTORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
78.0%; Score 32; DB 1; 185.7%; Pred. No. 2.9e+02; iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE SPENSING WITH THE SOURTH STREET: 1880 Century Park East - Suite 500 CITY: Los Angeles STATE: California COUNTRY: USA
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Sequence 893, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12
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                                                                                                                                                 APPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: Mre11 Orthologue and Uses Thereof
FILE REPERENCE: 1264
CURRENT APPLICATION NUMBER: US/09/835,654
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/198,570
PRIOR APPLICATION DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Levin, Joshua Z.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Potter, Sharon L.
Megrich, Lynette M.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 4; I
Pred. No. 4.4e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/480,921B CURRENT FILING DATE: 2000-01-11 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 2.1
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Patent No. 6387637
GENERAL INFORMATION:
                                                                            US-09-835-654-2

, Sequence 2, Application US/09835654

; Patent No. 6646182

; GENERAL INPORMATION:
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ORGANISM: Arabidopsis thaliana
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
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213 GNNSRPS 219
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ORGANISM: Zea mays
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US-09-976-594-893
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709, 2005-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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              Sequence 4, Application US/08504511A
Patent No. 5561224
GENERAL INFORMATION:
APPLICANT: Rosenefeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 442;
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                                                                                                                                                                                                                                                                                                                     COMPUTER REALISTIC Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/504,511A FILING DATE: 20-JUL-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.0%; Score 32; DB 4; I
85.7%; Pred. No. 3.6e+02;
tive 0; Mismatches 1;
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Pred. No. 3.5e+02;
                                                                                                                                       JUNESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%;
85.7%;
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Best Local Similarity 85...
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-504-511A-4
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: M.catarrhalis
US-09-540-236-3486
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COUNTRY:
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0
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83.3%; Pred. No. 8.4e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.6%; Score 31; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
REALSTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION INFORMATION:
TELEFONMUICATION INFORMATION:
TELEFONMUICATION INFORMATION:
TELEFONMUICATION INFORMATION:
TELEFONMUICATION OF SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2743049CD1
US-09-976-594-893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Cooper and Dunham LLP
T: 1185 Avenue of the Americas
New York
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 893
LENGTH: 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 38, Application US/08672345C; Patent No. 5948658
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            955 GDNYRP 960
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STREET: 11
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US-08-672-345C-38
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STATE:
                                                                                                                                   TYPE: PRT
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RESULT 16 US-08-672-345C-74

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Gaps
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Sequence 74, Application US/08672345C
Patent No. 594865B
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                              COMPUTER KEALMABLE FURNI;

MEDIUW TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUN-1996
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 4.35
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 74:
SEQUENCE CHARACTER STILES:
SEQUENCE CHARACTER STILES:
TUNFORMATION FOR SEQ 1D NO: 74:
SEQUENCE CHARACTER STILES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/09214095D
; Patent No. 62800987
; GENERAL INFORMATION:
; APPLICAMY: Landry, Donald
; TITLE OF INVENTION:
; FILE REPERENCE: 51400-A-PCT-US
; CURRENT PELICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFWARE: PatentIn version 3.0
; LENGTH: 7
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Matches 5; Conservative
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-38
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                                                                                                                                                                                                                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                             75.6%; Score 31; DB 4; Length 75; 71.4%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDERC ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                    1; Mismatches
            CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 5643
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0575/51400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
FILE REFERENCE: GENSET.054PR2
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amino acid
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 109 amino acid
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MOLECULE TYPE: protein
                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  50 GNEYQPS 56
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                         1 GNNYRPS 7
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                            ; NAME/KEY: SIGNAL
; LOCATION: -15..-1
US-09-621-976-5643
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.6%; Score 31; DB 3; Length 7; 100.0%; Pred. No. 38+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4090, Application US/09621976
; Patent No. 663963
; GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glocat, S.
; APPLICANT: Glocat, S.
; TILLE OF INVENTION: ESTS and FILLE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION WIMBER: US/09/621,976
; CURRENT FILLING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
                                               Sequence 74, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5643, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobett, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                ORGANISM: Murinae gen.
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2 NNYRP 6
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US-09-621-976-4090
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              RESULT 18
US-09-214-095D-74
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LENGTH: 74
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                                                                                                                                                                                                                                                                                               TYPE: PRT
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ORGANISM: Murine
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US-09-489-039A-10928
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US-08-672-345C-93
; Sequence 93, Application US/08672345C
; Pattent No. 5948658
; GENERAL INFORMATION:
    APPLICANT: Landry Donald, W.
    TITLE OF INVENTION: AWTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper and Dunham LLP
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-214-095D-3
; Sequence 3, Application US/09214095D
; Patent No. 6280987;
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REPERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 109
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REFRENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
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ORGANISM: Murinae gen. Sp.
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Best Local Similarity
Matches 5; Conserv
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| Sequence 121, Application US/09214095D |
| Septent No. Ga0087 |
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Sequence 1139, Ap
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APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawcon, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: for Making and Using Them
FILE REFERENCE: 01-799-A
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR FILING DATE: 2001-12-21
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
SEQ ID NO 656
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ORGANISM: Homo sapiens
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NAME/KEX: SITE
LOCATION: (195)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1561
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85.7%; Pred. No. 53;
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 Length 7;
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100.0%; Score 41; DB 16;
100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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; Sequence 8, Application US/10467721
; Publication No. US20040058366A1
; GENERAL INFORMATION:
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ALIGNMENTS

RESULT 1
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Sequence 656, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene

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85.7%;
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Matches 6; Conservative
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NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 599
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Best Local Similarity 85.7-
Lange 6; Conservative
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US-10-260-708-78
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ORGANISM: Homo sapiens
US-10-121-235-19
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1139
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1139
LENGTH: 591
                                                                                                                                                           Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Publication No. US20040058366A1
GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REFERENCE: A011-15PCT
CURRENT APPLICATION UNMBER: US/10/467,721
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: JP 2001/35743
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Pred. No. 1.5e+02;
1; Mismatches 0;
                                                                                                                                                         Score 36; DB 12;
Pred. No. 1.5e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-764-864-1139
Sequence 1139, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
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85.7%;
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 PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 85.7
That 6; Conservative
                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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124 GSNYRPS 130
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121 GSNYRPS 127
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                                                     SEQ ID NO 8
LENGTH: 588
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Length 599;
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APPLICANT: Maemura, Koji
APPLICANT: Haich, Chung-Ming
APPLICANT: Haich, Chung-Ming
FILLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILLE REPERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/10/121,235
CURRENT PILING DATE: 2002-04-12
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 19
IENGTH: 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 14; Length 602;
Pred. No. 1.6e+02;
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US-10-260-708-78

Sequence 78, Application US/10260708

Publication No. US20040063101A1

GENERAL INFORMATION:

APPLICANT: Lee, Sang-Yull

APPLICANT: Lee, Sang-Yull

APPLICANT: Lee, Sang-Yull

APPLICANT: Leo, Sang-Yull

APPLICANT: Looyd

TITLE REFERENCE: L00461/70138

CURRENT FILION NUMBER: US/10/260,708

CURRENT FILION DATE: 2002-09-30

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn version 3.1

LENGTH: 602
Score 36; DB 12;
Pred. No. 1.5e+02;
1; Mismatches 0
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Pred. No. 1.6e+02;
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Publication No. US20030032609A1
GENERAL INFORMATION:
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| PUDLICARION NO. USZU03022996A1
| PUDLICARION NO. USZU04022996A1
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| CURRENT APPLICATION NUMBER: US/10/293,418
| CURRENT FILING DATE: 2002-11-27
| PRIOR APPLICATION NUMBER: 60/340,817
| PRIOR APPLICATION NUMBER: 60/340,817
| PRIOR APPLICATION NUMBER: 60/293,499
| PRIOR PILING DATE: 2001-06-15
| PRIOR PILING DATE: 2001-06-25
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-03-16
| PRIOR PILING DATE: 2001-01-17
| PRIOR PILING DATE: 2000-06-16
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Pred. No. 1
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Pred. No.
                  CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PELING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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Publication No. US20030223996A1
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; ORGANISM: Homo sapiens
US-09-880-748-1555
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Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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; ORGANISM: Homo
US-10-293-418-1555
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
  0; Indels
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Publication No. US200400583661

GENERAL INFORMATION:

APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION

TITLE OF INFURION: Bmal2, novel clock genes

FILE REFERENCE: A011-15PCT

CURRENT APPLICATION NUMBER: US/10/467,721

FRIOR TILING DATE: 2003-08-11

PRIOR FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGHH: 622
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Sequence 2, Application US/10467721

Sequence 2, Application US/10467721

Publication No. US20040058366A1

GENERAL INFORMATION:

APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION

TITLE OF INVENTION: Bmal2, novel clock genes

TITLE OF INVENTION: Bmal2, novel clock genes

CURRENT APPLICATION NUMBER: US/10/467,721

CURRENT FILING DATE: 2003-08-11

PRIOR FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 63

SOSTWARE: Patentin Ver. 2.1
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  Mismatches
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Pred. No.
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Sequence 1555, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
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6; Conservative
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CORGANISM: Homo sapiens
US-10-467-721-2
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                                                                                                   135 GSNYRPS 141
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 636
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Matches
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APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26050-709.501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              publication No. US20030180296A1
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
ITLE OF INVENTION: Acceptors
FILE REFERENCE: PFS85
CURRENT APPLICATION NUMBER: US/10/322,673
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR PLICATION NUMBER: 60/349,877
PRIOR PLICATION NUMBER: 60/369,877
PRIOR PLICATION NUMBER: 60/403,370
PRIOR PLICATION NUMBER: 60/403,370
PRIOR PLING DATE: 2002-08-15
PRIOR PLING DATE: 2002-08-15
PRIOR PLING DATE: 2002-08-15
PRIOR PLING DATE: 2002-01-13
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 51
LENGTH: 243
TAVER: DATE
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Pred. No. 2.4e+02;
0; Mismatches 1
                                                                                                        FILE KEREAGEA. 2003-10.703,434
CURRENT APPLICATION NUMBER: US/10/723,434
CURRENT FILING DATE: 2003-11-26
PRIOR PLILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR PLILING DATE: 2002-04-17
PRIOR PLILOR DATE: 2002-04-17
PRIOR PLILOR DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 10/153,176
PRIOR PILING DATE: 2003-05-20
PRIOR PRILING DATE: 2003-05-20
PRIOR PRILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin version 3.1
LENGTH: 110
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Publication No. US20030180296A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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nilarity 85.7%;
Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
Wang, Kevin C.
                         Hsieh, Mark
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US-10-322-673-51
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                                                             APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1435
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CURRENT PELLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/2928B
PRIOR PELLING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 238
LENGTH: 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 15; Length 919;
Pred. No. 5.7e+02;
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Pred. No. 5.7e+02;
0; Mismatches 1; Indels
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Sequence 1435, Application US/10369493
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Publication No. US20040077039A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application US/10723434
Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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                      US20030233675A
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
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                      Publication No. US200
GENERAL INFORMATION:
APPLICANT: Cao, Yong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-369-493-1435
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US-10-149-310-238
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US-10-723-434-53
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Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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US-10-293-418-1993
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187 GNNQRPS 193
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Sequence 1998, Application Wo. US20030659937A1

GENERAL INFORMATION:

APPLICATY: Rublen et al.

ITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION WHMBER: US/09/880,748

FILE REPLING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-25

NUMBER: OF SEQ ID NOS: 3239
                                                                                     Sequence 1993, Application US/09880748
; Bublication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/216; PRIOR APPLICATION NUMBER: 60/216; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR PRIING DATE: 2001-03-21
; PRIOR PRIING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3229
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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Pred. No. 2.4e+02;
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SEQ ID NO 1998
LENGTH: 247
TYPE: PRT
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Best Local Similarity 85.7
Matches 6; Conservative
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US-09-880-748-1993
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Best Local Similarity
Matches 6; Conserv
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GNNYRPS

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Sequence 1937, Application US/1023118

Sequence 1937, Application US/1023118

Publication No. UEGG000223986A1

APPLICATY: Ruben et al.

TITLE OF INVENTION: Anti-bodies that Immunospecifically Bind BluyS

FILES PEREBRUCE: 12232E

CURRENT APPLICATION NUMBER: 04/0233,418

FRIGH RILNG DATE: 2001-11-34

PRIOR APPLICATION NUMBER: 04/0234,48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-48

PRIOR APPLICATION NUMBER: 04/03-49

PRIOR APPLICATION NUMBER: 04/03-49

PRIOR PRIING DATE: 2010-06-15

PRIOR PRIING DATE: 2010-10-15

PRIOR PRIING DATE: 2010-10-15

PRIOR PRIING DATE: 2010-10-15

PRIOR PRIING DATE: 2010-10-15

PRIOR PRIING DATE: 2010-10-15

PRIOR PRIING DATE: 2010-13-14

PRIOR PRIING DATE: 2010-13-14

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PRIOR PRIING DATE: 2
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
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Publication No. US20030223996A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
APPLICATION NUMBER: 60/277,379
FILING DATE: 2001-03-21
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h 80.5%;
Similarity 85.7%;
6; Conservative (
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Best Local Similarity 85...
6; Conservative
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CORGANISM: Homo sapiens
US-09-880-748-2000
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                      Best Local Similarity
Matches 6; Conserv
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    Query Match
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; Beduence 1976, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
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; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
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TITLE OF INVENTION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS
FILE REPERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.2
SEQ ID NO 44
LENGTH: 247
TYPE: PRT
CORGANISM: artificial
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Pred. No. 2.4e+02;
                                                                                                                     Score 33; DB 12; Length 247; Pred. No. 2.4e+02;
                                                                                                                                                                    1; Indels
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                                                                                                                                                                    0; Mismatches
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; Sequence 44, Application US/10779461
; Publication No. US20040166544A1
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SEQ ID NO 1976
LENGTH: 248
                                                                                                                     Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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  ; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1998
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US-09-880-748-1976
                                                                                                                                                                                                                                                                 187 GNNQRPS 193
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US-09-880-748-1976
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US-US-GOV. 740-2-00.

Publication No. US20030059937A1

FURBLEARTENCE: FURBLE ALL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: FF23
CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET: 2.0
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Length 248;
Score 33; DB 10;
Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
); Mismatches 1
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION WIMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PELLING DATE: 2000-6-15

PRIOR PLING DATE: 2000-6-15

PRIOR PLING DATE: 2000-0-17

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0; Mismatches 1; Indels
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Best Local Similarity 85.7%;
Matches 6; Conservative (
; SEQ ID NO 1976
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1976
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; ORGANISM: Homo sapiens
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                                                                     September 24, 2004, 01:33:11; Search time 10.434 Seconds (without alignments) 64.534 Million cell updates/sec
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            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Oy 1 GNNYRP 6	RESULT 2 H64422 type II restriction enzyme homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000	C;Accession: H64422. C;Accession: H64422. R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, r; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	A.Authors: Kaine, B.P.: Borodovsky, M.; Klenk, H.P.; Framer, C.M.; Smith, H.O.; Woese, C. A.Authors: Kaine, B.P.: Borodovsky, M.; Klenk, H.P.; Framer, C.M.; Smith, H.O.; Woese, C. A.Itle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A.Reference number: A64300; WUID:96337999; PMID:8688087	A,Statesbion: nowizz A,Statesbion: nowinary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-222 <bul></bul>	A;Cross=references: GB:U67541; GB:L77117; NID:g2826353; PIDN:AAB98987.1; PID:g1591646; TJ C;Genetics: A;Map position: FOR915789-916457 A;Gtart codon: GTG	Query Match  Query Match  Best Local Similarity 85.7%; Pred. No. 14;  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy. 1 GNNYRPS 7	RESULT 3 S61435 metalloproteinase (EC 3.4.24) precursor - Aspergillus fumigatus C.Species: Aspergillus fumigatus C.Species: Aspergillus fumigatus C.Decies: 14-Fb-1997 #sequence_revision 13-Mar-1997 #text_change 29-Jan-1999 C.Accesion: S61435, S61436, S61450 R.Jaton-Ogay, K.; Paris, S.; Huerre, M.; Quadroni, M.; Falchetto, R.; Togni, G.; Latge, i	Mol. Microbiol. 14, 917-928, 1994 A.Tile: Cloning and disruption of the gene encoding an extracellular metalloprotease of A.Reference number: S61435; WUID:95231298; PMID:7715453 A.Accession: S61435 A.Molecule type: DNA	A;Resdiues: 1-633 <4JAT> A;Cross-references: EMBL:Z30424; NID:g458475; PID:g458476 A;Experimental source: Btrain deltai8 A;Accession: S61436 A;Accession: S61436	A;Residues: 1-633 «JAN» A;Cross-references: EMBL:230424 A;Cross-references: EMBL:230424 A;Accession: 861450 A;Molecule type: protein A;Residues: 246-276;362-371;407-416;419-428;477-488;571-588 «JAF» C;Reywords: hydrolase; metalloproteinase; zinc; zymogen F;1-18/Domain: siqnal sequence #status predicted <sig»< th=""><th>F;19-245/Domain: propeptide #status predicted <pro> F;246-633/Product: metalloproteinase #status experimental <mat> F;428,432/Binding site: zinc, catalytic (His) (active) #status predicted F;429/Active site: Glu #status predicted</mat></pro></th><th>Query Match Best Local Similarity 100.0%; Pred. No. 39; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</th><th>Cy 2 NNYRPS 7                                    </th></sig»<>	F;19-245/Domain: propeptide #status predicted <pro> F;246-633/Product: metalloproteinase #status experimental <mat> F;428,432/Binding site: zinc, catalytic (His) (active) #status predicted F;429/Active site: Glu #status predicted</mat></pro>	Query Match Best Local Similarity 100.0%; Pred. No. 39; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Cy 2 NNYRPS 7
73.2 278 2 S54352 alpha-tocoph 73.2 288 2 S68197 regulatory p 73.2 297 2 T38372 RNA binding 73.2 344 2 F86267 T604.6 prote	30 73.2 351 2 JC4752 ferrochelatase (BC 30 73.2 355 2 T30873 dNDP-glucose dehyd 30 73.2 391 2 AG2536 hypothetical prote 30 73.2 396 2 C49904 L-lactate dehydrog 30 73.2 396 2 C91189 L-lactate dehydrog 30 73.2 396 2 D8636 L-lactate dehydrog 50 73.2 396 2 D8636	30 73.2 499 2 73.237 hypothetical proce 30 73.2 516 2 JE0301 inulinase (EC 3.2. 30 73.2 545 2 T51438 hypothetical proce 30 73.2 545 2 T51438 cMP2 non-tical	30 73.2 570 2 145712 Dpp receptor SAX p 30 73.2 570 2 116373 Dpp receptor SAX p 30 73.2 570 2 116373 hypothetical prote 30 73.2 661 2 A66252 3-hydroxyacyl-CoA	30 73.2 713 2 JC5870 poly(beta-D-mannur 30 73.2 741 2 T13677 NADH2 dehydrogenas 30 73.2 984 2 A22513 mineralocorticoid	30 73.2 1153 2 A971134 Franciscosase Trafe52 30 73.2 1153 2 A97179 ATP-dependent exon 30 73.2 1235 1 VGTHMJ F7742.12 protein pr 30 73.2 1376 1 VGTHMJ F7742.12 protein r	30 73.2 1376 1 30 73.2 1677 2 30 73.2 2254 2 30 73.2 2701 2	73.2 4063 2 T42993 73.2 4101 2 T23630 70.7 13 2 PH0805 70.7 103 2 E81030 70.7 120 2 T10814	29 70.7 120 2 T18015 hypothetical prote 29 70.7 120 2 Z21648 receptor al 29 70.7 152 2 C81262 probable lipoprore 29 70.7 162 2 T40662 peripheral-type be 29 70.7 183 2 A86819 peptide methionine 29 70.7 185 2 AE131 hypothetical prote 29 70.7 185 2 AE1702 hypothetical prote 29 70.7 185 2 AE1702	70.7 191 2 F783352 NADH-depend 70.7 191 2 B70042 hypothetics 70.7 195 2 G7874 hypothetics 70.7 197 2 E72743 hypothetics	ALIGNMENTS	149635 mouse Dhal protein - mouse mouse Dhal protein - mouse mouse Dhal protein - mouse C;Species: Mus musculus (house mouse) C;Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 C;Accession: 149635 R;Shobuike, T.; Sugano, S.; Yamashita, T.; Ikeda, H. Nucleic Acids Res. 23, 357-361, 1995	:: Characterization of cDNA encoding mouse homolog of fission yeast dhp1+ gene: st ence number: 149635; MUID:95192042; PMID:7885830 saion: 149635 is: preliminary; translated from GB/EMBL/DDBJ	1.1;	Query Match 90.2%; Score 37; DB 2; Length 947; Best Local Similarity 100.0%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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A;Accession: S4552
A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-919 <SMI>
A;Coss-references: EMBL:X76078; NID:g498748; PIDN:CAA53688.1; PID:g498760
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Cross-references: SGD:S0000237
A;Cross-references: SGD:S0000237
A;Note: YBR033W
C;Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster hc
C;Keywords: DNA binding; transmembrane protein; zinc finger
F;56-89/Region: zinc finger
F;56-85/Region: zinc finger
F;408-424/Domain: transmembrane #status predicted <TMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proportetical protein 311 - diatom (Cylindrotheca fusiformis) plasmid pCF1 C; Species: Cylindrotheca fusiformis C; Species: Cylindrotheca fusiformis C; Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000 C; Accession: S2533.
C; Accession: S2533.
R; Hildebrand, M.; Hasegawa, P.; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E. Plant Mol. Biol. 19, 759-770, 1992
A; Title: Nucleotide sequence of diatom plasmids: identification of open reading frames with Reference number: S23531; MUID:92353385; PMID:1322740
A; Recente number: S23533
A; Molecule type: DNA
A; Residues: 1-311 cHIL>
A; Cross-references: EMBL:X64302; NID:g17988; PIDN:CAA45582.1; PID:g17991
C; Genetics:
                                                                 right arm of chromosome II from
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DNA Res. 5, 1-9, 1998
A;Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sopB protein - Bscherichia coli plasmids po157 and F
N;Alternate names: plasmid partitioning protein; protein B
C;Species: Bscherichia coli
C;Decies: Bcherichia coli
C;Decies: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00244; $28096; 742169
R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota,
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C;Superfamily: Cylindrotheca fusiformis plasmid pCF1 hypothetical protein 311
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0; Mismatches 1; Indels
R,Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A;Title: The complete sequence of a 33 kb fragment on the
ly identified genes and a homologue of the SC01 gene.
A;Reference number: S46551; MUID:94378725; PMID:8091864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;408-424/Domain: transmembrane #status predicted <TM1>F;482-504/Domain: transmembrane #status predicted <TM2>F;547-503/Domain: transmembrane #status predicted <TM3>F;547-320/Domain: transmembrane #status predicted <TM3>F;709-806/Domain: transmembrane #status predicted <TM5>F;790-806/Domain: transmembrane #status predicted <TM5>
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Matches 5, Conservative
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A;Cross-references: EMBL:Z35902; NID:g536247; PIDN:CAA84975.1; PID:g536248; MIPS:YBR033w
A;Experimental source: strain S288C
                                                                                                                                                        C;Species: Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: Ob-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S42894
R;Jaton-Ogay, K.; Quadroni, M.; Falchetto, R.; Togni, G.; Paris, S.; Latge, J.; Monod, M submitted to the EMBL Data Library, March 1994
A;Description: Nucleotide sequence of genomic and cDNA clones encoding an extracellular A;Reference number: S42894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable regulatory protein YBR033w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YBR0318
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #equence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S45889; S46562
R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45889
                                                                                                                        metalloproteinase MEP - Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S42894
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100.0%; Pred. No. 73;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Regidues: 1-649 <JAT>
A;Regidues: 1-649 <JAT>
A;Roross-references: EMBL: Z30424; NID:g458475; PID:g458476
C;Genetics: A;Introns: 119/3; 251/2; 588/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 6; Conservative
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NNYRPS 313
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Status: preliminary
Molecule type: DNA
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A; Accession: G71607

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ઠે 셤 A, Molecule type: DNA

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R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                             A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Stasidues: 1-491 <SIM>
A;Croses-references: GB:AE003867; GB:AE003849; NID:g9104919; PIDN:AAF82951.1; GSPDB:GN001;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.E.A.; Ferriaira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.E.; Krieger, J.E.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, M.V.; Marcio, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.J.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, A;Reference number: Asilva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombination activating protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Sep-2000
C;Accession: I51556
R;Greenhalgh, P.; Olesen, C.E.; Steiner, L.A.
J:Immunol. 151, 3100-3110, 1993
A;Fitle: Characterization and expression of recombination activating genes (RAG-1 and RACA)
A;Reference number: I51555; MUID:99389137; PMID:89376769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide methionine sulfoxide reductase [imported] - Lactococcus lactis subsp. lactis (str
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86875
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Pred. No. 82;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-520 <GRE>
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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GNNFRP 230
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A; Residues: 1-323 <MOR>
A; Cross-references: EMBL:X04619; NID:g42429; PIDN:CAA28296.1; PID:g42432
A; Cross-references: EMBL:X04619; NID:g42429; PIDN:CAA28296.1; PID:g42432
B; Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A; Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher A; Reference number: Z22068; MUID:98391744; PMID:9722640
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R,Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K. submitted to the EMBL Data Library, May 1998
A;Reference number: Z17603
A;Recession: T13113
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                    A; Residues: 1-523 <MAK>
A; Residues: 1-523 <MAK>
A; Residues: 1-523 <MAK>
A; Residues: 1-523 <MAK>
A; Cross-references: EMBL: AB011549; NID: 94589740; FIDN: BAA31791.1; PID: 93337032
A; Experimental source: strain EHEC 0157: H7, substrain RIMD 0509952
B; Mori, H.; Kondo, A.; Obshima, A.; Ogura, T.; Hiraga, S.
D; Mol. Biol. 192, 1-15, 1986
A; Title: Structure and function of the F plasmid genes essential for partitioning.
A; Reference number: A92934; MUID: 87141188; PMID: 3029390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable sopB protein - phage N15
N.Alternate names: protein gp27
S.Species: phage N15
C.Species: phage N15
C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Sep-1999
C.Accession: T13113
R.Hendrix, R.W.; Ravin, V.K.; Casiens. S.R. Ford W.F. Parl
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Mar-2003
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Pred. No. 54;
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A; Reference number: Z14127; MUID:98290540; PMID:9628576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:AF074613; PIDN:AAC70137.1
Experimental source: strain EDL933; serotype 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 2;
Pred. No. 51;
2; Mismatches
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: plasmid
C;Superfamily: parB protein
C;Keywords: DNA binding; plasmid partition
                                                          A;Status: translated from GB/EMBL/DDBJ
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-342 <HEN>
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                                                                                               A; Molecule type: DNA
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F82843
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Ob-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
Cispecies: S35541
R;Goldsborough, A.S.; Healy, L.E.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Willison Nucleic Acids Ree: 21, 127-134, 1993
A;Title: Cloning, chromosomal localization and expression pattern of the POU domain gene A;Reference number: S35541; MUID:93181164; PMID:8441607
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C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
C;Keywords: alternative splicing: DNA binding; homeobox; nucleus; transcription regulatic
F:183-250/Domain: POU domain homology <POU>
F:275-331/Domain: homeobox homology <HOX>
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N;Alternate names: Skn-1a
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Dec-1997
C;Accession: A46216
R;Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearse II, R.V.; Singh, H.; Rosenfeld, M.(
                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Neurospora crassa
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Accession: 149791
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A; Reference number: 225022
A; Reference number: 225022
A; Status: preliminary
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A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 1; Length 403;
Pred. No. 1e+02;
0; Mismatches 1; Indels
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                                           Indels
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                                               7;
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Pred. No. 88;
1; Mismatches
   Pred. No. 87;
0; Mismatches
       85.7%; Pred. No.
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85.7%;
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83.3%;
                                           6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                    297 ĠNNSRPS 303
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Best Local Similarity
Matches 6; Conserv
Best Local Similarity
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A; Residues: 1-349 <SCH>
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A;Molecule type: mRNA
A;Residues: 1-403 <GOL>
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               A.Reference number: A86625; MUD:21235186; PMID:11337471
A.Steation: F86875
A.Status: preliminary
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A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A.Status: A
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
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A;Cross-references: GB:L23863; NID:g393221
A;Cross-references: GB:L23863; NID:g393221
C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
C;Reywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
P;101-168/Domain: POU domain homology <POU>
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Science 260, 78-82, 1993
A;Title: Skn-la and Skn-li: two functionally distinct Oct-2-related factors expressed in A;Reference number: A46216; MUID:93219836; PMID:7682011
A;Accession: B46216
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R;Lin, X.; Tang, J.
J. Biol. Chem. 265, 1990
A;Title: Purification, characterization, and gene cloning of thermopsin, a thermostable A;Reference number: A35009; MUID:90110209; PMID:2104843
A;Reference number: A35009
A;Retus: preliminary
A;Status: preliminary
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A;Cross-references: GB:AE005176; PID:g12725052; PIDN:AAK06104.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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Species: Sulfolobus acidocaldarius
Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 03-Jun-2002
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A; Status: preliminary; not compared with conceptual translation
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A)Cross-references: GB:J05184; NID:g152940; PID:g152941
C;Superfamily: Sulfolobus acidocaldarius thermopsin
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: pmsk
C;Superfamily: peptide methionine sulfoxide reductase
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Pred. No. 85;
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Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conserv
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hypothetical protein T4121.13 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: P96491 (Spacesion: Powar, R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Anthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker; M. Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome lof the plant Arabidopsis.

A.Title: Associated that Arabidopsis.
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C;Dacte: 24-May-2001 #text_change 03-Aug-2001
C;Dacte: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90564
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acida Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein MYPU 4220 [imported] - Mycoplasma pulmonis (strain UAB
   A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: H84862
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A;Cross-references: GB:AL445566; PID:g14089836; PIDN:CAC13595.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
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                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-564 cSTC>
A;Cross-references: GB:AE002093; NID:g3763926; PIDN:AAC64306.1; GSPDB:GN00139
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Pred. No. 1.3e+02;
1; Mismatches 0;
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Pred. No. 1.3e+02;
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83.3%;
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83.3%;
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A;Molecule type: DNA
A;Residues: 1-530 <STO>
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A, Map position: 2
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Best Local S:
Matches 5,
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Best Local 8
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hypotherical protein At2943170 [imported] - Arabidopsis thaliana
hypotherical protein At2943170 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #8680
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Benito, N.S.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nalternate names: Epoc-1 protein; POU domain protein Oct-11; POU-domain transcription in Sispecies: Mus musculus (house mouse)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Accession: JC2002; S09239
G;Accession: JC2002; S09239
G;Accession: J. Y.; Yamamoto, A.; Shiku, H.; Kishimoto, T.; Kikutani, H.
A;Yukawa, K.; Yasuti, T.; Yamamoto, A.; Shiku, H.; Kishimoto, T.; Kikutani, H.
A;Title: Epoc-1: A POU-domain gene expressed in murine epidermal basal cells and thymic
A;Reference number: JC2002; MUID:94040806; PMID:8224904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
K;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;183-250/Domain: POU domain homology <POU>
F;275-331/Pomain: homeobox homology <HOX>
                                        Oct-2-related factors expressed in
                                                                                                                                                                                                                                                                                                  domain homology
transcription regulati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor Oct-11, long splice form - mouse N;Alternate names: Epoc-1 protein; POU domain transcription
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A;Residues: 200-318 <GOL>
A;Cross-references: BMBL:X51960; NID:g53464; PIDN:CAA36219.1; PID:g930192
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A;Note: sequence extracted from NCBI backbone (NCBIP:128572)
S,Superfamily: transcription factor Oct-2; homeobox homology; POU C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; F;183-250/Domain: POU domain homology <POU>F;275-331/Domain: homeobox homology <POX>
                                                                                                                                       A; Status: preliminary; not compared with conceptual translation
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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Science 260, 78-82, 1993
Afritle: Skn-1a and Skn-1i: two functionally distinct Ox
A;Reference number: A46216; MUID:93219936; PMID:7682011
A;Accession: A46216
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85.7%; Pred. No. 1.1e+02;
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85.7%;
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Matches 6; Conservative
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A; Residues: 1-430 <AND>
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A; Residues: 1-431 <YUK>
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78.0%; Scor. 83.3%; Pred. No. 1...

5; Conservative

33 NNYRPT 38

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2 NNYRPS 7

Query Match Best Local Similarity Matches 5; Conserv

A; Genetic code: SGC3

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Disobable Athila retroelement ORF1 protein [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dacession: E84475
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffert, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.N. Nature 402, 761-768, 1999
A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: MRE11
C;Superfamily: double-strand break repair protein MRE11; phosphoesterase core homology
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C;Genetics:
Mrell protein homolog [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-0ct-2000 #sequence_revision 24-0ct-2000 #text_change 15-Sep-2003 C;Accession: T52564 C;Accession: T52564 A;Hartung, F. Sabal Data Library, July 1999 A;Reference number: Z26116 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: T52564 A;Accession: 
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A,Molecule type: DNA
A,Residues: 1-750 <STO>
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A, Map position: 2
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tibonuclease II [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. ptc 7120
C;Species: Nostoc sp. etrain PCC 7120
C;Accession: AB2362
C;Accession: AB2362
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Accession: AB2362
A;Status: preliminary
A;Molecule type: DNA
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Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1857
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                                                                                                                           Score 32; DB 2; Pred. No. 1.4e+02;
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Query Match Best Local Similarity 71.4%, Them 5; Conservative

A;Gene: all4450

A; Residues: 1-686 < KUR>

|| |:|| GNTYKPS 58

1 GNNYRPS

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Score 32; DB 2; Length 750;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                83.3%;
  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                     2 NNYRPS 7
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Search completed: September 24, 2004, 01:54:28 Job time : 15.434 secs

A;Residues: 1-692 «KUR» A;Cross-references: GB:BA000019; PIDN:BAB72363.1; PID:g17129750; GSPDB:GN00179

A;Status: preliminary

A; Molecule type: DNA

A, Experimental source: strain PCC 7120 C, Genetics: A, Gene: all0405

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Gaps

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Query Match 78.0%; Score 32; DB 2; Length 692; Best Local Similarity 83.3%; Pred. No. 1.7e+02; Matches 5; Conservative 1; Mismatches 0; Indels

373 GNDYRP 378

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
             Copyright
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OM protein - protein search, using sw model

April 28, 2005, 17:57:45; Search time 52.7188 Seconds (without alignments) 51.354 Million cell updates/sec Run on:

US-10-088-639A-2_COPY_49_55

Perfect score:

41 1 GNNYRPS 7 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

## SUMMARIES

AAU16186	ייי	7.8 588 5
ABU55255 ABG92867 ABAY79162 ABU56486 ADK52095 ADK14096 ABG928666 ABG9286665	20022222222222222222222222222222222222	6 6 0 2 2 2 2 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3

Add58094 Reg IV-ep Adp96371 Single ch Adp96371 Single ch Adp96371 Single ch Adp1878 Bacterial Adp11878 Bacterial Adg9120 Human aut Adg9138 Amino aci Abg21683 Novel hum Abg1575 Novel hum Abg21677 Novel hum Abg21671 Novel hum Abg21671 Novel hum Abg21671 Novel hum Abg21671 Novel hum Abg21671 Novel hum Abg21661 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21667 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21666 Novel hum Abg21666 Novel hum	Novel Novel Novel Human (
AD158094 ABP45544 AD695371 AAD18288 AD78288 AD78288 AD78288 AD791421 AAG80220 AD691398 ABG21572 ABG21572 ABG21677 ABG21677 ABG221677 ABG21701 ABG21701	ABG106/6 ABG04022 ABG24588 AAO31145
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#### ALIGNMENTS

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canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
                                              Canine immunoglobulin light chain variable domain CDR2 peptide 58
                                                                antiallergic, allergy, IgE, gene therapy, complementarity determining region, CDR2.
          ADM09121 standard; peptide; 7 AA.
                                  (first entry)
                                   20-MAY-2004
                       ADM09121;
RESULT 1
      ADM09121
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Canis familiaris. WO2003060080-A2.

24-JUL-2003.

20-DEC-2002; 2002WO-US041362.

21-DEC-2001; 2001US-0344874P.

(IDEX-) IDEXX LAB INC.

Lawton R; Guo H, Aiyappa A, Krah ER,

WPI; 2003-598521/56.

New canine heavy and light chain variable domain polypeptides, useful for treating canine allergy.

Disclosure; Page 24; 130pp; English.

The invention relates to a novel canine heavy or light chain variable domain polypeptide. The protein of the invention demonstrates antiallergic activity and may be useful for treating canine allergy, possibly via externer. The current sequence is that of a canine immunoglobulin light chain variable domain complementarity determining region (CDR) peptide of the invention.

Sequence 7 AA;

Gaps ; 0 Length 7; Indels Query Match 100.0%; Score 41; DB 7; Le Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0;

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They are useful for treating human metastatic and malignant disease, for in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                         tumour deposits in
                                                                              Sequence 249 AA;
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ABB64583
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    'note= "Complementarity determining region (CDR) 1 of the

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                                                                                                                                                                 Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                              An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                                                                                                                                                                       "Complementarity determining region (CDR)
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                                                                             AAB68087 standard; protein; 249 AA.
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note= "linker"
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N-PSDB; AAF84797.
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              GNNYRPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Score 41; DB 4; Length 249;
Pred. No. 20;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 20541
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100.0%; Score 41; 100.0%; Pred. No.
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                                                                                                                                                                  ABB64583 standard; protein; 182 AA
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
interactions.
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                               7; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; ABL08686.
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Query Match
Best Local Similarity
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1 GNNYRP 6

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heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alpha6beta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-anglogenic mechanism in humans.

The present sequence represents a Monkey antibody light chain linked to a

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(first entry)
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       26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and encoded proteins thereof. Specifically, it refers to the isolated proteins thereof. Specifically, it refers to the isolated brosophila odourant receptor genes, and compounds that bind to and modulate these receptors cause various behavioural responses such as mating, repulsion or flight. Accordingly, the present invention describes such compounds (both natural and synthetic) that are useful for attracting insects to traps or to localised toxins, for repelling insects from individuals or populated residential areas, or for interfering with the function of olfactory system such that insects are unable to locate food and hosts. As such, these compounds can be used to control insect damage and the spread of disease, and will significantly reduce dependence on toxic pesticides having a direct and immediate impact on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Anopheles gambiae odorant receptor polypeptides and nucleic acid encoding the polypeptides, useful as targets for identifying pest control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coordinated insect management programs. This polypeptide sequence is a
Drosophila melanogaster odourant receptor protein, which is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to novel Anopheles gambiae odourant receptor genes
                                                                                                                                                                                                                                                                                                                        odourant receptor; fruitfly; mating; repulsion; flight; insect damage; disease spread; pesticide; insect management program.
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                                                                                                                                                                                                                                                                             Fruitfly odourant receptor protein (SeqId 37).
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 37; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kloss B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB63795 standard; protein; 865 AA.
                                                                                                                                      ADD15285 standard; protein; 182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2001; 2001US-0317401P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nguyen TT,
                                                                                                                                                                                                                                   15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SENT-) SENTIGEN CORP.
||||||
GNNYRP 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003020913-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2003
                            134
                                                                                                                                                                                      ADD15285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents.
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Matches
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ADD15285
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ABB63795
ID ABB6
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AC ABB6
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                  Drosophila, developmental biology, cell signalling, insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 18177; 21pp + Sequence Listing; English
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Drosophila melanogaster polypeptide SEQ ID NO 18177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 4; Le
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU53195 standard; protein; 930 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWD,
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                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                  Drosophila melanogaster.
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This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, neutralising antibody, interleukin-12; IL-12; antiinflammatory, complementarity determining region, CDR; antirheumatic; antiarthritic; antisolarotic; neuroprotective; antigoriatic; antiasthmatic; cardiant, antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duncan AR;
                                                                                                                                               Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 527.
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Labkovsky B, Sakorafas P, Friedrich S, My
Lurbin A, Warne NW, Widom A, Blvin JG, D
Carmen S, Smith S, Holtet TL, Du Pou SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                               90.2%; Score 37; DB 4; Length 930; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 Example III; Page 809; 1095pp; English.
                                               (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB40011 standard; peptide; 7 AA.
99US-0149499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-2000; 2000WO-US007946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0126603P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n Z, Labroca,
I, Venturini A, I
E.T. Carmen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI ) BASF AG.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roguska M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-638250/61.
                                                                                                               WPI; 2001-327840/34.
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Best Local Similarity
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Veldman GM, Vent
Derbyshire EJ, (
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 930 AA;
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18-AUG-1999;
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                 28-SEP-1999;
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                                                                                   Wiemann S;
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New human antibody specific for human interleukin-12 (IL-12) used

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This invention relates to a new human antibody specific for human conterleukin-12 (IL-12). The invention also includes antigen binding contents that bind to IL-12. Sequences ABB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences. And also includes variable region antio acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39517-B39570 represent anti-IL-12 CDR3 related amino acid sequences AAB39517-B39771 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAC61062-CC G1071. The antibody of the invention is a neutralising antibody and has antibacterial and immunosuppressive activity. The antibodies or antigence antibacterial and immunosuppressive activity. The antibodies or antigence in the detrimental releases of human IL-12, especially Crohn's disease, multiple sclerosis and rheumacoid arthrities. They can also be used in the antibodies construction of a pharmacoutical composition to treat human IL-12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; carebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; cerebral ischaemia; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative; optiferation; skin ageing; food additive;
treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 3; Length 7;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel secreted protein, Seg ID 1561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU16608 standard; protein; 201 AA.
                                                         Claim 33; Fig 2G; 377pp; English
                     disease and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20000S-0184664P
20000S-0184664P
20000S-018464P
20000S-0189874P
20000S-0190076P
20000S-0190176P
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85.7%;
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Best Local Similarity
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1 GNDYRPS
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16-MAR-2000;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
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28-JUN-2000; 2000US-0216486P.
30-JUN-2000; 2000US-0216486P.
07-JUL-2000; 2000US-0216486P.
11-JUL-2000; 2000US-0216486P.
11-JUL-2000; 2000US-0216486P.
11-JUL-2000; 2000US-0216486P.
11-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0216890P.
14-JUL-2000; 2000US-022526BP.
14-JUL-2000; 2000US-022526BP.
14-JUL-2000; 2000US-022526BP.
14-JUL-2000; 2000US-022526BP.
14-JUC-2000; 2000US-022514P.
14-JUC-2000; 2000US-022514P.
14-JUC-2000; 2000US-022514P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
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16-SEP-2000; 2000US-023144P.
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16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-
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2000US-0240960P.
2000US-0241221P.
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2000US-0236369P.
2000US-0236370P.
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21-SEP-2000;
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27-SEP-2000;
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20-OCT-2000;
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2000US - 0241786P

2000US - 024180PP

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2000US-0251990P
2000US-0254097P
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01-NOV-2000;
08-NOV-2000;
08-NO
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01-DBC-2000;
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05-DBC-2000;
06-DBC-2000;
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08-DBC-2000;
08-DBC-2000;
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17-NOV-2000;
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Ruben SM Rosen CA, Barash SC, WPI; 2001-488783/53. N-PSDB; AAS26595.

and New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.

Claim 11; SEQ ID NO 1561; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used

2000US-0229344P. 2000US-0229345P. 2000US-0229509P. 2000US-0229513P.

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(ELISA). Disorders which are diagnosed or treated include autoimmune

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(ELISA). Disorders which are diagnosed or treated include autoimmune

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muscular disorder; respiratory disease; reproductive disorder;
gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
hyperproliferative disorder; inflammatory disease; allergic reaction;
blood related disorder; cancer; immunosuppressive; antiinflammatory;
cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
haemostatic; antiarteriosclerotic.
in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic
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85.7%; Pred. No. 1.3e+02;
cive 1; Mismatches 0; Indels
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11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0218290F.
14-JUL-2000; 2000US-0218290F.
26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
14-AUG-2000; 2000US-022451BP.
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2000US-0214886P.
2000US-0216647P.
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Best Local Similarity 85.,
6; Conservative
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lugus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left reart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. acthma), blood inflammatory diseases. Sequences Abusatalal inflamction) and cancerous diseases. Sequences Abusatalal inflamction and cancerous diseases. Sequences Abusatalal inflamction novel polypeptides of the invention
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85.7%; Pred. No. 1.3e+02;
iive 1; Mismatches 0; Indels
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2000US-0244617P.
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2000US-0234223P.
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2000US-0234997P.
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2000US-0236327P.
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nes 6; Conservat
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
08-SEP-2000;
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02-OCT-2000;
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Best Local S
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14-AUG-2000; 2000US-0224519P. 14-AUG-2000; 2000US-02526PP. 14-AUG-2000; 2000US-025268PP. 14-AUG-2000; 2000US-025270P. 14-AUG-2000; 2000US-0225447P.

2000US-0225757P

14-AUG-2000;

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antibody; single-chain fragment; human; replication inhibitor; hepatitis C virus; variable region; VL; VH; light chain; heavy chain; viral protein; B1; E2; core protein; NS3-protease; NS3-helicase; NS4A cofactor; NS5B RNA polymerase; virucide; hepatotropic; antiinflammatory; vaccine; passive immunisation; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New single-chain human antibody fragment, useful for treating or diagnosing hepatitis C virus infection, has affinity for an essential viral protein.
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                                                                                                                                                                                                                                                                                                       "Linker fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 58; 78pp; German.
                                                                   sFv antibody fragment from clone 42
                                                                                                                                                           Location/Qualifiers
                ¥.
                                                                                                                                                                                                                                                                                      "J-segment"
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.61
..= "CDR-L2"
              ADH44202 standard; protein; 249
                                                                                                                                                                                              "CDR-L1"
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193. .224
/note= "FR-H3"
225. .249
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L63. .176
                                                                                                                                                                                                                                                                                                                       "FR-H1"
                                                                                                                                                                                                                                                                                                                                                                            "CDR-H2"
                                                                                                                                                                                                                                                                                                                                                                                                               'note= "CDR-H3'
                                                                                                                                                                            "FR-L1"
                                                                                                                                                                                                       10. .54
/note= "FR-L2"
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'note= "FR-L3"
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/note= "Li
                                                  25-MAR-2004 (first entry)
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                                                                                                                                                                                                                                                                            .116
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                                                                                                                                                                      . 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200293519-A2
                                                                                                                                           Homo sapiens.
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RESULT 10
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This invention describes a novel single-chain fragment of human antibody

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that inhibits replication of hepatitis C virus (HCV) and comprises the variable regions (VL and VH) of the light and heavy chains of an antibody directed against at least one essential viral protein. The invention also describes a method of identifying antibody fragments that inhibit replication of HCV. The protein is an envelope, core or non-structural protein, especially B1, B2, core, NS3-protease or -helicase, NS4A coffector or NS5B RNA polymerase (especially a NS3 helicase). The VL and VH regions may be linked covalently or through a linker, particularly a hydrophilic and/or flexible peptide. The single chain fragment may also be linked to a non-protein polymer and where intended for diagnosis, it may include disulfide bridges. The method of the invention involves identifying a DNA library of antibody fragments against one or more essential HCV proteins prepared from bone marrow of patients with chronic HCV infection. The library is cloned and expressed on the surface of phages. Phages that express fragments with high affinity for essential proteins are selected by many cycles of selection and reamplification (panning). Sequences that encode the selected fragments are then copic as soluble proteins, in bacteria (particularly Escherichia coli) and recovered from the periplasmic space. The products of the invention or for gene. The invention have virucide, hepatotropic and antiinflammatory activity. The covers single chain fragments are used to prepare vaccines, especially for passive immunisation and for diagnosis of HCV infection or for gene therapy of HCV. The sequence and structure of single chain fragment can be used for design of HCV protein inhibitors. This sequence represents a human continuely fragment described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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85.7%; Pred. No. 1.7e+02;
ive 1; Mismatches 0; Indels
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55 GNNHRPS 61
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in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                         sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents MOP9, a novel member of the PAS superfamily, where PAS stands for PER/ARNT/SIM domains. MOP9 cDNA (see AAXS8988) was cloned from human brain mRNA. MOP9 displays extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 4; Length 438; Pred. No. 2.9e+02; 1; Mismatches 0; Indels
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                              Claim 20; SEQ ID NO 41037; 103pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, aleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
homology to MOP3 (see AAY06291). It pairs with CLOCK and MOP4 (see AAY06292) and binds an B-box element with flanking region specificity. The invention provides novel MOP 2-9 nucleic acids (see AAX06289-97). These we useful in a variety of research, diagnostic and therapeutic applications. Several of the MOP8 are alphaclass, hypoxia-inducible factors. Others are involved in circadian signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
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                                                                                                                                                                   Score 36; DB 2; Length 585;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #4.
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85.7%; Pred. No. 3.8e+02;
.ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                      ABG92868 standard; protein; 588 AA.
                                                                                                                                                                   87.8%;
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                                                                                                                                    Sequence 585 AA;
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29-SEP-2000;
02-OCT-2000;
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13-OCT-2000;
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17-NOV-2000;
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25-SEP-2000;
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                                                                                                                                                                                                                                                                                   29-SEP-2000;
  Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; optalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardia arthritis; hyperproliferative disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                               Human novel secreted protein, Seg ID 1139
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                                                   AAU16186 standard, protein; 591
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01-SEP-2000; 2000US-022943P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-022945P.
05-SEP-2000; 2000US-0229509P.
                                                                                                                                                                                                                                                                                                                        2000US-0179065P

2000US-0180652P

2000US-018063P

2000US-0189814P

2000US-0199076P

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2000US-0191515P

2000US-0209467P

2000US-02148667P

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2000US-022548P

2000US-022548P
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                                                                                           (first entry)
  GSNYRPS 127
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23-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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07-JUL-2000;
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                                                                      AAU16186;
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                               RESULT 14
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muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory;

Human; neural disorder; immune system disorder; renal disorder;

Human novel polypeptide #342.

18-MAR-2003 (first entry)

ABU55255;

cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.

Homo sapiens.

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. raddioimmunoassays or erzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune coplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, transplantation, for supporting cell culture of primary tissues, to respend the content of the perverse storage and in chemotrais. The polypeptides can also be used to as a content of primary tissues, to respond the content of the perverse storage and in chemotrais. The polypeptides can also be used to as a content of primary tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; Score 36; DB 4; Length 591;
85.7%; Pred. No. 3.8e+02;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Barash SC, Ruben SM;
                                       17-NOV-2000; 2000US-0249245F.
17-NOV-2000; 2000US-0249264F.
17-NOV-2000; 2000US-0249265F.
17-NOV-2000; 2000US-024929F.
17-NOV-2000; 2000US-0249299F.
17-NOV-2000; 2000US-0249299F.
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05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
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08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
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2000US-0254097P
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N-PSDB; AAS26173.
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Matches 6; Conserv
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2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
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2000US-0229287P.
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2000US-0234997P.
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                                                            US2002132753-A1.
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Gaps
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ABUS5255 standard; protein; 591 AA.

RESULT 15 ABUSS2SS ID ABUSS

6; Conservative

|:||||| 124 GSNYRPS 130

1 GNNYRPS 7

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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Barash SC; Rosen CA, Ruben SM,

WPI; 2003-147444/14. N-PSDB; ABX73514.

New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 11; SEQ ID NO 1139; 402pp; English

The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. can mustiple sclerosis), pulmonary disorders, reproductive disorders, can quality and ployps and sinusitis), reproductive disorders, congenital heart defects, Ebstein's anomaly and hypoplastic left cheart syndrome), renal disorders (e.g. acute kidney failure and end-stage congenital), inflammatory diseases (e.g. septic shock, bursitis and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial merrals and candersous diseases. Sequences ABUSSA914-ABUSSS99 and ABU55748 represent human novel polypeptides of the invention 

Sequence 591 AA;

ö Query Match 87.8%; Score 36; DB 6; Length 591; Best Local Similarity 85.7%; Pred. No. 3.8e+02; Matches 6; Conservative 1; Mismatches 0; Indels

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Search completed: April 28, 2005, 18:17:21 Job time : 55.7188 secs

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Sequence

Sequence Sequence

4846, Ap

Sequence 19693,

5033, Ap 3408, Ap 161, App

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Sequence

Sequence 4628 Sequence 405, Sequence 42,

Perfect score:

Sequence:

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Scoring table:

Searched:

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Sequence 44201, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REPRESENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44201
LENGTH: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09374454

Patent No. 6395548

GENERAL INFORMATION:
APPLICANT: Lee, Mu.En
APPLICANT: Haich, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/09/374,454
CURRENT APPLICATION NUMBER: US (0/096,515)
EARLIER FILING DATE: 1998-08-13
ARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 19
LENGTH: 602

LENGTH: 602

TYPE: PRT

ONGANISM: Homo sapiens
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US-09-207-844-2
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US-09-107-532A-633
US-09-583-110-3408
US-09-902-540-11116
US-08-443-104-4
US-08-398-489-4
US-08-398-489-4
US-08-398-489-4
US-08-398-489-4
               -09-270-767-46152
-09-107-433-4846
-09-489-039A-10928
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100.0%; Pred. No. 27;
ive 0; Mismatches (
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US-09-199-637A-405
US-09-443-780C-42
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ORGANISM: Drosophila melanogaster
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Best Local Similarity
Matches 6; Conserv
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RESULT 1
US-09-270-767-44201
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US-09-374-454-19
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Sequence 11409, A
Sequence 11252, A
Sequence 4, Appli
Sequence 7214, Ap
Sequence 7214, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
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2, Appli
24557, A
8, Appli
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Appli
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                                                                                                 April 28, 2005, 18:06:50 ; Search time 14.2188 Seconds (without alignments) 36.750 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-489-039A-11252
US-08-345-039A-11252
US-08-345-321-4
US-09-621-976-4449
US-09-107-532A-7214
US-08-035-392-4
US-08-504-511A-2
US-08-504-511A-4
US-09-540-236-3486
US-09-540-236-3486
US-09-540-236-3486
US-09-2480-921B-8
US-09-345-345-386
US-09-346-345-386
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US-09-21-976-4993
US-09-21-976-920-74
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US-08-672-345C-93
US-09-214-095D-3
US-09-214-095D-121
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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HETEROHYBRIDOMAS PRODUCING HUMAN MONOCLONAL ANTIBODIES TO HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4449; Application US/09621976;
Patent No. 6639063;
GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TILLE OF INVENTION: ESTS and Encoded Human Proteins.;
FILE REPRENCE: GENSET.054FR2
CURRENT APPLICATION NUMBER: US/09/621,976;
CURRENT APPLICATION NUMBER: 2000-07-21
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
; LENGTH: 159
; TYPE: PRT
                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,321
                                                                                  ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZOLLA-PAZNER1B
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PULDA PELICATION DATA:
APPLICATION NUMBER: US/07/872,675
                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ELOWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ZO TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 132 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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  TITLE OF INVENTION: HET
TITLE OF INVENTION: MON
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                               Sequence 11409, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PNEUDORICE ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQUENCE FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11252, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KNEWN THILNG AFFE: 2709-2004001
CURRENT FILL REPERBORE: 2709-2004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11252
LENGTH: 324
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  85.7%; Pred. No. 1.4e+02;
tive 1; Mismatches 0; Indels
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Pred. No. 2.5e+02;
2; Mismatches 0,
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Patent No. 5914109
GENERAL INFORMATION:
APPLICANT: SOLLA-PAZNER, Susan
APPLICANT: GORNY, Miroslav K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 83.3
Matches 5; Conservative
    Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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135 GSNYRPS 141
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153 GNDYRPT 159
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                                                                    1 GNNYRPS 7
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US-09-489-039A-11409
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APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,511A
FILING DATE: 20-UUL-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (619) 678-5070
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

ZIP: USA
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Pred. No. 4e+02;
                  E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2607
TELECHONE: (619) 455-510
TELECHONE: (619) 455-510
TELECHONE: (619) 455-510
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08504511A Patent No. 5561224
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-035-392-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                            CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 GNNSRPS 303
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                                                                                                                                                                        APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 4; Length 223;
Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENTING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATIMIELLO, PAMELA DERORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...23
; SEQUENCE DESCRIPTION: SEQ ID NO: 7214:
US-09-107-532A-7214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 7214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                       Sequence 7214, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 223 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity 83.3
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37 GNNERPS 43
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Patent No. 5484732
GENERAL INFORMATION:
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 1; Length 430;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                    Score 32, DB 1; Length 348;
Pred. No. 4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-504-511A-4
Sequence 4, Application US/08504511A
Patent No. 5561224
GENERAL INFORMATION:
APPLICANT: ROSENÉEIG, M. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.0%;
                                                                                                                                                      78.0%;
85.7%;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                  Query Match
Best Local Similarity 85...
Lag 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-035-392-4
                                                                                                                                                                                                                                                                   297 GNNSRPS 303
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                                                                                                                 US-08-504-511A-2
                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-035-392-4
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARFITILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
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APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 430;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%; Score 32; DB 4; Length 442; 85.7%; Pred. No. 5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                             COMPUTER READABLE FORM:

"MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 20-JUL-1995
CLASSIFICATION: 435
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APPLICATION.
FILING DATE: 20-C.
FILING DATE: 20-C.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
FELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4:
FELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3486, Application US/09540236
Patent No. 6673910
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Best Local Similarity 85.7
Matches 6; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-3486
                                                                                                                                                CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 GNNSRPS 385
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Best Local Similarity
Matches 6; Conservi
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                                                                                                                                                                                                              92037
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US-09-835-654-2
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Score 32; DB 3; Length 720;
Pred. No. 7.8e+02;
1; Mismatches 1; Indels
    ; CURRENT APPLICATION NUMBER: US/09/480,921B; CURRENT FILING DATE: 2000-01-11; NUMBER OF SEQ ID NOS: 29; SEQ ID NO 8; SEQ ID NO 8; LENGTH: 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 720; TYPE: PRT 72
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 GNOYRPT 302
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Patent No. 6447137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 24557
LENGTH: 612
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78.0%; Score 32; DB 4; Length 612;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%; Score 32; DB 4; Length 552; 71.4%; Pred. No. 6.1e+02; tive 1; Mismatches 1; Indels
Sequence 2, Application US/09835654
; Patent No. 6646182
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mre11 Orthologue and Uses Thereof;
TITLE REPERENCE: 1264
CURRENT APPLICATION NUMBER: US/09/835,654
CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/198,570
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Levin, Joshua Z.
APPLICANT: Levin, Joshua Z.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Potter, Sharon L.
APPLICANT: Wegrich, Lynette M.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09480921B
Patent No. 6387637
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.0
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 GNOYRPT 302
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455 GKNYKPS 461
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CRGANISM: Zea mays
US-09-835-654-2
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NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-248-796A-24557
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US-09-480-921B-8
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LENGTH: 552
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               April 28, 2005, 18:24:46; Search time 43.4219 Seconds (without alignments) 53.700 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1426032 segs, 333106140 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                               US-10-088-639A-2_COPY_49_55
                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                   Run on:
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			Description	Sequence 656, App	Sequence 527, App	Sequence 1561, Ap	Sequence 8, Appli	Sequence 1139, Ap	Sequence 6, Appli	Sequence 19, Appl	Sequence 78, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 334, App	Sequence 1555, Ap	Sequence 1555, Ap
SUMMAKIES			ID	US-10-327-598-656	US-10-884-830-527	US-09-764-864-1561	US-10-467-721-8	US-09-764-864-1139	US-10-467-721-6	US-10-121-235-19	US-10-260-708-78	US-10-467-721-4	US-10-467-721-2	US-10-783-311-334	US-09-880-748-1555	US-10-293-418-1555
			DB	16	16	О	15	6	15	14		15	15	17	10	15
		Query	Length	7	7	201	588	591	599	602	602	622	636	123	251	251
	ф	Query	Match	100.0	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	85.4	85.4	85.4
			Score	41	36	36	36	36	36	36	36	36	36	35	35	35
		Result	No.	п	8	m	4	ß	9	7	89	6	10	11	12	13

	is, and	
Sequence 1435, Ap Sequence 238, Appl Sequence 51, Appl Sequence 1993, Ap Sequence 1998, Ap Sequence 1998, Ap Sequence 1998, Ap Sequence 2000, Ap Sequence 1176, Appl Sequence 1958, Ap Sequence 1958, Ap Sequence 2083, Ap Sequence 2083, Ap Sequence 1958, Ap Sequence 1958, Ap Sequence 1958, Ap Sequence 1958, Appl Sequence 1958, Appl Sequence 112, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequ	ns, Caninized Antibodies,	h 7; 1s 0; Gaps 0;
S US-10-369-493-1435 S US-10-149-310-238 S US-10-322-673-53 US-10-322-673-51 US-09-880-748-1993 US-09-880-748-1998 S US-10-293-418-1998 S US-10-293-418-1998 S US-10-293-418-1998 S US-10-293-418-1998 S US-10-293-418-1998 S US-10-293-418-1998 S US-10-293-418-1976 S US-10-293-418-1976 S US-10-293-418-1976 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-293-418-2083 S US-10-327-598-698 S US-10-327-598-698 S US-10-327-598-698 S US-10-277-155-114 S US-10-273-916A-75	riable em	Score 41; DB 16; Length Pred. No. 1.38+06; 0; Mismatches 0; Indel.
34 82.9 919 15 35 80.5 110 16 36 80.5 140 16 37 80.5 247 10 38 80.5 247 10 39 80.5 247 10 39 80.5 247 10 31 80.5 247 10 32 80.5 248 10 33 80.5 248 10 33 80.5 248 10 34 80.5 248 10 35 80.5 258 10 36 80.5 258 10 37 80.5 258 10 38 80.5 258 10 39 80.5 258 10 30 80.5 258 10 31 80.5 258 10 32 78.0 16 17 32 78.0 7 16 33 78.0 7 16 34 78.0 7 16 35 78.0 111 17	Application US/11 No. US20040181039A No. US20040181039A No. US20040181039A No. US20040181039A No. US20040181039A Alyapa, Honliang Alyapa, Ashok Lawton, Robert Lawton, Robert NVENTION: Canie Im VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTION: Canie Makin VENTI	Query Match  Best Local Similarity 100.0%; Pred  Matches 7; Conservative 0; Mi  Matches 1 GNNYRPS 7                   Db 1 GNNYRPS 7  SESULT 2  US-10-884-830-527  ; Sequence 527, Application US/10884830
, 1111111222222222222222222222222222222	RESULT 1 US-10-327-598- Sequence 655 Publication GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPL	Query Match Best Local ( Matches ( Qy 1) Db 1 RESULT 2 US-10-884-830; Sequence 52'

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LOCATION: (465)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (485)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-864-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (338)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1139, Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENEUS: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

PHIOR APPLICATION ADDRESS CONTONEY

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                          Score 36; DB 15; Length 588;
Pred. No. 2e+02;
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                     0; Indels
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Publication No. US20040058366A1
GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REPERENCE: A011-159CT
CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                       1; Mismatches
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PRIOR APPLICATION NUMBER: JP 2001/35743
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 8
LENGTH: 588
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OTHER INFORMATION: Xaa equals any
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Similarity 85.7%;
6; Conservative
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Local Similarity 85.7%;
Loc 6; Conservative
                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   121 GSNYRPS 127
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Best Local Similarity
Matches 6; Conserv
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US-09-764-864-1139
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LENGTH: 591
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Best Local S
Matches 6
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                                    TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing FILE REFERENCE: BEI-093CP
FILE REFERENCE: BEI-093CP
CURRENT PELLING DATE: 2004-07-01
PRIOR APPLICATION NUMBER: US/10/884,830
CURRENT FILING DATE: 2000+07-01
PRIOR PELLING DATE: 2000-03-24,717
PRIOR FILING DATE: 2000-03-25,1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PATCHIN VET. 2.0
SEQ ID NO 527
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (195)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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| Patent No. US20020132753A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILE REFERENCE: PTZ23
| CURRENT PELLING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper
| NUMBER OF SEQ ID NOS: 1792
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 1561
| LENGTH: 201
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; Publication No. US20040058366A1
; GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Bmal2, novel clock genes
FILE REFERENCE: A011-15.PCT
; CURRENT APPLICATION NUMBER: US/10/467,721
; CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 16;
Pred. No. 1.3e+06;
1; Mismatches 0
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Pred. No. 69;
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85.7%;
  Publication No. US20050004354A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-527
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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85.7%; Pred. No. 2.1e+02;
tive 1; Mismatches 0; Indels
                          Indels
                                                                                                                                                                                                        Sequence 4, Application US/10467721
| Publication No. US20040058366A1
| GENERAL INPORMATION:
| APPLICANT: JAPAN SIENCE AND TECHNOLOGY CORPORATION
| TITLE OF INVENTION: Bmal2, novel clock genes
| TITLE OF INVENTION: Bmal2, novel clock genes
| CURRENT APPLICATION WUMBER: US/10/467,721
| CURRENT FILING DATE: 2003-08-11
| PRIOR PRILING DATE: 2001-02-13
| NUMBER OF SEQ ID NOS: 63
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10467721
; Sequence 2, Application US/10467721
; Publication No. US20040058366A1
; GENERAL INFORMATION:
; APPLICAMT JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Bmal2, novel clock genes
; FILE REFERENCE: A010-15PCT
; CURRENT APPLICATION NUMBER: US/10/467,721
; CURRENT FILING DATE: 2003-08-11
; FRIOR APPLICATION NUMBER: UP 2001/35743
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO S: 63
; LENGTH: 636
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      85.7%; Pred. No. 2e+02; tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.8%;
    Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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169 GSNYRPS 175
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135 GSNYRPS 141
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155 GSNYRPS 161
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Best Local Similarity
Matches 6; Conserv
                                                                  1 GNNYRPS 7
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US-10-783-311-334
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US-10-467-721-2
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US-10-467-721-4
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85.7%; Pred. No. 2e+02;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Macmura, Koji
APPLICANT: Haich, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OP ANGIOGENESIS
TILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/10/121,235
CURRENT FILING DATE: 2002-04-12
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 602
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US-10-260-708-78

Squence 78, Application US/10260708

Publication No. US20040063101A1

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew

APPLICANT: Lee, Sang-Yull

APPLICANT: Loy

TITLE OF INVENTION: Human Sarcoma-Associated Antigens

PIE REPERENCE: L00461/70138

CURRENT APPLICATION NUMBER: US/10/260,708

CURRENT FILING DATE: 2002-09-30

NUMBER OF SEQ 1D NOS: 96

SOFTWARE: PatentIn version 3.1

SEQ 1D NO 78

LENGTH: 602
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PRIOR APPLICATION NUMBER: JP 2001/35743
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 19, Application US/10121235; Publication No. US20030032609A1
EBERRAL INFORMATION:
APPLICANT: Lee, Mu-En
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                            TYPE: PRT
GRGANISM: Homo sapiens
US-10-467-721-6
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US-10-121-235-19
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132 GSNYRPS 138
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135 GSNYRPS 141
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PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILLING DATE: 2001-12-19
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/273,799
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-06-16
SEQ ID NO 1555
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1435, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Publication No. US20040077039A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-10-369-493-1435
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Similarity 85.7%;
6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-293-418-1555
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REFERENCE: PF523P2
CURRENT APPLICATION UMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1555, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REPERENCE: PF5.3
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 35; DB 17; Length 123; 100.0%; Pred. No. 66; 0; Mismatches 0; Indels
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US-10-783-311-334
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TITLE OF INVENTION: PAPP-A LIGANDS
FILE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US 60/448,515
PRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 394
SOFTWARE: PASTEEQ for Windows Version 4.0
SEQ ID NO 334
LENGTH: 123
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/273,499
PRIOR FILING DATE: 2001-05-25
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1555
LENGTH: 251
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
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58 NNYRPS 63
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                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown
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US-09-880-748-1555
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US-10-293-418-1555
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 6/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1435
LENGTH: 919
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0
    Length 251;
                                          1; Indels
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Score 35; DB 15;
Pred. No. 1.3e+02;
0; Mismatches 1;
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Pred. No. 7.2e+02;
0; Mismatches 1.
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TITLE OF INVENTION: Modulation of Secondary Metabolite Production by TITLE OF INVENTION: Zinc Binuclear Cluster Proteins FILE REPERENCE: 14184-019US1
CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2031-02-19
PRIOR APPLICATION NUMBER: PCT/US01/29288
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 238
LENGTH: 919
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                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-10-149-310-238
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Search completed: April 28, 2005, 19:02:13 Job time : 44.4219 secs

130 GNNYLPS 136

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55; Search time 9.625 Seconds Run on:

(without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_49_55 41 1 GNNYRPS 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: piri: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	mouse Dhm1 protein	type II restrictio	metalloproteinase	metalloproteinase	probable integral		heti	sopB protein - Esc	probable sopB prot	aminopeptidase A/I	recombination acti	peptide methionine	C 3.4.23.42 thermo	transcription fact	hypothetical prote	6	transcription fact	¢	hypothetical prote			ribonuclease II [i	hypothetical prote	Mrell protein homo	probable Athila re	hypothetical prote	ribosomal protein	ribosomal protein	cobN protein - Syn
SUMMAKIES	ΩI	I49635	H64422	S61435	S42894	G71607	S45889	S23533	T00244	T13113	F82843	151556	F86875	A35009	B46216	T49791	S35541	A46216	JC2002	H84862	F96491	F90564	AB2362	AD1857	T52564	E84475	S66306	S52680	T50348	875635
	DB	5	7	7	7	7	7	7	α.	~	~	~	~	7	Н	~	-	٦	Н	~	7	7	~	N	~	7	~	7	~	0
	Length	947	222	633	649	1182	919	311	323	342	491	520	172	340	348	349	403	430	431	504	530	572	989	692	720	750	935	105	108	184
de	Query. Match	90.2	85.4	85.4	85.4	85.4	82.9	80.5		80.5	80.5	80.5	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0		•	•	75.6		
	Score	37	35	35	35	35	34	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31
	Result No.	-	7	٣	4	2	9	7	ω	6		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56		28	

carbonate dehydrat hypothetical prote	probable exported probable exported probable transcrip	probable diphthine protein ZC53.6 [im carbonate dehydrat	carbonate dehydrat 2-dehydro-3-deoxyg 2-dehydro-3-deoxyg	hypothetical prote 2-dehydro-3-deoxyg llm protein - Stap	F21H2.9 protein - uncharacterized pr
A60519 T27260	AD0486 AF0209 T51689	T41424 E89472 S12579	CRHUS AI0985 AG0485	T10238 C55215 A55856	D86470
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200	234 236 258	283 292 298	305 309 314	318	365
75.6	75.6 75.6	75.6 75.6 75.6	75.6 75.6 75.6	75.6	75.6
31	333	3333	######################################	31	31
30 31	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 37	38 39 40	44 4 1 2 4	4 4 4 73

### ALIGNMENTS

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accesion: 149635
R;Shobuike, T.; Sugano, S.; Yamashita, T.; Ikeda, H.
Nucleic Acids Res. 23, 357-361, 1995
A;Thle: Characterization of CDNA encoding mouse homolog of fission yeast dhpl+ gene: stranspacence number: 149635; MUID:95192042; PMID:7885830
A;Reference number: 149635
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-947 <RES>A;Residues: 1-947 <RES>A;Cross-references: GB:D38517; NID:g1060920; PIDN:BAA07524.1; PID:g1060921
                                                                                             - monse
                                                                                    mouse Dhml protein
RESULT 1
                                                149635
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### Query Match 90.2%; Score 37; DB 2; Length 947; Best Local Similarity 100.0%; Pred. No. 24; Matches 6; Conservative 0; Mismatches 0; Indels 843 GNNYRP 848 9 1 GNNYRP 셤 à

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Trestriction enzyme homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64422
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reon, J.D.; Sadow, D.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borddovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Authors: Melecane sequence of the methanogenic archaeon, Methanococcus jannaschii.
A;Recession: H64422
A;Accession: H64242
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A;Accession: H644243
A;Accession: H64

A;Map position: FOR915789-916457 A;Start codon: GTG C;Superfamily: Methanobacterium mthZIM protein

Gaps ö Query Match 85.4%; Score 35; DB 2; Length 222; Best Local Similarity 85.7%; Pred. No. 15; Matches 6; Conservative 0; Mismatches 1; Indel8

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C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C.Accession: G7160
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1182 <GAR>
A;Cross-references: UNIPROT:096240; GB:AE001414; GB:AE001362; NID:g3845260; PIDN:AAC71936
A;Cross-references: clone 3D7
A;Gsperimental source: clone 3D7
A;Gsperimental source: clone 3D7
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N,Alternate names: hypothetical protein YBR0318
C,Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #equence_revision 09-Sep-1994 #text_change 16-Aug-2004
C;Accession: $45889; $46562
R;Girvell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: $45875
A;Accession: $45889
A;Accession: $45889
A;Accession: $45889
A;Accession: $45889
A;Residues: 1-919 <GRI>A;Residues: 1-919 <GRI>A;Residues: 1-919 <GRI>A;Residues: 1-919 <GRI>A;Texperimental source: strain $288C
A;Experimental $288C
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A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: 1-919 <cMI>
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A;Status: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Cross-references: SGD:S0000237
A;Map posttion: 2R
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Species: Plasmodium falciparum
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Matches 6; Conserv
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Reference number: S61435; MUID:95231298; PMID:7715453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
S42894
S42894
C; Species: Aspergillus fumigatus
C; Species: Aspergillus fumigatus
C; Species: Aspergillus fumigatus
C; Species: Aspergillus fumigatus
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
R; Jacon-Ogay, K; Quadroni, M.; Falchetto, R.; Togni, G.; Paris, S.; Latge, J.; Monod, M submitted to the EMBL Data Library, March 1994
A; Description: Nucleotide sequence of genomic and cDNA clones encoding an extracellular A; Accession: S42894
A; Status: preliminary
                                                                                                                                                                                                                                                                 RESULT 3
$61435
metalloproteinase (EC 3.4.24.-) precursor - Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 29-Jan-1999
C;Accession: $61435; $61436; $61450
R;Jaton-Ogay, K.; Paris, S. Huerre, M.; Quadroni, M.; Falchetto, R.; Togni, G.; Latge, Mol. Microbiol. 14, 917-928, 1994
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G71607
probable integral membrane protein PFB0735c - malaria parasite (Plasmodium falciparum)
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A,Molecule type: protein

C,Residues: 246-276;362-371;407-416;419-428;477-488;571-588 cJAF>

C,Keywords: hydrolase; metalloproteinase; zinc; zymogen

F;1-18/Domain: signal sequence #status predicted cSIG>

F;19-245/Domain: propeptide #status predicted cPRO>

F;246-631/Product: metalloproteinase #status experimental cMAT>

F;428,432/Binding site: zinc, catalytic (His) (active) #status predicted

F;429/Active site: Glu #status predicted
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A Residues: 1-633 <JAT>
A Cross-references: EMBL: 230424, NID: 9458475; PID: 9458476
A; Experimental acurce: strain deltal8
A; Accession: S61436
A; Accession: S61436
A; Accession: S6136
A; Accession: S633 <JAMA>
A; Cross-references: EMBL: Z30424
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C;Genetics:
A;Introns: 119/3; 251/2; 588/2
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100.0%; Pred. No. ...
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Best Local Similarity 100..
--- 6; Conservative
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                                                                                                     147 GGNYRPS 153
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A;Cross-references:
A;Accession: S61450
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A; Cross-references: UNIPROT: 064340; EMBL: AF064539; NID: 93192683; PID: 93192710; PIDN: AAC15
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C;Species: Xylella fastidiosa
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A85115, MID:20365717, PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A,Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme C.Dado, M.A.; Madeira, M.E.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre, C.Dado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Ollveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr. V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, Atthores: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
                                                                                                                                                                                                                                                                                                                                                                                NiAlternate names: protein gp27
C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13113
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K. submitted to the EMBL Data Library, May 1998
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56;
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Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
Pred. No. 53;
2; Mismatches
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Pred. No. 5
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71.48;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                    5; Conservative
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A; Contents: annotation
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155 GNDYRPT 161
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Best Local Similarity
Matches 5; Conserv
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A;Accession: T42169
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT: P08867; EMBL:AB011549; NID:g4589740; PIDN:BAA31791.1; PID:g3
A;Experimental source: strain EHEC O157:H7, substrain RIMD 0509952
B;Mori, H.; Kondo, A.; Ohshima, A.; Ogura, T.; Hiraga, S.
A;Mol. Biol. 192, 1-15, 1986
A;Title: Structure and function of the F plasmid genes essential for partitioning.
A;Reference number: A92934; MUID:87141188; PMID:3029390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: plasmid partitioning protein; protein B
C;Species: Bscherichia coli
C;Date: (0.Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00244; S28096; T42169
R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota,
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A;Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrha
A;Reference number: Z14127; MUID:98290540; PMID:9628576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:Q39500; EMBL:X64302; NID:g17988; PIDN:CAA45582.1; PID:g1799
                                                                                                                                                                    hypothetical protein 311 - diatom (Cylindrotheca fusiformis) plasmid pCF1
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 823533
R;Hildebrand, M.; Hasegawa, P.; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E. Blant Mol. Biol. 19, 785-770, 1992
A;Title: Nucleotide sequence of diacom plasmids: identification of open reading frames A;Reference number: 823531; MUID:92353385; PMID:1322740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Cylindrotheca fusiformis plasmid pCF1 hypothetical protein 311
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C, Keywords: DNA binding; plasmid partition
       GNINYLPS 136
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GNNYQP 113
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A;Molecule type: DNA
A;Residues: 1-323 <MOR>
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A;Molecule type: DNA
A;Residues: 1-311 <HIL>
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Matches 5, Conserv
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C;Superfeet
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C;Accession: B46216
R;Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearse II, R.V.; Singh, H.; Rosenfeld, M.C
Science 260, 78-82, 1982
A;Title: Skn-la and Skn-li: two functionally distinct Oct-2-related factors expressed in A;Reference number: A46216; MUID:93219836; PMID:7682011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L23863; NID:g393221
A;Cross-references: GB:L23863; NID:g393221
A;Note: sequence extracted from NCBI backbone (NCBIP:128574)
C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatic
F;101-168/Domain: POU domain homology <POU>
F;103-249/Domain: homeobox homology <HOX>
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R;Schulte, U.; Ajgn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
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A;Cross-references: UNIPROT: Q9P555; EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.280
A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Rattus norvegicus (Norway rat)
Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Neurospora crassa
Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                             A;Residues: 1540 <LIN>
A;Cross-references: UNIPROT:P17118; GB:J05184; NID:g152940; PID:g152941
C;Superfamily: Sulfolobus acidocaldarius thermopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                             78.0%; Score 32; DB 2; Length 340; 71.4%; Pred. No. 88;
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A; Reference number: A35009; MUID:90110209; PMID:2104843
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Pred. No.
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Pred. No.
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85.7%;
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83.3%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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246 GNNYTPN 252
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                               A;Accession: A35009
A;Status: preliminary
A;Molecule type: DNA
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;Residues: 1-172 <STO>
;Cross treferences: UNIPROT:Q9CE42; GB:AE005176; PID:g12725052; PIDN:AAK06104.1; GSPDB:G
;Bxperimental source: strain IL1403
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Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT: Q91830; GB:L19325; NID: g401812; PIDN: AAA49943.1; PID: g401813
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C;Species: Lactococcus lactis subsp. lartie
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(3.4.23.42 thermopsin () precursor - Sulfolobus acidocaldarius
(5.5pecies 20.5ulfolobus acidocaldarius
(5.5pecies 20.5ul-1990 #sequence_revision 20.Jul-1990 #text_change 09.Jul-2004
(5.5pecies 20.5ul-1990 #sequence_revision 20.Jul-1990 #text_change 09.Jul-2004
(5.5pecies 20.5ul-1990 #sequence_revision 20.Jul-1990 #text_change 09.Jul-2004
(5.5pecies 20.5ul-1990 #sequence_revision 20.Jul-1990 #text_change 09.Jul-2004
(5.5pecies 20.Jul-1990 #text_change 09.Jul-1990 #text_change 09.Jul-2004
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(5.5pecies 20.Jul-2004
(5.
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A,Accession: IS1556
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Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
Accession: I51556
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Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
   Gaps
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C;Superfamily: peptide methionine sulfoxide reductase
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C,Superfamily: recombination-activating protein RAG-2
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   Mismatches
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Pred. No.
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Best Local Similarity 83.3
   Conservative
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Best Local Similarity
Matches 5; Conserv
                                                              1 GNNYRPS 7
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A; Residues: 1-520 <GRE>
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92 GDNYRP 97
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AND MEMBER 21394685; PUDPMEGGE 1246685;

AND OKAZAKI Y., FURTHO M., KASUKAWA T., Adachi J., BODO H., KONGO S.,

RA NIKARIGO I., OSAICO R., SAICO R., SUZUKI H., YAMMANAR I., KIYOSAWA H.,

RA BAIGARELII R., HILLI D.P., BUIL C., HUME D.A., QUACKENDUBH J.,

RA SCHRIML L.M., KANADAIN A., MATCHIA H., SCHONDACH C., GOJODORI T.,

RA BAIR E., DYRAGANI T.A., FIETCHER C., CORDANI L.B., COUSINS S.,

BAIRE J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., COUSINS S.,

RA BAIR B., DYRAGANI T.A., FIETCHER C.F., FORTERS A., GOUGH J.,

RA RANAJI H., KAWASAWA Y., KEGAZIERSKI R.M., KANAJI H.,

RA MARIOTH C., MATCHIONNI L., MCKENZIE L., MIKH H.,

RA MAGOLT D.R., MAILTIS L., MATCHIONNI L., MCKENZIE L., MIKH H.,

RA MAGOLT D.R., MAILTIS L., MATCHIONNI L., MCKENZIE L., MIKH H.,

RA RAVASI T., Reed D.G., Reed D.J., RINGWAR K.,

SANGELIN A., SCHNEIGER C., SEMDLE C.A., SECTOW M., Shimada K.,

SANGELIN A., SCHNEIGER C., SEMDLE C.A., SECTOW M., Shimada K.,

RA SCHOLL R.W. WASHAW BOTIS A., YANAGAIR R.D., TOMITA M.,

RA WILLIAM R., TAKENBAW BOTIS A., YANAGAIR R.D., TOMITA M.,

RA HINDZAND-KISHIKAWA T., KONDO H., WAKAMUTA M., KARAWA I.,

RA HINDZAND-KISHIKAWA T., KONDO H., WAKAMUTA M., KARAWA I.,

RA HINDZAND-KISHIKAWA T., KONDO H., NAKAMUTA M., KARAWA I.,

RA HINDZAND-KISHIKAWA T., KONDO H., WAKAMUTA M., KARAWA T.,

RA BARINZUME W., IMDLANIK, RAWAI J., AIZAWA T., ITOM M., KARAWA I.,

RA BARINZUME W., IMDLANIK K., KAWAI J., SARAYA T., FUNUGA S.,

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RA BANDASI OF THE MOUSE TRANSCHIPOM
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REPUBLICATION OF THE STREET AND MARKED SECURING STRAIN—CS7BL/6, and Czech II; TISSUB—Brain, and Mammary gland;

RAMENINE—22388257; Pubméd—12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RAMESTONIS E.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhar N.K.,

RAMESTONIS R.F., Jordan H., Moore T., Max S.I., Wang J., Hisieh F.,

RAD Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RAD Altespleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RAMESTONIS S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.A., McEwan P.J., McKernan K.J., Match J., Gunzardne P.H.,

RAD Bosak S.A., McEwan P.J., McKernan K.J., Match J.J., Hulyk S.W.,

RICHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RAD Helton E., Ketteman M., Madan A., Gabs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RAD Robert S., McC., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Possesses 5'->3' exoribonuclease activity and may be involved in homologous recombination and RNA metabolism, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA synthesis and RNA trafficking.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lsoId=Q9DBR1-2; Sequence=VSP_007235;
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MEDLINE=22354683; PubMed=12466851;
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   STRAIN=C57BL/6J; TISSUE=Embryo, Eye, Forelimb, and Lung;
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DNA Res. 9:189-197(2002).
-!- FUNCTION: Catalyzes the desulfonation of aliphatic sulfonates (By
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MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.
                                                                                                                                                                              SMART; SM00343; ZnF_C2HC; 1.
PROSTIE; PSS0158; ZF_CCHC; PALSE NEG.
MENA processing; Hydrolase; Nuclease; Exonuclease; Nuclear protein;
RNA-binding; Zinc-finger; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alkanesulfonate monooxygenase (EC 1.14.14.5) (FMM2-dependent
                                                                                                                                                                                                                                                                   Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 951; 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                 C (in isoform 2)
/FTId=VSP_007235
                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 AA.
                                                                           EMBL, AK004800, BAB23573.1; -- EMBL, AK031247; BAC27318.1; -- EMBL, AK031247; BAC35458.1; -- EMBL, BC004028; AAM04028.1; ALT_INIT. EMBL, BC054743; AAM54743.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aliphatic sulfonate monooxygenase).
SSUD OR BLL7010.
                                                                                                                                  MGD; MGI:894687; Xrn2.
InterPro; IPR004859; Put 53exo.
InterPro; IPR001879; Znf_CCHC.
Pfam; PP03159; XRN_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
                                                                   EMBL; D38517; BAA07524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          951 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GNNYRP 6
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Q89ER2;
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VARSPLIC
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

BUDINES-9633-9999; PubMed=8688087;

BULL C.J., White O., Olsen G.J., Flou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstook K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
-!- CATALYTIC ACTIVITY: An alkanesufonate (R-CH(2)-SO(3)H) + FMNH(2) O(2) = an aldehyde (R-CHO) + FMN + sulfite + H(2)O. -!- SIMILARITY: Belongs to the ssub family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Type II restriction enzyme MjaI (EC 3.1.21.4) (Endonuclease MjaI)
(R.MjaI).
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"Method for screening restriction endonucleases.";
Patent number W09911821, 11-MAR-1999.
-i- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 387;
Pred. No. 5.1;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    EMBL), MF 01229; -; 1.
INTERPRO, IPR002103; Bac_luciferase.
InterPro, IPR002103; Bac_luciferase.
Pro0226; bac_luciferase; 1.
Oxidoreductase; Monooxygenase; FMN; Complete proteome.
SROUENCE 387 AA; 42411 MW; C63361B034AD8431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA.
                                                                                                                                                                                                                                                                         EMBL; AP005960; BAC52275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      87.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
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Best Local Similarity 85. والمادية
المادية وفي Conservative أ
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T2M1_METJA
ID _T2M1_META
AC Q58391;
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NCBI_TaxID=5085;
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                                                                                                                                            SEQUENCE
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               PROPEP
CHAIN
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ELM2_ASPFU
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(See http://www.isb-sib.ch/announce/
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular elastinolytic metalloproteinase precursor (EC 3.4.24.-)
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Isolate 13;

BUDLINE=95012603; PubMed=7927676;

Sirakova T.D., Markaryan A., Kolattukudy P.E.;

"Molecular cloning and sequencing of the cDNA and gene for a novel

elastinolytic metalloproteblase from Aspergillus fumigatus and its

expression in Escherichia coli.";

Infect. Immun. 62:4208-4218(1994).
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Markaryan A., Morozova I., Yu H., Kolattukudy P.E.; "Purification and characterization of an elastinolyric metalloprotease from Aspergillus funigatus and immunoelectron microscopic evidence of secretion of this enzyme by the fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invading the murine lung.";
Infect. Immun. 62:2149-2157(1994).
Infect. Immun. 62:2149-2157(1994).
Infect. Immun. 62:2149-2157(1994).
Infect. Immun. 62:2149-2157(1994).
Infect. Immun. 62:2149-2157(1994).
Infect. Immun. 63:2149-2157(1994).
                                                                                                                                                                                                                                                                     Length 222;
                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                222 AA; 25962 MW; 9A254A208AB8AC02 CRC64;
                                                                                                                                                                                      Restriction system; Hydrolase; Nuclease; Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; M36.001; ... ... ... ... ... InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001842; Peptidase_M36.
Ffam; PF02128; Peptidase_M36; I.
PRINTS; PR00999; FUNGALYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Zymogen. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus fumigatus (Sartorya fumigata).
Eukaryota, Fungi, Ascomycota, Pezizomycotina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 530-542.
                                                                                                                                                                                                                                                                     Score 35; DB Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
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85.7%;
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                                                                                                  EMBL; U67541; AAB98987.1; -. PIR; H64422; H64422.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7%
Conservative 6;
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                                                                                                                                                                                                                                                                                                                                                                                                  147 GGNYRPS 153
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                                                                                                                                            REBASE; 1221; MjaI.
TIGR; MJ0984; -.
                                                                                                                                                                                                                                                                                                                                                        1 GNNYRPS 7
                                                                                                                                                                                                            Complete proteome.
SEQUENCE 222 AA;
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P46074;
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Extracellular elastinolytic metalloproteinase precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                Gaps
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Jaton-Ogay K., Paris S., Huerre M., Quadroni M., Falchetto R., Togni G., Latge J.-P., Monod M.;
"Cloning and disruption of the gene encoding an extracellular metalloprotease of Aspergillus fumigatus.";
Mol. Microbiol. 14:917-928(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.
                                                  (CATALYTIC) (BY SIMILARITY).
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                                                                                                           SIMILARITY)
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to peptidase family M36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 634;
                                                                                                                                                                                          DB 1; Length 634;
14;
EXTRACELLULAR ELASTINOLYTIC
                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                    B94E274BF767F911 CRC64;
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MEROPS, M36.001; -..

InterPro; IPR001842; Pept M Zn BS.

InterPro; IPR001842; Peptidase M36.

PERM; PR01218; Peptidase M36; I.

PRIMT, PR001999; FUNGALYSIN.

PROSITE, PS00142; ZINC PROTEASE; I.

Hydrolase; Metalloprotease; Zinc; Signal; Zymogen.
                                                                               BY SIMILARITY.
ZINC (CATALYTIC) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METALLOPROTEINASE
                            METALLOPROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 AA.
                                                                                                                                                                                          85.4%; Score 35; DB 100.0%; Pred. No. 14; ive 0; Mismatches
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                                                           ZINC
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                                                                                                                                       68726 MW;
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                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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433
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634 AA;
                                                                                                                                                                                                                                                                                                                                                         309 NNYRPS 314
                                                                                                                                       634 AA;
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      2 NNYRPS 7
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01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                       outbreak."
                                                                                                                                                                                        PLASMID=F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                         Smits P.H.M., de Haan M., Maat C., Grivell L.A.;
"The complete sequence of a 13 kb fragment on the right arm of chromosome Il from Saccharomyces cerevisiae reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene.";
Yeast 10:875-S80(1994).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                 Gaps
                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative 103.4 kba transcriptional regulatory protein in RPL4A-HWT1
intergenic region.
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 32;
                 Indels
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                                                                                               919 AA
        Pred. No. 14;
                 Mismatches
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                                                                                                                                                                                                                                   MEDLINE=94378725; PubMed=8091864;
100.0%; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X76078; CAA53688.1; -. EMBL; Z35902; CAA84975.1; -.
                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                               STANDARD;
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GermOnline; 138576; -
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                                           309 NNYRPS 314
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      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=S288C;
                                 2 NNYRPS 7
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                                                                                                                                                                                              NCBI_TaxID=4932;
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P08867;
                                                                                               YEAST
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Nucleic Acids Res. 26.4196-4204 (1998).
-!- FUNCTION: CONTROL OF PLASMID PARTITIONING; REQUIRED TO RECCGNIZE
-IFUNCTION: CONTROL OF PLASMID PARTITIONING THE DNA SEGMENT CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / CR63; PLASMID=F;
Shimizu H., Saitch Y., Suda Y., Uchara K., Sampei G., Mizobuchi K.;
"Complete nucleotide sequence of the F plasmid: its implications for organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952; PLASMID=p0157;
MEDLINE=98290540; Pubmed=9628576;
Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
Yutsudo H.C., Kubota Y., Yamaichi Y., Iida T., Yamamoto K.,
Han C.G., Ohtsubo E., Kasamatsu M., Hayashi T., Kuhara S.,
                                                                                                                                                                              Bscherichia coli 0157:H7.
Plasmid F, and Plasmid p0157.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bichenlaub R.;
"F plasmid DNA complete mini-F region (F coordinates 40.301F to
49.869F).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of enterohemorrhagic Escherichia coli 0157:H7 derived from Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE SOPC REGION. SOPB IS TRANS-ACTING.

- MISCELLANEOUS: OVERPRODUCTION OF SOPB PROTEIN CAUSES INCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mori H., Kondo A., Ohshima A., Ogura T., Hiraga S.; "Structure and function of the P plasmid genes essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98391744; PubMed=9722640;
Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.869F).";
Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.
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STRAIN=0157:H7 / EDL933 / ATCC 700927; PLASMID=pO157;
           SopB protein (Plasmid partition protein B).
   Last sequence update)

    -!- SIMILARITY: Belongs to the parB family.

                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-KI2; PLASMID-F;
MEDLINE-87141188; PLDMed-3029390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF074613; AAC70137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 192:1-15(1986).
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                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562, 83334;
(Rel. 09,
                                                                                                                                              Escherichia coli, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 5:1-9(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partitioning.";
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
As Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
R.A. Adril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.B. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Beeson K.Y., Denos P.V., Berman B.P., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouke C., Davenport L.B., Davies P.,
R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Posler C., Gabrielian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
R. Adlali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R. Hostin D., Houston K.A., Heiman T.J., Hernandez J.R., Houck J.,
R. Almel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,
R. Marke P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morpherson D.,
R. Markulov G., Milshina N.V., Mobarry C., Morris J., Morris J., Morris J., Morris J., Morris J., Pallon D.R.,
R. Ralush R., Moy M., Murphy B., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Willer D., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullard J., Pullar
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                   EcoGene; EG40060; sopB.
InterPro; IPR004437; ParB_part.
InterPro; IPR004135; ParBc.
Pfan; PF02195; ParBc; I.
SWART; SW00470; ParB; I.
TIGRPAMS; TIGR00180; parB part; I.
Plasmid; Plasmid partition; DNA-binding; Complete proteome.
DNA BIND 180 199 HT-T-H MOTIF (BY SIMILARITY).
SEQÜENCE 323 AA; 35372 MM; 3CC19C873CED3CIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Powers P.A., Ganetzky B.; "On the components of segregation distortion in Drosophila
                                                                                                                                                                                                                                                                                         80.5%; Score 33; DB 1; Length 323; 71.4%; Pred. No. 18; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster. V. Molecular analysis of the Sd locus.";
Genetics 129:133-144(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS2S_DROME STANDARD; PRT; 349 AA. P25722; Q9VIW4; 01-MAY-1992 (Rel. 22, Created) 28-FB2-003 (Rel. 41, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Heparin sulfate O-sulfotransferase (EC 2.8.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Oregon-R;
MEDLINE=92038937; PubMed=1936954;
                                                                                                                                                                                                                                                                                                                    Local Similarity 71.4
nes 5, Conservative
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T00244; T00244.
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SEQUENCE FROM N.A.
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Matches
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodege T., Worlbey K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM S1).

STRAIN=Berkeley, TISSUE=Head;
MRDINIE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
-: SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFRKLLIKWWILLRPTHWLILIALC -> MKRSAECSEWQAF
FESDDGFRQPGIITIDEAFEAII (in isoform S2).
FTId=vSP 004382.
Missing (in isoform S4).
/FTId=vSp_004383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Transmembrane; Glycoprotein; Golgi stack; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUMENAL (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P25722-3; Sequence=VSP_004383; CAUTION: Was originally (Ref.1) thought to be SD. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.5%; Score 33; DB 1; Length 349; 71.4%; Pred. No. 19; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DN -> EH (IN REF. 1).
E4655D92D7615C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ALTERNATIÚE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P25722-2; Sequence=VSP_004382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [sold=P25722-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X60218; CAA42779.1; ALT_FRAME.
EMBL; AE003663; AAF53800.1; -.
EMBL; AY058422; AAL13651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AA; 41273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0024230; Hs2st.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007734; HS2ST.
Pfam; PF05040; HS2ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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107
126
282
24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing.
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Best Local Similarity .
5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, S18765; S18765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=S4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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1 GNNYRPS 7

METAL

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FFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity).

CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaar | - Xbb., in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. COFACTOR: Binds 2 manganese ions per subunit (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2013 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, ME_00181; -; 1.

InterPro; IRR00819; Peptidase M17_C.

InterPro; IRR00819; Peptidase M17_N.

Fram; PR00883; Peptidase M17, 1.

Pfam; PR00789; Peptidase M17, 1.

PRNITS; PR00481; LAMNOPPTDASE.

PROSITE; PS00631; CYTOSOL AP; 1.

Hydrolase; Aminopeptidase; Mangamese; Complete proteome.
                                                                                                                                                                                                                                                    490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE012005; AAM38399.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Leucyl aminopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 host specificities.";
Nature 417:459-463(2002).
                                                                                                                                                                                                                                                    STANDARD;
|:||||:
179 GDNYRPN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR XAC3556
                                                                                                                                                                                                                                                    AMPA XANAC
QBPGRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METĀL
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STRAINB=20365717; PubMed=10910347;
Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Bala G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., R., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carraro J.M., Ranca S.C., Franco M.C., Frome M., Furlan L.R., A acriner M., Goldman G.H., Goldman M.H., Kemper B.L., Kitajima J.P., Rrieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., R. Arcieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., R. Arcieger J.E., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mardera B.G.M., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mardera B.G., Miyaki C.Y., Monteiro-Vitozello C.B., Monon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Monon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., A Mani A. Jr., Nobrege R.G., Miyaki C.Y., Monteiro-Vitozello C.B., Pereira G.A.G., Pereira H.A. Jr., Perquero J.B., Roberto P.G., Santelli R.V., Sawasaki H.E., A Silva A.M., A Silva A.M., A Silva A.J.M., A Silva A.C., A Silva A.M., A Silva A.J.M., A Silva A.W., Thuffi D., Tsai Silva A.W., Nations B.G., Silva A.M., Tauhako M.H., Nagoon M.H., Nature G.H., Marinella S., Vettore A.L., R. A. A. Sago M.A., Zatz M., Midais J., Stubella G., Setubal J.C., Sayani H. R., R. A. A. Sago M.A., Zatz M., Midais J., Setubal J.C., Sayani H. R., R. A. A. Sago M.A., Satz M., Midais J., Setubal J.C., Sayani H. R., R. A. Sago M.A., Satz M., Metore B. J. Setubal J.C., Sayani H. R., R. A. Sago M.A., Satz M., Midais J., Setubal J.C., Sayani H. B., R. A. Sago M.A., Satz M., Midais J., Satubal J.C., Sayani H. B., R. Midais J., Satubal J.C., Sayani H. B., R. Mature G. H. B., Roberto G. H. B., Roberto G. H. B., Roberto G. H. B., Roberto G. H. B., Roberto M. M., Sayani H. W., Sayani H. W., Sayani H. W., Sayani H. W., Sayani H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. --- CORACTOR: Binds 2 manganese ions per subunit (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                              Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
E3D2A310638965E9 CRC64;
                                                                                                                                                ö
                                                                                               DB 1; Length 490;
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                          491 AA.
                                                                                                                    Pred. No. 27;
0; Mismatches
                                                                                                  Score 33;
344 344 M
346 346 M
490 AA; 51181 MW;
                                                                                                                                                                                                                                                                                                                                                                       AMPA XYLFA STANDARD;
Q9PHQ8;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Leucyl aminopeptidase)
                                                                                               85.78;
                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                321 GNAYRPS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kylella fastidiosa.
                                                                                                                                                                                               7
                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                 1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPA OR XF0138.
                                                 SEQUENCE
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                        RESULT 10
AMPA_XYLFA
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AMPA_XANCP
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Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Nan Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

A Takita M.A., Lemos B.G., Mandado M.A., Ferro M.T.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Garrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

Coutinho L.L., Kimura B.T., Ferro B.S., Harakava R., Kuramae B.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Enrille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

A Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,

Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (Leucyl aminopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 185:1018-1026(2003).
-!- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 POTENTIAL.
264 MANGANESE 2 (BY SIMILARITY).
287 MANGANESE 2 (BY SIMILARITY).
387 MANGANESE 1 (BY SIMILARITY).
348 MANGANESE 1 (BY SIMILARITY).
348 MANGANESE 1 (BY SIMILARITY).
349 MANGANESE 1 AND 2 (BY SIMILARITY).
51723 MM; 3D0576F9A7CAP3EE CRC64;
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Xanthomonadaceae; Xylella.
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use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                         HAMAP; MF_00181; -; 1.
InterPro; IPR000819; Peptidase_M17_C.
InterPro; IPR008283; Peptidase_M17_N.
Pfam; PF00883; Peptidase_M17_N.
Pfam; PF00789; Peptidase_M17_1.
Pfam; PF00789; Peptidase_M17_N; 1.
PRINTS; PR00481; LAMNOPPTDASE.
PROSITE; PR06511; CYTOSOL_AP; 1.
Hydrolase; Aminopeptidase; Manganese; Complete proteome.
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Xylella fastidiosa (strain Temeculal / ATCC 700964)
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85.7%;
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HSSP; P00727; 1LAM.
MEROPS; M17.003; -.
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Q87F32;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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SEQUENCE FROM N.A.

SEQUENCE 33913 / NCPPB 528;

X. MEDLINE-2202145; PubMed=12024217;

A lausgio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A laves L.M.C. do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A laves L.M.C. do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorry H.,

A paria J.B., Ferreira A.J.S., Ferreira R.C.C., Fruber A.,

A pormighieri E.P., Franco M.C., Graggio C.C., Gruber A.,

A paria B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Manck C.F.M., Mayaki C.Y., Moon D.H.,

Martins B.C., Maddanis J., Menck C.F.M., Mayaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira W.R.,

Bereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
-!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
-!- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBLIBLY: Belongs to peptidase family M17.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (Leucyl aminopeptidase).
PEPA OR XCC0649.
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MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Pred. No. 27;
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InterPro; IPR00819; Peptidase_M17_C.
InterPro; IPR00829; Peptidase_M17_N.
Pfam; PF00883; Peptidase_M17; I.
Pfam; PF00789; Peptidase_M17; I.
PRINTS; PR00481; I.AMNOPPTASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
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FUNCTION: During lymphocyte development, the genes encoding
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                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    similarity).
    CATALVIIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-Xbb., in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
    COPACTOR: Binds 2 manganese ions per subunit (By similarity).
    SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
    SIMILARITY: Belongs to peptidase family M17.

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                        -I- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93389137; PubMed=8376769; Greenhalgh P.H., Olesen C.E., Steiner L.A.; Greenhalgh P.H., Olesen C.E., Steiner L.A.; "Characterization and expression of recombination activating genes (RAG-1 and RAG-2) in Xenopus layevis."; J. Immunol. 151:3100-3110(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
764A6FAD2BBDB775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.5%; Score 33; DB 1; Length 493; 85.7%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Aminopeptidase; Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V(D)J recombination activating protein 2 (RAG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00181; -; 1
InterPro; IPR000819; Peptidase_M17_C.
InterPro; IPR008819; Peptidase_M17_N.
Pfam; PF00881; Peptidase_M17; I.
Pfam; PF00481; LAMNOPPIDASE.
PRINTS; PR00481; LAMNOPPIDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                           EMBL; AE012163; AAM39965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51590 MW;
                                                             Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 GNAYRPS 327
                                            host specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=HD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAG2 XENLA
Q91830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT SITE
ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
RAG2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METĀL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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immunoglobulins and Teal receptors are assembled from variable (V), diversity (D), and joining (J) gene segments. This combinatorial process, known as V(D) Tecombination, allows the generation of an enormous range of binding specificities from a limited amount of genetic information. The RAGI/RAG2 complex initiates this process by binding to the conserved recombination signal sequences (RSS) and introducing a double-strand break between the RSS and introducing a double-strand break conserved in two steps, nicking of one strand (hydrolysis), followed by hairpin formation (transesterification). RAGI/2 has also been shown to function as a transposase in vitro, and to possess RSS-independent endonuclease activity (end processing) and hairpin opening. RAGI alone can bind to RSS but stable, efficient binding requires RAG2. All known catalytic activities require the presence of both proteins (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone marrow of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Aizawa M., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Is expressed within the thymus, liver and spleen in juvenile frogs, and within the thymus and bone mark adults. A lower level expression is seen in the ovaries. SIMILARITY: Belongs to the RAG2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foulon V., Casteels M., Mannaerts G.P., Van Veldhoven P.P.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1; Length 520; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520 AA; 58636 MW; E5105425D5295BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Endonuclease; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPCL MOUSE STANDARD; PRT; 581 AA. 090XE0; 09DAV1; SerBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 2-hydroxyphytanoyl-CoA lyase (EC 4.1.-.-) (2-HPCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Placenta;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L19325; AAA49943.1; -.
PIR; I51556; I51556.
InterPro; IPR004321; RAG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03089; RAG2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 GNNFRP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA recombination.
SEQUENCE 520 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GNNYRP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausher R.D., Collins F.S., Wagner L., Schmenen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buchow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buchow K.H., Schaefer C.F., Bhat N.K.,

B Altschul S.F., Zeeberg B., Buchow K.H., Schaefer C.F., Bhat N.K.,

A Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Erownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

R Achards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R A. Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Souffard G.G.,

RA Alting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Refereration and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)

C -1- FUNCTION: Catalyzes a carbon-carbon cleavage reaction; cleaves a

2-hydroxy-3-methylacyl-CoA into formyl-COA and a 2-methyl-branched

Eatty aldehyde (By similarity).

C -1- CARALYIC ACTIVITY: 2-hydroxyphytanoyl-COA and a 2-methyl-branched

Eatty aldehyde (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blowersein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: Binds 1 thiamine pyrophosphate and 1 magnesium ion per subunit (By similarity).
-!- PATHWAY: Alpha-oxidation of 3-methyl branched fatty acids (phytamic acid); third step.
-!- SUBUNIT: Homoterramer (By similarity).
-!- SUBCELLULAR LOCATION: Peroxisomal (By similarity).
-!- SIMILARITY: Belongs to the TPP enzyme family.
                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00205; TPP_enzymes; 1.
Pfam, PF02775; TPP_enzymes C; 1.
Pfam, PF02776; TPP_enzymes N; 1.
PROSITE; P$00187; TPP_ENZYMES; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016829; F:lyase activity; IDA.
GO; GO:0006629; P:lipid metabolism; IDA.
InterPro; IPR000399; Pyruvate_decarb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AJ132139; CAB65550.1; -. EMBL, AKO05505; BAB24088.1; -. EMBL, BC021360; AM121360.1; - MGD; MGI:1929657; Hpcl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
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Thiamine pyrophosphate; Magnesium; Peroxisome.

SIMILARITY)

581

Flavoprotein; Lyase; SITE 579 58

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ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURACE FROM N.A.

REDLINE=21618749; PubMed=11780052;

REDLINE=21618749; PubMed=11780052;

REDLINE=21618749; PubMed=11780052;

REDLINE=21618749; PubMed=11780052;

REDLINE=21618749; PubMed=11780052;

REDLINES=21618749; PubMed=11780052;

REDLINES P., Marthew D.H., Bartes D.M., Beare D.M.,

Reasley O.P., Blard C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Reasley O.P., Blurill W.D., Bultler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,

R. Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,

R. Chapman J.C., Clamp M., Clark G., Clark S.Y., Clee C.M.,

R. Chapman J.C., Clamp M., Clark G., Clark J.D., Dunn M.,

R. Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

R. Ellington A.G., Frankland J.A., Fraser A., Hoden J.L., Howden P.J.,

R. Hunche E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

R. Kan M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

R. Milne S.A., Mistry D., Mocore M.J.F., Mullikin J.C., Nickerson T.,

R. Millimcr K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

R. Spann R.M., Sycamore N., Taylor R., Thomas D., M., Tracey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M.,

R. Sycamore N., Tromans A.C., Vaudin M., Walli M., Wallis J., Williams S.A.,

Milning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

M. Mitcheed S.L., Whitteker P., Willey D.L., Williams B.A.,

M. Milming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

M. Walliming L., Wray P.W., Rubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).

TISSUB=Lung, and Tonsillar carcinoma;

Kawakami T., Noguchi S., Itoh T., Shigata K., Senba T., Matsumura K.,

Rawakami T., Noguchi S., Itoh T., Shigami A., Fujiwara T., Ono T.,

Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,

Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,

Isogai T., Sugano S.,

"NEDO human cDNA sequencing project.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity to N-cadherin.";
Submitted (UT-1999) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kools P.F.J., Van Roy F.; "Identification and characterization of a novel human cadherin with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      QBIXHB; QBTCH3; Q9BQN4; Q9NRU1;
10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
Cadherin-like protein 26 precursor (Cadherin-like protein VR20).
                                                                                                                   0;
                                                                80.5%; Score 33; DB 1; Length 581;
85.7%; Pred. No. 32;
1ive 0; Mismatches 1; Indels
252 M -> I (IN REF. 1).
63660 MW; ·7CABBFC780A32A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 405-847 FROM N.A. (ISOFORM 3).
                                                                                           Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 414:865-871(2001)
                                                                                                                                                                                                              315 GNNVRPS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                           581 AA;
                                                                                                                                                                  1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       CADO HUMAN
  CONFLICT
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roders
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5; Conservative
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ID MSRA
 Matches
                                                                        RESULT 16
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                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K -> KDLEEVPPSAASQSAQARCALGSWGYGKPFEPRSVK
NIHSTP (in isoform 2 and isoform 4).
/FTId=VSP 008331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKERNRFSLSRGCII PQGRATAGRGLPQDIYKEMMPRRLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAVSG -> KLHVANVLEDDPGYLPHVYSEEGECGGAPSLS
SLASLEQELQPDLLDSLGSKATPFEEIYSESGVPS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKRKHGALARTPSFKKVVYDHKEDEENKAGRKORSHLFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQLRNEQGGVRVQSAHSPSPLNKKACFPGDYRGESAGGHNC
                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO0205; CADHERIN.
SMART; SM00112; CA, 4.
PROSTE; PS00232; CADHERIN.1; 2.
PROSTE; PS50269; CADHERIN.2; 4.
Cell adheaion; Glycoprotein; Transmembrane; Calcium-binding; Repeat; Signal; Alternative splicing.
manner in connecting cells; cadherins may thus contribute to the
           sorting of heterogeneous cell types.
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                  Name=2; Synonyms=b;
Isold=081XH8-2; Sequence=VSP_008331, VSP_008334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        () (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2).
/FTId=VSP 008333.
KGTSAQ -> MKPLIW (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48A378DC655EBA5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CADHERIN-LIKE PROTEIN 26. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CADHERIN 3.
CADHERIN 4.
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
N-LINKED (GLCNAC. .) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                         Isold=Q81XH8-4; Sequence=VSP 008331;
Note=No experimental confirmation available;
SIMILARITY: Contains 4 cadherin domains.
                                                  Name=1 Synomyms=a,
IsoId=08IXH8-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                       Note=No experimental confirmation available;
                                                                                                                          IsoId=Q8IXH8-3; Sequence=VSP_008332;
Note=No experimental confirmation available;
                                          Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soform 3).
FIId=VSP 008332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTIG=VSP
                                                                                                                                                                                                                                                                                     EMBL; AK055202; -; NOT ANNOTATED_CDS.
EMBL; AL109928; CAD5557.1; ALT_TERM.
EMBL; AF16690; AAF89687.1; -I_TERM.
EMBL; AL109928; CAD55556.1; -.
                                                                                                                                                                                                                                                                                                                                          Genew, HGNC:15902; CDH26.
InterPro; IPR002126; Cadherin.
Pfam, PF00028; cadherin, 4.
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71.4%;
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                                                                                                                                                 Name=4;
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TRANSMEM
DOMAIN
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CARBOHYD
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Best Local Similarity

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Genome Res. 13:1042-1055(2003).

-!- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversable oxidation-reduction of methionine sulfoxide in proteins to methionine (By similarity).

-!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.

-!- SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=SS1-1 / Serotype M3;
MEDLINE=226831-21, Serotype M3;
MEDLINE=226831-218; PubMed=12793345;
Nakagawa I., Kurokawa K., Yamaabhita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MGAS315 / Serotype M3;
MEDLINE=2213808; Pubmed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlistevert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                       28-FBE-2003 (Rel. 41, Created)
28-FBE-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last aequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Peptide methionine sulfoxide reductase marA (BC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met (O) reductase).
SARA-2 OR SPNM3 03129 OR SPS1528.
Streptococcus pyogenes (Serotype M3).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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   Indels
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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   2; Mismatches
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InterPro; IPR002569; PMSR.
Pfam; PF01625; PMSR; 1.
ProDom; PD003489; PMSR; 1.
                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                |||:||:
263 GNNHRPA 269
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Best Local Similarity
                                                                       1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=198466;
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Matches

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                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (BC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Methionine-S-oxide reductase) (Peptide Methionine-S-oxide reductase).
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Peppide methionine sulfoxide reductase marA 2 (BC 1.8.4.6) (1)
methionine-S-oxide reductase 2) (Peptide Met(O) reductase 2)
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MEDLINE=21235186; PubMéd=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
                                                                                                                    Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY. SEEE1E1823A1BE30 CRC64;
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                                                                                                                                                                                                                                                         Serotype M1;
                                                                                                                                                                                                                                                         STRAIN=SF370 / ATCC 700294 / Serot
MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00401; msrA; 1.
Oxidoreductase; Complete proteome.
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ilarity 83.3%;
Conservative
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TPR002569; PMSR.
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                                                                                                                                                                                         NCBI_TaxID=1314;
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Q9CE42;
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SEQUENCE
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       셤
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-1- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaussee M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to methionine (By similarity).
CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin
protein L-methionine S-oxide + reduced thioredoxin.
SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (RC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met(O) reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROW N.A.
STRAIN-MGAS8232 / Serotype M18;
MEDLINE-21927593; PubMed=11917108;
Smot J.C., Barbian K.D., Van Gompel J.J., Smot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Rapur V., Daly J.A., Veasy L.G., Musser J.M.;
Genome sequence and comparative microarray analysis of serotype N group A Streptococcus strains associated with acute rheumatic feve outbreaks.";
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         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7800C67F3237891C CRC64;
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       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 pyogenes (serotype M18)
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Oxidoreductase; Complete proteome.
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Q9A149;
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MSRA_STRP8

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MEDLINE=90110209; PubMed=2104843;
MIX.-L., Tang J.;
Tang J.;
Thermostable acid protease from Sulfolobus acidocaldarius.";
Thermostable acid protease from Sulfolobus acidocaldarius.";
J. Biol. Chem. 265:1490-1495(1990).
T. PINATION: MAY REPRESENT A NEW CLASS OF ACID PROTEASES. IT DIGEST PROFEINS AND PEPTIDES IN ACIDIC SOLUTION, AND IS THERWOSTABLE. IT HAS MAXIMAL PROTEOLYTIC ACTIVITY AT PH 2 AND 90 DEGREES CELSIUS.
THAN MAXIMAL PROTEOLYTIC ACTIVITY AT PH 2 AND 90 DEGREES CELSIUS.
THROUGH SOME SIDE CHAINS.
THROUGH SOME SIDE CHAINS.
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THROUGH SOME SIDE CHAINS.
THROUGH SOME THERMOSTIN HAS PERHAPS A DIFFERENT TYPE OF ACTIVE
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                                                                                                    -!- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine (By similarity).
-!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
-!- SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
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Oxidoreductase; Complete proteome.
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ProDom; PD003489; PMSR; 1.
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InterPro; IPR002569; PMSR.
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01-AUG-1990 (Rel. 15,
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HSSP; P54149; 1FVG.
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92 GDNYRP 97
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There are no restrictions on ng as its content is in no
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"A novel gene expressed in human hypothalamus.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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E2758C0BC287FCE1 CRC64;
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28 POTENTIA
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71.4%;
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Science 260:78-82(1993)
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Boandado M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.C., Hake T. G., Abramson R.D., Mullahy S.J.,
Richards S.W., Mczup N.C., Hake G.J., Abramson R.D., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N. Krzywinski M.I., Skalska W.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length
Ill Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
POU domain, class 2, transcription factor 3 (Octamer-binding
transcription factor 11) (Oct-11) (Transcription factor Skn-1)
POUST3 OR OTF11 OR SKN1 OR SKN-1.
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BAA91243).
BAB14083).
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E -> K (IN REF. 2;
D -> G (IN REF. 2;
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CONFLICT 53 53 R ->
CONFLICT 219 219 D ->
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InterPro; IPR004000; Actin_like.
Pfam; PF00022; actin; 1.
SMART; SM00268; ACTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF220190; AAF67655.1; -. EMBL, AK0000544; BAAB1433.1; -. EMBL, AK025534; BAB14083.1; -. EMBL, BC011997; AAH11997.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.7 es 6; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MYNLEPMHTEIKMSGDVADSTDARSTFGGVESGNDRNGLDF
NORIKTEDLEGDTLHESLSHRPCHLTEGPTMMPGNQMSGDMA
SLHPLQQLVLVPGHLQSVSQFLLSQTPPGQQ -> MYSMFS
LSFKWPGFCLFVCFLCPFVLPCHS (in isoform 2).
                                                                                                                                                                                                                 -!- FUNCTION: Transcription factor that binds to the octamer motif (ATTTGCAT'). Activates cytokeratin 10 (K10) gene expression. May serve a regulatory function with respect to epidermal development. Isoform 2 inhibits transactivation by OCT-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=Skn-1a;
Isold=P42571-1; Sequence=Displayed;
Name=2; Synonyms=Skn-1i;
Isold=P42571-2; Sequence=VSP_002332;
-!- TISSUE SPECIFICITY: Expressed in epidermis.
-!- SIMILARITY: Belongs to the POU transcription factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 123863; -; NOT ANNOTATED CDS.

EMBL; 123863; -; NOT ANNOTATED CDS.

EMBL; 123863; -; NOT ANNOTATED CDS.

EMBL; 123863; -; NOT ANNOTATED CDS.

InterPro; IPR00135; Octamer-bind_TP.

InterPro; IPR00132; POU domain.

InterPro; IPR00132; POU domain.

InterPro; IPR00132; POU domain.

InterPro; IPR00132; POU domain.

INTERPROSED POUDOMAIN.

INTERPROSED PR00101; Homeobox; 1.

INTERPROSED POUDOMAIN.

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MEDLINE=94069332; PubMed=8248794;
Andersen B., Schonemann M.D., Flynn S.E., Pearse R.V. II,
Singh H., Rosenfeld M.G.;
Science 262:1499-1499(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       MEDLINE=93181164; PubMed=8441607; Goldsborough A.S., Healy L.E., Copeland N.G., Gilbert D.J., Jenkins N.A., Willison K.R., Ashworth A.; "Cloning, chromosomal localization and expression pattern of the POU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikutani H.; "Bpoc-1: a POU-domain gene expressed in murine epidermal basal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Transcription factor that binds to the octamer motif
                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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In; Transcription regulation; Homeobox.
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-!- TISSUE SPECIFICITY: Skin, thymus, stomach and testis.
-!- DEVELOPMENTAL STAGE: During embryogenesis and in adults.
-!- SIMILARITY: Belongs to the POU transcription factor family.
Class-2 subfamily.
                                        01-JUL-1993 (Rel. 26, Created)
01-NV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POU domain, class 2, transcription factor 3 (Octamer-binding transcription factor 11) (Got-11) (Epoc-1).
POUZE3 OR OTF11 OR OFF-11 OR OCT11 OR EPOC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=94040806; PubMed=8224904;
Yukawa K., YaBui T., Yamamoto A., Shiku H., Kishimoto T.,
      431 AA
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HOMEOBOX.
SER-RICH.
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MGD; MGI:102565; Pou2f3.
InterPro; IPR001356; Homeobox.
InterPro; IPR000972; Octamer-bind_TF.
InterPro; IPR000327; POU domain.
InterPro; IPR007103; POU_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                              domain gene Oct-11.";
Nucleic Acids Res. 21:127-134(1993)
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ProDom; PD000583; POU domain; 1.
SMART; SM01389; HOX; T.
SMART; SM00382; POU; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; F.V. HOMEOBUM. 2, DNA-binding; Nuclear protein; PAO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z18537; CAA79222.1; -. EMBL; L14677; AAA16855.1; -. PIR; S35541; S35541. HSSP; P14859; IOCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and thymic stromal cells.";
Gene 133:163-169(1993).
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Pfam; PF00157; pou; 1.
PRINTS; PR00029; OCTAMER.
PRINTS; PR00028; POUDOMAIN.
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PROSITE; PS00465; POU 2; 1.
PROSITE; PS50071; HOMĒOBOX
    STANDARD;
                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ('ATTTGCAT')
                                                                                                                                                                                                                                                                                                          TISSUE=Thymus;
PO23_MOUSE
P31362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99403087; Pubmed=10473598;
Hildesheim J., Foster R.A., Chamberlin M.E., Vogel J.C.;
Hildesheim J., Foster R.B., Chamberlin M.E., Vogel J.C.;
Hildesheim of the regulatory domains of the human skn-la/Epoc-1/Oct-11 POU transcription factor.";
J. Stol. Chem. 274:26399-26406(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jimenez-Mateco O., Castrillo J.L.;
Jimenez-Mateco O., Castrillo J.L.;
"PLA-1. a novel human POU transcription factor, regulates the placental lactogen-3 gene expression."
Submitted (CGT-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcription factor that binds to the octamer motif ('ATTGGAT'). Regulated the expression of a number of genes such as SPRRZA or placental lactogen.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Specifically expressed in epidermis and
R -> A (IN REF. 1).
P -> A (IN REF. 1).
P -> A (IN REF. 1).
P -> A (IN REF. 1).
SQUWALLT (IN REF. 1).
7E283E797EA8D3FA CRC64;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SIMILARITY: Belongs to the POU transcription factor family.
Class-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO23 HUMAN STANDARD; PRT; 436 AA.

G9UKIG; Q9UKIG; Q9YSO4;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
POU domain, class 2, transcription factor 3 (Octamer-binding transcription factor 11) (Oct-11) (Transcription factor Skn-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Fischer D.F., Hemelaar J., Backendorf C.;
Characterisation of the Numan transcription factor Oct-11:
involvement in the regulation of the SPRR2A gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     DB 1; Length 431
                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                  Score 32; DB 1
Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 homeobox domain.
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                                                                                                                                        431 AA; 47071 MW;
                                                                                                                                                                                                  78.0%;
85.7%;
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EMBL, AJ012214; CAB45383.1;
HSSP; P14859; 1OCT.
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                                                                                                                                                                                              Ouery Match 78.0
Best Local Similarity 85.7
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLA-1 protein).
POU2F3 OR OTF11 OR PLA1.
                                                                                                                                                                                                                                                                                                                                                                                                379 GNNSRPS 385
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      139
249
396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human chromosome 19413.2 and mouse chromosome 7.";

bubmitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: May function as a transcription factor.

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

-!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r protein; Transcription regulation; Homeobox.
257 POU.
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Shannon M., Branscomb E., Hauser L., Gordon L., Ashworth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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37 N -> K (IN REF. 2).

152 N -> D (IN REF. 2).

351 V -> D (IN REF. 1).

47451 MW; C674482739963C5B CRC64;
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Pred. No. 38;
0; Mismatches
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                                    InterPro; IPR001356; Homeobox.
InterPro; IPR000972; Octamer-bind_TF.
InterPro; IPR00127; POU domain.
InterPro; IPR007103; POU homeo.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
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                                                                                                                                                                                                                                                                                                      PRINTS; PR00029; OCTAMER.
PRINTS; PR00029; PCTAMER.
PRODOM; PR00010; HOMEOBOX; 1.
PRODOM; PD000583; POU domain; 1.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 1; 1.
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85.7%;
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PROSITE; PS00465; POU_2; 1
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Best Local Similarity
Matches 6; Conserv
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    MIM; 607394;
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224 HUMAN
10-0CT
DT 16-0CT
DT 16-0CT
DT 10-0CT
DT 10-0CT
DT 10-0CT
DT 20-0CT
DR HODER DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR BOOK DOR
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EMBL; AF187990; AAF04106.2; -.

HSSP; P08047; 1SP2. Genew; HGNC:13017; ZNF224.

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PROSITE; PSS00865; ZINC FINGER C2H2 1; 17.
PROSITE; PSS01057; ZINC FINGER C2H2 2; 18.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
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0
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157D9F7D4FCE39A7 CRC64;
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                                                                                                                                                                                                KRAB.

CC2H2 - TYPE.

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CC2H2 - TYPE.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF001352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 18.
ProDom; PD000003; Znf_C2H2; 9.
SWART; SW00349; KRAB; 1.
SWART; SW00355; Znf_C2H2; 18.
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82267 MW;
                                                                                                                                                                                    Nuclear protein, Repeat
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150 GNGYKPS 156
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ZN_FING
SEQUENCE
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Q8ex31 mycoplasma
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DE Jacalin-related lectin.  GN PALB. OS Phlebodium aureum. OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Moniliformopses; Filicophyta; Filicopsida; Filicales; Polypodiaceae; OC NCBI_TaxID=218620; RN [1] RP SEQUENCE FROM N.A. RC TISSUB=Rhizome;	RX MEDINTE=22538483; PubMed=12538884; RA Tateno H., Harry W.C., Petryniak J., Goldstein I.J.; RT "Purification, Characterization, Molecular Cloning, and Expression of RT Novel Members of Jacalin-related Lectins from Rhizomes of the True RT Pern Phlebodium aureum (L) J. Smith (Polypodiaceae)."; RL J. Biol. Chem. 278:10891-10891(2003). DR GO, GO:0005129; F:sugar binding; IEA. DR GO, GO:0005157; P:heterophilic cell adhesion; IEA. DR InterPro; IPR001229; Jacalin_lectin. KW Lectin. SCO: GO:UNDECTION CONTROL OF TAXARIRERAGA CRC64:	Duery Match  Duery Match  Best Local Similarity 100.0%; F  Attches 6; Conservative 0;  1 GNNYRP 6  117 GNNYRP 122	RESULT 2  Q9W316  1D Q9W316  AC Q9W316; Q96FF;  DT 01-MAY-2000 (TEMBLrel. 13, Created)  DT 01-CCT-2002 (TEMBLrel. 22, Last sequence update)  DT 01-CCT-2003 (TEMBLrel. 25, Last annotation update)  DT 01-CCT-2003 (TEMBLrel. 25, Last annotation update)  DT 032698 protein (GH2663p).  GN CG32698 OR CG9678 OR CG9678  OS Drosophila melanogaster (Fruit fly).  OC Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  OC Ropotera; Endopterygota; Diptera; Brachycera; Muscomorpha;  OC Ephydroides; Drosophilidae; Drosophila.	RN [1]  RN [1]  RD SEQUENCE FROM N.A.  CTRAIN=Berkeley;  RX MEDLINE=20196066; PubMed=10731132;  RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  RA George R.A., Lewiss S.E., Richards S., Ashburner M., Henderson S.N.,  RA Brandon R.C., Rogers YH.C., Plazej R.G., Champe M., Pfeilfer B.D.,  RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  RA Man K.H., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,  RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  RA Borkova D., Botchan M.R., Bouck J., Broketen P., Brotter P.,  RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center R., Chandra I.,  RA Burtis K.C., Busam D.A., Batler H., Cadleu E., Center R., Chandra I.,  RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei MH., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kennison J.A., Ketchum K.A., RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kennison J.A., Katchum K.A., RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liin X.,
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A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Pacteb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A G.J., Yeh. Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou K., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                            Celniker S. E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
By Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Perriers S., Frise B., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B., Scheeler F.,
A phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.; Shobmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yn C., Lewis S.B., Rubin G.M., Celniker S.,
Submitted (AuG-2001) to the EMBL/Genbank/DDBJ databases.
EMBL, AE003448; AAF46521.2; --
EMBL, ANCOSIC20; ARK930441; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMBL; Arubises,
HSSP; 043570; 1JD0.
FlyBase; FBGN0652699; CG12698.
GO; GO:0004089; F:carbonate dehydratase activity; IEA.
GO; GO:0008270; F:ainc ion binding; IEA.
GO; GO:0006710; F:ainc ion binding; IEA.
InterPro; IPR001149; Euk COanhd.
Fram; PF00194; carb anhydrase; 1.
FroDom; PD000865; Euk COanhd, 2.
FroDom; PD000865; Euk COanhd, 2.
FroDom; PJ000865; Euk COanhd, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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90.2%; Score 37; DB 5; Length 327;

Query Match

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REAUGRICE FORWAN NA.

REAUGRICE FORWAN NA.

REAGAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Fashburner M., Henderson S.N.,

Bandarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Augustica G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazel, R.G., Champe M., Pfeiffer B.D.,

Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basue M., Barcandale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Banu A., Barchan B.P., Bhandari D., Bolphakov S.,

RA Berkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Daliker C., Davenport L. B., Davise P.,

RA Cherry J.M., Cawley S., Daliker C., Davenport L. B., Davise B.,

RA Cherry J.M., Cawley S., Daliker C., Davenport L. B., Davise B.,

RA Cherry J.M., Cawley S., Daliker W., Dugan-Rocha S., Punkov B.C., Dunn P.,

RA Cherry J.M., Cawley S., Daliker W., Dugan-Rocha S., Platschmann W.,

RA Chopen R., Downes M., Dugan-Rocha S., Platschmann W.,

RA Cholek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Hahman T.J., Hernandez J.R., Houck J.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J., Laid Y., Ling M.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.,

Ander M. Houston K.A., Howland T.G., Morris S., Kulp D., Lai Z.,

Luu X., Mattei B., McInton T.C., Mreisod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Wei M., Pecchel J.M.,

Rabarzolo M., Pittanan G.S., Pan S., Pollard J., Pari W.,

Rabarzolo M., Pittanan G.S., Pan S., Pollard J., Wang X.,

Rainer K., Remington K.A., Murphy L., Murny D.M., Nelson D.L.,

Raper E., Spadling A.C., Stapheton M., Strong R., Sung K., Shen H.,

Raper E., Spadling A.C., Stapheton M., Strong R., Sung X.,

Mulliams S.M., Woodager, Worley K.C. Wu D., Yang S., Yao Q., Xeng L.,

Rapen R.H., Wayer E.W., Rubin G.M., Venter E., Wang R., Sanith H.O.,

Rapen R. S., Myers E.W., Rubin G.M., Venter E., Stapher S., Stapher 
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Misra. S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F.,
Lewis S.E.;
Lewis S.E.;
                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Arthropoda; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                            447 AA
                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:2185-2195(2000).
                                            PRELIMINARY;
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                                            Q86BA6
RESULT 3
Q86BA6
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28 GNNYRP 33
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                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                   1 GNNYRP 6
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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0
                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neopiera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                              90.2%; Score 37; DB 5; Length 447; 100.0%; Pred. No. 43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.2%; Score 37; DB 5; Length 569; 100.0%; Pred. No. 56; ive 0; Mismatches 0; Indels
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                    Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                         48394 MW; 5AB7FD629E1B62FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63587 MW; 4463ECE6092EAE59 CRC64;
                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) P120 (Fragment).
                                                                                                                                                                                                                                                                           569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY121618; AAM51945.1; -. FlyBase; FBgn0037720; CG8312. InterPro; IPR006020; PTB_PID.
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                                                                                                                EMBL; AE003683; AAO41527.1; SEQUENCE 447 AA; 48394 M
                                                                                                                                                                       6; Conservative
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1es 6; Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                          Best Local Similarity
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GNNYRP 11
                                  SEQUENCE FROM N.A.
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                            1 GNNYRP 6
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Matches
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RRDLINE=20196005, PubMed=10731312,
A Adams M.D., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Davies P.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunn P.,
RA Dodson K., Doug L.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherfi A.,
RA Meiner S.M., Moy M., Murphy B., Murphy L., Murny D., Puri V., Pallson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Sun B.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Wang R.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Wang R.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Wang R., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 742; 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
Ciesiolka M., Vanlandschoot A., Staes K., van Roy F.;
"Armadillo-related proteins in Xenopus laevis.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 1 1 1 SEQUENCE 742 AA; 82927 MW; E51D3A3A5CB95FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.2%; Score 37; DB 100.0%; Pred. No. 74; cive 0; Mismatches
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                                                                                                                                                        InterPro; IPR008938; ARW.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 4.
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50176; ARM_REPEAT; 3.
                                                                                                                           EMBL; AF150746; AAG45945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Lage 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Gaps

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Biochem. Biophys. Res. Commun. 275:493-502(2000).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                            Paulson A.F., Mooney E., Fang X., Ji H., McCrea P.D., "Xarvcf: Xenopus Member of the p120 Catenin Subfamily Associating with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ikeda M., Yu W., Hirai M., Ebisawa T., Honma S., Yoshimura K., Honma K., Nomura M.; Honna K., Nomura M.; Honna K., Inding of a novel bHLH-PAS transcription factor superfamily gene, BMAL2; Its mRNA expression, subcellular distribution, and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB039921; BAB01485.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:sagnal transducer activity; IEA.
GO; GO:0003700; F:transduccription factor activity; IEA.
GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001067; MLL basic.
InterPro; IPR001067; MLC translocat.
InterPro; IPR001601; PAC.
InterPro; IPR001619; PAC.
InterPro; IPR001619; PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                            90.2%; Score 37; DB 13; Length 907;
100.0%; Pred. No. 91;
.ive 0; Mismatches 0; Indels
                                                                        Cadherin Juxtamembrane Region.";
J. Biol. Chem. 275:30124-30131(2000).
BMBL; AF287051; AAG00555.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR008938; ARM; 3.
SMART; SM00185; ARM; 3.
SEQUENCE 907 AA; 101572 MW; A3B9EF7A0E5B9B86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transcription factor BMAL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 AA
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MEDLINE=20422287; PubMed=10964693;
       MEDLINE=20459074; PubMed=10899158;
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRFAM8; TIGR00229; sensory_b
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PROSITE; PS50888; HLH 2; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE 551 AA; 61786 MA
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Best Local Similarity 100.0
Matches 6; Conservative
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Pfam; PF00989; PAS; 2.
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                                                                                                                                                                                         Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Renas C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Barson J.A. An H., Baldwin D., Eanzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

I begwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Amintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Amiliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.",

Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yed J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu K., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Snith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Catenin arvef-2ABC protan clawed frog).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Similarity 85.7%; Pred. No. 85, 6, Conservative 1; Mismatches 0; Indels

Best Local Similarity Matches 6; Conserva

Query Match

Kenopodinae; Xenopus.

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[1] SEQUENCE FROM N.A.

61786 MW; FF93B29B660E218D CRC64;

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Pfam; PF00010; HLH; 1.
Pfam; PF00989; PAS; 2.
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SEQUENCE 572 AA; 64
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105 GSNYRPS 111
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Matches 6: Conserv
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
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SEQUENCE FROM N.A.
SEQUELINE=20325577; Pubmed=10864977;
HOGENESCH J.B., Gu Y.Z., Moran S.M., Shimomura K., Radcliffe L.A.,
Takahashi J.S., Bradfield C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC000172.3 AAH00172.2; -. GO, GO:0005634; C:nucleus; IEA. GO, GO:0004891; F:signal transducer activity; IEA. GO, GO:0004891; F:signal transcription dactor activity; IEA. GO, GO:0007165; F:transcription dactor activity; IEA. GO, GO:0007165; P:regulation of transcription, DNA-dependent; IEA. GO, GO:0007165; P:signal transduction; IEA. InterPro; IPR001092; HLH basic. InterPro; IPR001067; Nuc translocat. InterPro; IPR001661; PAC. InterPro; IPR001661; PAC. InterPro; IPR00161; PAC. PEGM: PF00189; PAS; 2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to transcription factor BMAL2.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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85.7%; Pred. No. 85;
ive 1; Mismatches
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGREAMS; TIGR00229; sensory_box; 2.
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                                                                                                                                                                                                               PRELIMINARY;
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84 GSNYRPS 90
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GNNYRPS
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DT Q1-UN-:
DE BHLH-PAGN MOP9.
GN MAMMAII:
OX MAMMAII:
OX NCBI Tan
RP SEQUENCI
RX MEDLINE:
RX HOGENER
RA HOGENER
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"The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors."; J. Neurosci. 20:RC83-RC83(2000).

-!-- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
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Hogenesch J.B., Gu Y.Z., Moran S.M., Shimomura K., Radcliffe L.A.,
Hadanasch J.B., Gu Y.Z., Moran S.M.,
Hadanasch J.B., Bradfield C.A.;
Takahashi J.S., Bradfield C.A.;
"The basic helix-loop-helix-PAS protein MOP9 is a brain-specific
heterodimeric partner of circadian and hypoxia factors.";
J. Neurosci. 20;RC83-RC83(2000).
-! SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:00003700; F:transcription franscription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001092; HILL basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001061; PAC.
InterPro; IPR001014; PAS. domain.
PF00010; HIH; 1.
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HSSP; P3656; 1AM9.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004801; F:signal transducer activity; IEA.
GO; GO:0004100; F:transcription factor activity; IEA.
GO; GO:000315; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0001165; P:signal transduction; IEA.
InterPro; IPR001092; HIM-basic.
InterPro; IPR001167; Nuc.ranslocat.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS_domain.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 88;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E4056207B02D1FD1 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
BHLH-PAS transcription factor MOP9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0785; NCTRNSLOCATR, SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGR00229; sensory
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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599 AA

PRT;

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PRELIMINARY;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                      Gaps
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Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF246663; AAL50342.1; -. GO GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003701; F:signal transducer activity; IEA.
GO; GO:0003705; F:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001092; HIH basic.
InterPro; IPR0010161; PAC.
InterPro; IPR0010161; PAC.
InterPro; IPR0010161; PAS.
Fam; PF0010; HLH; 1.
Pfam; PF0010; HLH; 1.
Pfam; PF0010; HLH; 2.
Pfam; PF0010; HLH; 3.
Pfam; PF0010; HLH; 3.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 91;
ive 1; Mismatches 0; Indels
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85.7%; Pred. No. 91;
ive . 1; Mismatches 0; Indels
                                                                                                                                                                                      585 AA; 65556 MW; F7F44D78BB8ADF15 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2d.
              SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TICRFAM9; TIGR00229; SENSOTY_box; 2.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE 585 AA; 65556 MW; F7F44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plani; Fronos, NCTRNSLOCATR. SMART; SM00353; HLH; 1. SMART; SM00086; PAC; 1. SMART; SM00091; PAS; 2. TIGREAMS; TIGR00229; sensory box;
  PR00785; NCTRNSLOCATR
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PROSITE; PS50888; HLH 2; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE 588 AA; 65553 MK
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Best Local Similarity 85.7
Matches 6; Conservative
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121 GSNYRPS 127
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AC 08WYA
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RESULT 13 Q8WYA2

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"Identification of a novel ARNT-like transcription factor, hBMAL2.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
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MEDLINE=20538426; PubMed=11018023;
MEDLINE=20538426; PubMed=11018023;
Masemuzz K., de La Monnte S.M., Chin M.T., Layne M.D., Hsieh C.M.,
Yet S.F., Perrella M.A., Lee M.B.;
"CLIF, a Novel Cycle-like Factor, Regulates the Circadian Oscillation
of Plasminogen Activator Inhibitor-1 Gene Expression.";
J. Biol. Chem. 275:36847-36851(2000).
-I- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF246962; AAL50341.1; -.

R GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004370; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001092; HIM basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001067; Nuc_translocat.
R InterPro; IPR001067; PAS.
InterPro; IPR001067; PAS.
R PFam; PF00019; PAS; 2.
R PRMRT; SN00091; PAS; 2.
R SMART; SN00091; PAS; 1.
R SMART; SN00091; PAS; 1.
R SMART; SN00091; PAS; 1.
R PROSITE; PS08089; HIM 1; 1.
R PROSITE; PS08089; HIM 1; 1.
R PROSITE; PS08089; HIM 1; 1.
R PROSITE; PS08089; HIM 1; 1.
R PROSITE; PS08089; HIM 251 1.
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
Fukada Y.;
                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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85.7%; Pred. No. 93;
ive 1; Mismatches 0; Indels
Q8WYA2;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2c.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cycle-like factor CLIF.
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Best Local Similarity 85.77
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                                                                                                                                                                      Homo sapiens (Human)
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Gaps

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Indels

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Pred. No. 97; 1; Mismatches

85.7%; Pred. No.

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6; Conservative
Best Local Similarity
Matches 6; Conserv
                                                                     1 GNNYRPS
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01-JUN-2003
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PROSITE; E
SEQUENCE
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R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0004871; F:signal transducer activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR001092; HILH basic.

DR InterPro; IPR001001; Mac_translocat.

DR InterPro; IPR00101; PAC_

DR InterPro; IPR00101; HAH; PAS_domain.

DR PRINTF; PR00785; NCTRNBLOCATR.

DR SMART; SM00001; PAS; 2.

DR SMART; SM00001; PAS; 2.

DR SMART; SM00001; PAS; 2.

DR SMART; SM00001; PAS; 2.

DR SMART; SM00001; PAS; 3.

DR TIGRRAMS; TIGRRO229; sensory_box; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0009649; P:entranment of circadian clock; NAS.
GO; GO:0006355; P:entranment of transcription, DNA-dependent; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPR001092; Hill basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR0010610; PAC.
InterPro; IPR001014; PAS.
InterPro; IPR001014; PAS.
InterPro; IPR001014; PAS.
InterPro; IPR001014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. SARANCE K., Okano K., Hirota T., Takanaka Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 36; DB 4; Length 602;
85.7%; Pred. No. 93;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         67208 MW; AD8937DD526D8B45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DI-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-JUN-2003 (TYEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 AA
                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00229; sensory_box; 2. PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1. PROSITE; PS50112; PAS; 2. SEQUENCE 602 AA; 67208 MW; AD893
                                                                                                                                                                                                                               PRINTS, PR00785; NCTRNSLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
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PROSITE; PS50888; HLH 2;
PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Length 622;

DB 4;

87.8%; Score 36;

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"Identification of a novel ARNT-like transcription factor, hBMAL2."; Submitted (MAK-2000) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMBL; AF246960; AAL50339.1; -.
RGO; GO:0005634; C:nucleus; IEA.
GO; GO:000471; F:stanscription factor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
RGO; GO:000765; P:regulation of transcription, DNA-dependent; IEA.
RGO; GO:000765; P:regulation of transcription, DNA-dependent; IEA.
RGO; GO:0007165; P:signal transduction; IEA.
RITEFPO; IPR001067; Nuc_translocat.
RITEFPO; IPR001067; Nuc_translocat.
RR InterPro; IPR001014; PAS.
RR Pfam; PF00099; PAS.
RR Pfam; PF00099; PAS.
RR Pfam; PF00099; PAS.
RR SWART; SW00353; HLH; 1.
RR SWART; SW00096; PAS.
RR SWART; SW00091; PAS.
RR SWART; SW00091; PAS.
RR PIGRRAMS; ITGR00202; Sensory_box; 2.
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Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(TrEMBLrel. 25, Last annotation update)
(Novel protein similar to human AT-hook protein AKNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70887 MW; 972CE2BC5B05B1F3 CRC64;
                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2a.
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                                                                                                                                                                                               636 AA
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85.7%; Pred. No. 99;
ive 1; Mismatches
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(TrEMBLrel. 24, Last sequ
(TrEMBLrel. 25, Last anno
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00038; HLH 1; 1. PROSITE; PS50888; HLH 2; 1. PROSITE; PS50112; PAS; 2.
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                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                    155 GSNYRPS 161
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Best Local Similarity
Matches 6; Conserv
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                636 AA;
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2807W7
10 0807W
AC 0807W
AC 0807W
DT 01-JU
DT 01-JU
DT 01-JU
DE BM340
GE BM340
GS BM340
CS Muks m
OC Mamma M
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MEDLINE-2215703; PubMed=12228297;
Brouta F., Descamps F., Monod M., Vermout S., Losson B., Mignon B.;
"Secreted metalloprotease gene family of Microsporum canis.";
Infect. Immun. 70:5676-563 (2002).
EMBL; AJ490184; CAD35289.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004222; F:metalloendopeptidae activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001042; Peptidase M36.
InterPro; IPR001042; Peptidase M36.
Pfam; PF02128; Peptidase M36.
Pfam; PF02128; Peptidase M36.
PRONTS; PR0999; FUNNALYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichophyton rubrum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.4%; Score 35; DB 3; Length 632; 100.0%; Pred. No. 1.6e+02; tive. 0; Mismatches 0; Indels
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Capoccia S., Lechenne B., Zaugg C., Monod M.;
"Trichophyton rubrum encoding metalloprotease.";
Submitted (40G-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407185; AAN03636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 632 METALLOPROTEASE, MEP1.
632 AA; 69770 MW; D2FF2E8E8FABEBAF CRC64;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                     01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Metalloprotease, MEP1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative secreted metalloprotease 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0999; FUNGALYSIN.
PROSTITE; PS001142; ZINC PROTEASE; 1.
Metalloprotease; Protease.
SEQUENCE 635 AA; 70126 MW; EA11:
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InterPro; IPR006025; Pept M_Zn_BS.
Pfam; PF02128; Peptidase_M36; I.
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Best Local Similarity
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                                                                                                                           Microsporum canis.
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                                                                                                                                                                                                          NCBI_TaxID=82078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Protease.
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Viruses; daDNA viruses, no RNA stage; unclassified dsDNA viruses.
VCBI_TaxID=29250;
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                                                         Matthews L.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
By Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
R BEMBL; ALG83829; CAB62265.1; --
PIR; PT0636; PT0698.
GG; GG:0005576; C:extracellular; IEA.
GG; GG:0005179; F:hormone activity; IEA.
GG; GG:0005215; F:hormone activity; IEA.
GG; GG:0005215; F:transporter activity; IEA.
GG; GG:0006810; F:transporter activity; IEA.
R GG; GG:0006810; F:transporter; IEA.
R GG; GG:0006810; P:transport; IEA.
R InterPro; IPR002012; GnRH.
R InterPro; IPR002012; GnRH.
R PROSITE; PS00473; GNRH; TRANSPORT 1; 1.
R PROSITE; PS004216; SUGAR TRANSPORT 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                         87.8%; Score 36; DB 11; Length 1404;
85.7%; Pred. No. 2.3e+02;
ive 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.4%; Score 35; DB 12; Length 274;
85.7%; Pred. No. 65;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng C.H., Haiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF451898; AAN044281.; ---
InterPro: WW Rsp5. WW PROSITE; PS01159; WW DOWAIN 1; 1.
SEQUENCE 274 AA; 30555 WW; 978CE42F9FFCA83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Bust Local Similarity 85.7°,
Bust Local Similarity 65.7°,
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NCBI_TaxID=10090;
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Q8JKH7;
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Q8JODS
ID Q8JODS
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MEDLINE=22354719; Pubmed=12466555;
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SEQUENCE 1046 AA
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PROSITE;
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096240
ID 09624
AC 09624
DT 01-MA
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Q8EX31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                   Gaps
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STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%; Score 35; DB 17; Length 982; 85.7%; Pred. No. 2.5e+02;
                        Length 635;
                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Buryarchaeota orders incertae
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                     85.4%; Score 35; DB 3; L. 100.0%; Pred. No. 1.6e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
BEMBL, AE013485; AAM2117.1;
GO, GO:0005524; F:ATP binding; IEA.
GO, GO:0003754; F:chaperone activity; IEA.
InterPro; IPR003594; ATP
                                                                                                                                                                                                                                                           982 AA
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PRINTS; PR00775; HEATSHOCK90
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Query Match
Beet Local Similarity 100.0v
Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                              310 NNYRPS 315
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                                                                                                           NNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                    protein.
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Q8PUB4;
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08 PUB4
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087171
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Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 361:743-749(2003).
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NCBI_TaxID=28227,
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096240;
01-MAY-1999 (TYEMBLrel. 10, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
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100.0%; Pred. No. 2.6e+02;
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PS00013; PROKAR_LIPOPROTEIN; 1.
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InterPro; IPR001060; GGDEF.
InterPro; IPR0001060; GGDEF.
InterPro; IPR0000100; PAS-assoc C.
InterPro; IPR0000141; PAS domain.
InterPro; IPR0000143; ProK_lipoprot_S.
Pfam; PF00563; EAL; 1.
Pfam; PF00785; PAC; 2.
PROSITE; PS50883; EAL; 1.
PROSITE; PS50883; EAL; 1.
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Search completed: September 24, 2004, 02:18:33 Job time : 42.5472 secs
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MEDLINE=21189316; PubMed=11292810;
Cucarella C., Solano C., Valle J., Amorena B., Lasa I., Penades J.R.;
Hap, a Staphylococcus aureus surface protein involved in biofilm
formation.";
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                                                                                                                                       MEDLINE-99021743; PubMed=9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium
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                                  Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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EMBL; AE001414; AAC71936.2; -.
PIR; G71607; G71607.
Hypothetical protein.
SEQUENCE 1377 AA; 167626 MW; 99E2C9D0D9E0B7A8 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
PFB0735C.
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NCBI_TaxID=1280;
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Science 282:1126-1132(1998)
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01-MAY-2000 (TYEMBLEEL. 13, Created)
01-OCT-2002 (TYEMBLEEL. 22, Last sequence update)
25-OCT-2004 (TYEMBLEEL. 28, Last annotation update)
CG32698-PA (GHZ6663p).
Name=CG9683; ORFNames=CG32698;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Bidopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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099VHA6
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1: uniprot_sprot:*
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Filicophyta; Filicopsida; Filicales; Polypodiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Rhizome;
MBDLJRB=22538482; PubMed=12538584; DOI=10.1074/jbc.M211840200;
Tateno H., Harry W.C., Petryniak J., Goldstein I.J.;
Tateno H., Harry W. C., Petryniak J., Goldstein I.J.;
Purification, characterization, molecular cloning, and expression novel members of jacalin-related lectins from rhizomes of the true fern Phlebodium aureum (L) J. Smith (Polypodiaceae).";
J. Biol. Chem. 278-110899 (2003).
GO. GO.0005529; Psugar binding; IEA.
InterPro; IPR001229; Jacalin_lectin.
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            087tj7
086x31
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07w819
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 28pub4
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07X3P2
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O96240
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Best Local Similarity
Matches 6; Conserv
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327 AA.

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,
R. George R.G., Worten J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
R. Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
R. Beson K.Y. Basu A., Baxendall J., Bayzakarolu L., Beasley E.M.,
Beson K.Y. Banos P.V., Berman B.P., Bhandari D., Blothakov S.,
R. Burtis K.C., Buuam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R. Burtis K.C., Buuam D.A., Dalle C., Davenport L.B., Davise P.,
R. Burtis K.C., Buuam D.A., Dalle C., Perraz C., Ferrar C., Ferrar C., Ferrar C.,
R.A Burtis K.C., Buuam D.A., Dalle C., Perraz C., Perrar C., Perrar C.,
R.A Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.,
R.A Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C.,
R.A Glodek A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris M.L., Harvey D., Heiman T.J., Harris M.,
A Harris M.L., Harvey D., Heiman T.J., Wei M.H., Ibeywam C.,
A Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,
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A Lasko P., Lei Y., Leviseky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lu X., Matteel B., Morthcoh T.C., McLeodo M.P., Moshrefi A.,
Nount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
R. Rainert K., Pennigton K., Saunders R., Vent R., Pecleb J.M.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
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A Les C., Siden-Kiamos I. Simpson M., Stung S., Zhu X., Smith H.O.,
R. Jahen S.M., Woodager, World W., Wang G., Zhoo Q., Zheng L.,
R. Hang Z.Y., Wassarman D.A., Wainstock G.M., Weissenbach J.,
R. Hillams S.M., Woodager, World W., Shue B., Solnec 287:2185-219
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Maninker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drygdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426070; PubMed=12537573;
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)

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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Lib PW., Hoskins R.A., Galle R.E., Anderson R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogars Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Barter B.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Antis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Antris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Andrews D., Borchan M.R., Buller H., Cadieu E., Conter A., Chandra I., Andrews D., Bolcher A., Danke B.D., Dew I., Davies P., Andrews D., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borshi K.J., Evangelista C.C., Ferraz C., Ferritera S., Fleischmann W., Rosler C., Gabriellu J.H., Gu Z., Guan P., Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Ghavez C., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.B., Rubin G.M., Celniker S.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR063448; AAR46321.2, --
EMBL, AX051620; AAK93044.1; --
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                   FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0006730; P:one-carbon compound metabolism; IEA.
InterPro; IPR001148; Euk Coanhd.
Pfan: PF00194; Cab anhydrase; 1.
SEQUENCE 327 AA; 37182 MW; 9574C0BBBBA9FD01 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last anno
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RESULT 4
Q8MRF2
Kimmel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lak Y., Lei Y., Levitsky A.A., Li J. J., Li Z., Liang Y., Lin X., Lai X., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K., Nixon K., Nusskern D.R., Pacled J.M., Nelson D.E., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G., Reinett K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden Känmos I., Simpson M., Strong R., Sun E., Spradling A.C., Staplecon M., Strong R., Sun E., Spradling A.C., Staplecon M., Strong R., Sun E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Walliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Zhong Y., Zhong W., Zhou X., Zhu S., Zhan M., Zhong W., Zhou S., Zhu X., Smith H.O., Alberg R.A., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22445665; PubMed=12537568;
MEDLINE=22445665; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Peiffer B.D., Richards S., Sodergren B.J., Kichards S., Sodergren B.J., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finiahing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome:
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0037720; CG8312.
SEQUENCE 447 AA; 48394 MW; 5AB7FD629E1B62FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426069; PubMed=12537572;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Clampe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Prise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 2; Length 569; 100.0%; Pred. No. 61; 0; Indels ive 0; Mismatches 0; Indels
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFLS0746; AR4G45945.1; -
InterPro; IPR00838; ARM.
InterPro; IPR00825; Armadillo.
                                                                                                                                                                                                                                                                                                               (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                             EMBL; AY121618; AAM51945.1; -.
RIVBase; REGN0037720; CG8312.
InterPro; IPRO11036; PH related.
SEQUENCE 569 AA; 63587 MW; 4463ECE6092EAE59 CRC64;
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                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 80;
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SMART; SM00185; ARM; 5.
PROSITE; PS50176; ARM_REPEAT; 3.
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PRELIMINARY;
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RAMANDATION C. CALNIKER S.E., HOLD R.A., EVANS C.A. GOCARD J.D.,

RAMANDATION C.C., ROGERS Y.H., Blazel R.G., Champe M., Felifer B.D.,

RAMANDATION C.C., ROGERS Y.H., Blazel R.G., Champe M., Felifer B.D.,

RAMANDA R.C., ROGERS Y.H., Blazel R.G., Champe M., Felifer B.D.,

RAMANDA R.C., ROGERS Y.H., Blazel R.G., Champe M., Felifer B.D.,

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RAMANDA R.M., Band A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Benos P.V., Berman B.P., Brandari D., Bolahakov S.,

RAMANDA R.A.

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RAMANDA R.J. Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RAMANDA R.J. Benos P.V., Berman B.P., Brottler P., Cadieu E., Center A., Chanfra I.,

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RAMANDA R.J. Benos P.V., Howland T.J., Hernandez J.R., Houck J.,

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Alalai M., Kalush P., Karpen G.H., Ke Z., Kalp D., Lai Z.,

Liasko P., Lei Y., Leviteky A.A., Li J., Liang Y., Lin X.,

Liux X., Mattei B., McIntosh T.C., McLeod M.P., McIny D.M., Nalson D.L.,

RAMANDA R.M. Polascon K.A., Nixon K., Nixony D.M., Nalson D.L.,

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Surekas R. Y. Remington K., Stupleton M., Stupski M.P., Smith T.,

Surekas R., Tector C., Turner E., Wang A., Wang S., Yao Q.A., Ye J.,

RAMANDA R.W. Pittman D.A., Weinstock G.M., Sunba B.,

Surekas R., Woodager, Wan, Lian, Wang S., Zhu X., Smith H.O.,

RAMANDA R.M. Worley K., Wansatman D.A., Weinstock G.M., Weissenbach J.,

Ramanda R., Shong R.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Ramanda R., Shong R., Rubin G.W., V
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endoptervygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                   Created)
Last sequence update)
Last annotation update)
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                     866 AA
                                                                                   01-OCT-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                 PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                             ORFNames=CG8312;
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                                                 Q9VHA6
             RESULT 6
Q9VHA6
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Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

R. Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

R. Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Uddin T.B., Toshiyuki S., Carnino P., Prange C.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Atchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

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Raywinski M.I., Skalska U., Sachmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;
Ashburner M., Celniker S.E.; ^{\prime} "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Flybase; FBgn0037720; CG8312.
Interpro; IPR011036; PH related.
SEQUENCE 866 AA; 95236 MW; E1B0226E79A64A05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                          a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Xenopus laevis (African clawed frog)
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NCBI_TaxID=10090;
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   XRN2 MOUSE
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"Xarvef: Xanoyus Member of the pl20 Catenin Subfamily Associating with
"Cadherin Juxtamembrane Region.";
J. Biol. Chem. 275:30124-30131(2000).
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                   TISSUBESpleen;
BEDLINES-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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MEDLINE=20459074; PubMed=10899158; DOI=10.1074/jbc.M003048200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 2; Length 907; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.2%; Score 37; DB 2; Length 868; 100.0%; Pred. No. 94; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S., Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072124; AAH72124.1; -.
Interpro; IPR000238; ARM.
Interpro; IPR000225; Armadillo.
Pfam; PR00114; Arm; 4.
SWART; SM00185; ARM; 6.
PROSITE; PS00176; ARM_REPEAT; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .l protein. — 868 AA; 96907 MW; 433B1B5FB6CCF08F CRC64;
                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. >c,
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Xenopus laevis (African clawed frog)
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RM REPEAT; 3.
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InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
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Best Local Similarity 100...
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nes 6; Conservative
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SMART; SM00185; ARM; 5.
PROSITE; PS50176; ARM F
SEQUENCE 907 AA; 101
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155 GNNYRP 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
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SEOUENCE 86
                                                                                                                                                                                                                                                                                                                                          initiative.
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Q9DFB2;
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RC STRAIN=CS7BL/63; TISSUE=EmbryO. Eye, Forelimb, and Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y. Furuno M., Kasukawa T., Adachi J., Bono H., Kondoo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Badarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,
RA Balka J., Bragin T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Ronagaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Ronagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Ravasi T., Reed J.C., Remple C.A., Setou M., Shimada K.,
Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,
RA Verardo R., Wapner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynhaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Nilming L.G., Whimbaw-Boris A., Yanagisawa M., Yang I.,
RA Nilming L.G., Whimbaw-Boris A., Yanagisawa M., Zakezwa T., Fukuda S.,
RA Shiraki T., Waki K., Kawa J., Aizawa K., Arakawa T., Pukuda S.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sakazum I.,
RA Hara A., Hashizume W., Imotani K., Ishia Y., Ishiayaka A.,
Banishin A., Yoshaki K., Sasaki D., Shibata K., Shinagawa A.,
B., Ravasi Y., Sawai K., Sasaki D., Shibata E.S., Rogers J.,
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SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-C57BL/6, and Czech II; TISSUE-Brain, and Mammary gland;

XX MEDINE-2538825; PubMed=12477932; DOI=-0.1073/pnas.242663899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsiah F.,

Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiah F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley D.M., Sodersten B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                        Shobuike T., Sugano S., Yamashita T., Ikeda H.; "Characterization of cDNA encoding mouse homolog of fission yeast dhp1+ gene: structural and functional conservation.";
XRN2_MOUSE STANDARD; PRT; 951 AA.
Q9DBRI; Q61489; Q99KS7;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
5'-3' exoribonuclease 2 (EC 3.1.11.-) (Dhml protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 23:357-361(1995).
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95192042; PubMed=7885830;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                   Name=Xrn2; Synonyms=Dhml; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 420:563-573(2002).
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843 GNNYRP 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903 (2002).
-!- FUNCTION: Possesses 5'->3' exoribonuclease activity and may be involved in homologous recombination and RNA metabolism, such as RNA synthesis and RNA trafficking.
-!- SUBCELIULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                   IsoId=Q9DBR1-2; Sequence=VSP_007235;
Note=No experimental confirmation available. May result from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYPREGRKYPLPPPSGRYSWN -> VISTMWAVEGKQHTAH
                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: Expressed in the spleen, testis, heart, brain, lung, liver, skeletal muscle, and kidney.
-1- SIMILARITY: Belongs to the 5'-3' exonuclease family.
-1- SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03159; XRN N; 1.
PROSITE; PS50158; ZF_CCHC; FALSE_NEG.
Alternative splicing; Exonuclease; Hydrolase; mRNA processing;
Nuclear protein; Nuclease; RNA-binding; Zinc-finger.
ZN_FING 262 278
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R (in Ref. 1).

L (in Ref. 1).

H (in Ref. 2; BAC27318).

K (in Ref. 2; BAC27318).

L (in Ref. 1).

K (in Ref. 1).
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-> QV (in Ref. 2; BAC27318).
CF57479291DD18B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005634; C:nucleus; IC.
GO:0004534; F:5'-3' exoribonuclease activity; NAS.
GO:0016049; P:cell growth; IGI.
GO:0006310; P:DNA recombination; NAS.
GO:0006281; P:DNA repair; NAS.
GO:0007017; P:microtubule-based process; TAS.
GO:0016070; P:RNA metabolism; IGI.
                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.2%; Scor.
100.0%; Pred. No. 10.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 2
                                                                                                                                                                                                                                                                                                                                retention of an intron in the cDNA;
                                                                                                                                                                                                                                           IsoId=Q9DBR1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKE -> IKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0007283; P:spermatogenesis; IEP.
InterPro; IPR004859; Put 53exo.
InterPro; IPR001878; Znf CCHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AK004800; BAB23573.1; --
EMBL, AK031247; BAC27318.1; --
EMBL, AK053643; BAC35458.1; --
EMBL, BC004028; AAH04028.1; ALT_INIT.
EMBL, BC054743; AAH54743.1; --
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712
734
837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
221
332
336
493
563
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                                                                                                                                                                                                                                                               Name=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- CATALYTIC ACTIVITY: An alkanesufonate (R-CH(2)-SO(3)H) + FMNH(2) +
0(2) = an aldehyde (R-CHO) + FMN + sulfite + H(2)O.
-!- SIMILARITY: Belongs to the ssuD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- FUNCTION: Catalyzes the desulfonation of aliphatic sulfonates (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                  ORFNames=AER120C;
Ashbya gossypii, (Yeast) (Eremothecium gossypii).
Bukaryota; Fungi; Ascomyoota; Saccharomycotina; Saccharomycetes;
Saccharomyvetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alkanesulfonate monooxygenase (EC 1.14.14.5) (FMNH2-dependent aliphatic sulfonate monooxygenase).
Name-ssuD, OrderedLocusNames=bll7010;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 10895;
Gates K., Dietrich F.S., Brachat S., Voegeli S.E., Lerch A.,
Philippsen P., Gaffney T.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016818; AAS52804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 2; Length 1369; 100.0%; Pred. No. 1.5e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                             1369 AA; 151311 MW; 606DE612FEF0281A CRC64;
                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
  1369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 AA
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619 GNNYRP 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GNNYRP 6
                                                                                                                                                                                                                              NCBI_TaxID=33169;
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                                                                                                                 AER120Cp.
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Conservative

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Matches

Query Match

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Length 951;

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PRELIMINARY;
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ARNTL2;
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Q96J63;
                                                               Q9NYQ4
                      RESULT 13
Q9NYQ4
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2042287; PubMed=10964693; DOI=10.1006/bbrc.2000.3248; Ikeda M., Yu W., Hirai M., Ebisawa T., Honma S., Yoshimura K., Honma K., Nomura M.;
"CDA cloning of a novel bHLM-PAS transcription factor superfamily gene, BMAL2; Its mRNA expression, subcellular distribution, and chromosomal localization.";
Biochem BLophys. Res. Commun. 275:493-502(2000).
-!- SiMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain. HSSP; Q99814; 1P97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 000553; C: nucleus; IEA.
GO; GO: 0004871; F: signal transducer activity; IEA.
GO; GO: 0004871; F: signal transducer activity; IEA.
GO; GO: 0001700; F: transcription factor activity; IEA.
GO; GO: 0007165; P: signal transduction; IEA.
InterPro; IPR001092; Hill basic.
InterPro; IPR001067; Muc_translocat.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS.
Pfam; PP00010; Hill; 1.
Pfam; PP00010; Hill; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                        87.8%; Score 36; DB 1; Length 387;
85.7%; Pred. No. 66; .
ive 1; Mismatches 0; Indels
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85.7%; Pred. No. 94;
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C63361B094AD8431 CRC64;
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Last annotation update)
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or send an email to license@isb-sib.ch)
                                                                                  HAMAP; MF 01229; -; 1.

InterPro; IPR002103; Bac luciferase.
InterPro; IRR011251; Luciferase like.
Pfam; PF00296; Bac luciferase; I.
Complete Proteome; FNN; Monooxygenase; SEQUENCE 387 AA; 42411 MW; C63361B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                         EMBL; AP005960; BAC52275.1; -.
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SWART; SM00353; HLH; 1.
SWART; SM00086; PAC; 1.
SWART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor BMAL2
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                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        375 GNDYRPS 381
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84 GSNYRPS 90
                                                               HSSP; P80645; 1M41.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-2025557; PubMed=10864977;

Hogenesch J.B., Gu Y.Z., Moran S.M., Shimomura K., Radcliffe L.A.,

Takahashi J.S., Bradfield C.A.;

Takahashi J.S., Bradfield C.A.;

Takahashi J.S., Bradfield C.A.;

The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors.";

J. Neurosci. 20:RCB3-RCB3(2000)

J. Neurosci. 20:RCB3-RCB3(2000)

J. Neurosci. 20:RCB3-RCB3(2000)

Homain. BMBL; AF231339; AAF71307.1;

HSSP; Q99814; 1P97.
                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 98;
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                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BHLH-PAS transcription factor MOP9.
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01-DRA-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ARNIL2 protein (Fragment).
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stehetz T.B., Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.
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SEQUENCE FROM N.À.
MEDLINE=20325577; PubMed=10864977;
MEDLINE=20325577; PubMed=10864977;
Takahashi J.S., Bradfield C.A.;
Takahashi J.S., Bradfield C.A.;
The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors.";
J. Neurosci. 20:RC83-RC83(2000).
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:00003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IRR01092; HLL basic.
InterPro; IRR0100167; Wuc_translocat.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 99;
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PROSITE; PS50112; PAS; 2.
10N TER
SEQÜENCE 578 AA; 64621 MW; 280AF59AC0B082FD CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pfam; PF00989; PAS; 2.
PRINTS; PR00785; NCTRNSLOCATR.
SWART; SM00353; HLH; 1.
SWART; SM00091; PAS; 2.
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Best Local Similarity 85,77,
Thes 6; Conservative
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TISSUE=Placenta;
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ALIGNMENTS
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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

AAO15005 ID AAO15005 standard; peptide; 11 AA.

An anti-alpha6beta4 integrin light chain linked to a heavy chain Synthetic. Macaca fascicularis. 

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note= "Complementarity determining region (CDR) 1 of the
light chain"

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/note="Complementarity determining region (CDR) 1 of
heavy chain"
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/note= "Complementarity determining region (CDR) 1 of
heavy chain"
                                                                                                                           3 of
                                                                                                                                                                                                 "Complementarity determining region (CDR) 1 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tordsson MJ, Kearney PP;
                                                                                                /note= "Complementarity determining region (CDR)
11ght chain"
110. .127
                                                                      /note= "Complementarity determining region (CDR)
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Pred. No. 0.011;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsson LG,
              .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 55-56; 75pp; English.
                                                                                                                                                                /note= "linker"
158. .162
/note= "Complemer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-2000; 2000WO-SE002082.
                                                                                                                                                                                                             heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brodin TN, Karlstroem PJ,
Nilson BHK;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ACTI-) ACTIVE BIOTECH AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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N-PSDB; AAF84797.
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                                                                                                                                                                                                                                                                                                                              WO200130854-A2
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                                                                                                                                                        Peptide
              Key
Region
                                                                                                               Region
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The invention comprises a method (ribosome display system) for obtaining a specific binding pair (sbp) member that binds a complementary sbp member of interest. The method involves incubating mRNA molecules encoding an sbp and lacking an in-frame stop codon, allowing ribosome translation of the mRNA to produce the encoded sbp member, forming complexes comprising ribosome, mRNA, and encoded sbp member displayed on the ribosome. The ribosome display system is useful for the selection of an sbp member able to bind a complementary sbp member. The present amino acid sequence represents a GPI-linked cell surface receptor-specific VL
                                                                                                         Ribosome display system; specific binding pair; sbp; anti-FITC; VL CDR3; scFv antibody generation; GFI-linked cell surface receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              Obtaining specific binding pair member (I) that binds a complementary specific binding pair member of encapsidating specific binding pair member/ribosome complexes in a viral coat, comprises the use of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Engineered template; single primer amplification; antibody library; nucleic acid amplification.
                                                                           GPI-linked cell surface receptor-specific VL CDR3 peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 5; Length 11;
Pred. No. 0.077;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 42; 61pp; English.
                                                                                                                                                                                                                                                     26-MAR-2001; 2001WO-GB001319.
                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0193802P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.5%;
81.8%;
                                              16-AUG-2002 (first entry)
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ses 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
                                                                                                                                                                                      WO200175097-A2
                                                                                                                                                          Unidentified.
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                                                                                                                                                                                                                      11-OCT-2001.
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                AA015005;
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The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at the other, and contracting (S) with a primer having the predetermined sequence in the presence of a polymers contactides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for ilbrary. M1 is useful for producing an antibody librard into a suitable expression vector, where the vector can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of the present uncleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence. Our also sequence located on the same or different uncleic acid molecules. Acc62635 to Acc62753 and ABR54811 to antibuted accomplex library such as ABR54811 to antibute accomplex library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulator; immunosuppressive; immunostimulator; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematoeus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                           Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
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                                                                                                                                                                Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.4%; Score 49; DB 6; Length 110; 88.9%; Pred. No. 2.1; ive. 0; Mismatches 1; Indels
                                                                                                                                                                Lin Y,
                                                                                                                                                                Maruyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv SEQ ID 1115.
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                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 8e; 68pp; English.
                                          19-SEP-2002; 2002WO-US029889.
                                                                                   19-SEP-2001; 2001US-0323455P.
                                                                                                                                                                Frederickson S,
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                                                                                                                       (ALEX-) ALEXION PHARM INC.
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nes 8; Conserv
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27-MAR-2003
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Matches
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Gaps

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WO200202641-A1 Homo sapiens.

15-JUN-2001; 2001WO-US019110.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWS) super family and induces B cell tumour necrosis factor (TWS) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent the introduces antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 1733-1734; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                             17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0275248P.
21-MAR-2001; 2001US-0273799.
25-MAY-2001; 2001US-0293499P.
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72.7%;
                                                                 15-JUN-2001; 2001WO-US019110
                                                                                                                                              16-JUN-2000; 2000US-0212210P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114799/15
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10-JAN-2002
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This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and immunodeficiency (CVID) and content and activity and activity and activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer suppressing protein PP844 SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                   Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1734-1735; 3148pp; English.
                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB06006 standard; protein; 508 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer suppression; cancer
                                                                                                                                                                                                                                                                                                                     Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI INST ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000; 2000CN-00111997.
                                                                                                    2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
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                                                                           2000US-0212210P
                                                                                                                                                                                  25-MAY-2001; 2001US-0293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                       SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 HSWDSSGNH 234
                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-114799/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 247 AA;
                                                                                                    17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                           16-JUN-2000;
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                                                                                                                                                                                                                                                                                                                     SM,
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                                                                                                                                                                                                                                                                                                                        Ruben
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Gaps

10-JAN-2002

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The present invention describes human proteins with cancer suppressing activity. Also described are the polynucleotides encoding the proteins and a process for preparing the proteins by DNA recombination. The proteins and polynucleotides can be used in the treatment of diseases
                                                                                                      human protein able to suppress growth of cancer cells and its
                                                                                                                                                                                                                                                                   such as cancer. The present sequence represents a human cancer suppressing protein from the present invention
                                                                                                                                                         Claim 1; Page 39 (Disclosure); 65pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                         encoding polynucleotide.
                                                  WPI; 2002-042196/06.
                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                      N-PSDB; ABL39592
                                                                                                                                                                                                                                                                                                                       Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Score 43; DB 5; Length 508; Pred. No. 1.1e+02; 3; Indels 0; Mismatches 66.2%; 70.0%; 1 NSWDSSGTHP 10 ઠે

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Gaps

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160 NSWSSSSRHP 169 셤

ABP45969 standard; protein; 246 AA. ABP45969; RESULT 7 ABP45969 

Human BLyS binding scFv SEQ ID 1980. 19-AUG-2002 (first entry)

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatocid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

10-JAN-2002.

WO200202641-A1

15-JUN-2001; 2001WO-US019110. 16-JUN-2000;

17-OCT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P.

25-MAY-2001; 2001US-0293499P

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Hilbert Choi GH, Vaughan T, Ruben SM, Barash SC, Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

This invention describes novel antibodies that immunospecifically bind to

Claim 1; Page 2763-2764; 3148pp; English

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IGBP) polypeptides that specifically bind to a ligand for one or more disulphide bonds with polypeptides in transferted cells, to generate an IGBP that binds to a ligand, and transformed plant cells are selected, and preparing an IGBP array in plant cells. At least one peptide sequence has at least 75%

Disclosure; Page 14; 129pp; English.

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           tumour necrosis factor (TMS) where family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BuyS. The antibodies bind to BuyS and so may be used to detect and quantitate the presence of BuyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BuyS. They may also be administered to treat diseases oused with aberrant BuyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency syndrome (InDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                             Gaps
B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
                                                                                                                                                                                                                                                                                                           Length 246;
                                                                                                                                                                                                                                                                                                           Score 41; DB 5; Length 246
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lambda III light chain CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU70345 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001WO-US014349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000US-00563222.
                                                                                                                                                                                                                                                                                                            63.1%;
81.8%;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.0.,
Best Local Similarity 81.0.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           225 NSRDSSGTHLV 235
                                                                                                                                                                                                                                                                                                                                                                      1 NSWDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055482/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hein MB;
                                                                                                                                                                                                                                                                              Sequence 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200183806-A1.
                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU70345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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otitidis in the biological sample, (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (1) can be used in gene therapy. The polynucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials. The polynucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis

8X8888888888X8

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Gaps

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2; Indels

1; Mismatches

7; Conservative 1 NSWDSSGTHP 10

Matches

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Score 40; DB 6; Length 107; Pred. No. 63;

61.5%;

Query Match Best Local Similarity

Sequence 107 AA;

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The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, despendant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polynucleotide that is comprised in the expression vector; (6) a pharmaceulical composition comprising the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immuniaing against Alloiococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloiococcus
                                                                                                                                                                                                                                                                                      ö
sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD. IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (GHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The GHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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                                                                                                                                                                                                                                            Score 40; DB 5; Length 13; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alloiococcus otitis antigenic protein SEQ ID NO:3442.
                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 33; SEQ ID NO 3442; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Russell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB09502 standard; protein; 107 AA.
                                                                                                                                                                                                                                              61.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-NOV-2002; 2002WO-US036123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2002; 2002US-0426742P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcmichael JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                             2 SWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alloiococcus otitis.
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                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   2 AWDSSSDHP
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                                                                                                                                                                                                      Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-2003
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                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
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This polypeptide sequence comprises the VL domain of human scFv antibody 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the
                                                                                                                                                                                                                                 Transforming growth factor beta-1; TGF-beta-1; human; antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular dideases; cataract; glaucoma; scarring; glomeaulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthitis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agent contg. antigen-binding domain of human antibody to transformin growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jackson RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green JA, Jauner
PP. Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thompson JE, Vaughan TJ, Williams AJ, Green
Bacon L, Johnson KS, Wilton AJ, Tempest PR,
                                                                                                                                                                                                      Anti-TGF beta-1 scFv antibody 10A6 VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Fig 1b(ii); 184pp; English.
                                                                                                   AAW15538 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95GB-00020486.
96GB-00001081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-00020920.
                                                                                                                                                                    (first entry)
: | | | | | | | 65 SSWSSSGTWP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1995;
19-JAN-1996;
                                                                                                                                                                    27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                GB2305921-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1997.
                                                                                                                                   AAW15538;
                                                                RESULT 10
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The chimaeric anti-RhD antibodies can be used for diagnosis and therapy,

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adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retrinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty neural scarring and glomerulonephritis, also (not claimed) osteoporosis, or (ii) immune and inflammatory diseases (e.g. rheumatoid archritis, macrophage deficiency diseases (e.g. rheumatoid archritis, cids encoding human antibody WH and WL can be used for prodn. Of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding complementary determining regions - of human anti-rhesus antibodies, useful in prodn. of monoclonal antibodies and for passive
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                  Score 40; DB 2; Length 110;
Pred. No. 65;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody, rhesus D; blood-typing; CDR; haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-human RhD PAG-1 MAb (VL chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AAR12264 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLOO-) CENT BLOOD LAB AUTHORITY
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/label= CDR1
49. .55
/label= CDR2
                                                                                                                                                                                                                61.5%;
88.9%;
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                               Local Similarity 88.5
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                    88 NSRDSSGTH 96
                                                                                                                                                                                                                                                                           1 NSWDSSGTH 9
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                                                                                                                                                                                       Sequence 110 AA;
                                                                                                                                                              neutralisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughesjone N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunisation
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15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9107492-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                        AAR12264;
                                                                                                                                                                                                                   Query Match
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Region
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The invention relates to regulating a gammadelta T-cell mediated immune response in a mammal and involves administering to the mammal a soluble gammadelta T cell receptor (TCR). The method is useful for treating patients having, or are at risk of developing an intestinal condition, e.g. Crohn's disease, ischaemic colitis, irritable bowel disease, and color cancer; a lung condition associated with inflammation such as a condition associated with inflammation such as a metastatic lung tumour; a skin condition associated with inflammation or cancer as skin legion caused by bacterial infection, viral infection or laceration, and a skin cancer; or a condition associated with inflammation of the reproductive tract such as infection caused by bacterial or viral infection that involve the epithelial mucosal lining, a tubal infection, preventing tubal factor infertility, and a cancer selected from ovarian, cervical, uterine, prostate or testicular cancers selected from ovarian, cervical, uterine, prostate or testicular cancers selected from several controls.
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell receptor; TCR; gastrointestinal; antiinflammatory; cytostatic; tuberculostatic; dermatological; antibacterial; virucide; gynaecological; cell therapy; Vgamma; mouse.
               and are capable of providing blood- typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulating a gammadelta T-cell mediated immune response in a mammal, useful for treating inflammation in intestine, skin, lungs or reproductive tract, comprises administering to the mammal a soluble
                                                                                                                                                                                   ö
                                                                                                                                             DB 2; Length 111; 66;
                                                                                                                                                                                 Indels
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                                                                                                                                         61.5%; Score 40; DB 75.0%; Pred. No. 66; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine T cell receptor.Vgamma6 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 58-59; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                 ABR82488 standard; protein; 112 AA.
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gammadelta T cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                           Born WK,
                                                                                                                                                                                                                     3 WDSSGTHP 10
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N-PSDB; ACF35982.
                                                                                                          Sequence 111 AA;
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ABP44529 standard; protein; 249 AA

ABP44529 RESULT

112 WDSSGFHKV 120

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Human BLyS binding scFv SEQ ID 540.

(first entry)

19-AUG-2002

ABP44529;

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The invention relates to regulating a gammadelta T-cell mediated immune response in a mammal and involves administering to the mammal a soluble gammadelta T cell receptor (TCR). The method is useful for treating patients having, or are at risk of developing an intestinal condition, e.g. Crohn's disease, ischaemic colitis, irritable bowel disease, and colon cancer; a lung condition associated with inflammation such as airway hyperresposiveness, pneumonia, tuberculosis, and a primary or metastatic lung tumour; a skin condition associated with inflammation caused by bacterial infection, viral infection or laceration, and a skin cancer; or a condition associated with inflammation of the reproductive tract such as infection caused by bacterial infection caused by bacterial factor infection caused by bacterial infection used infection that involve the epithelial mucosal lining, a tubal infection, preventing tubal factor infertility, and a cancer selected from ovarian, cervical, uterine, prostate or testicular cancers. Sequences ABRR82485-489 represent murine TCR Vgamma chains used in the
                                                     ö
                                                                                                                                                                                                                                                                                                                                                       T cell receptor; TCR; gastrointestinal; antiinflammatory; cytostatic; tuberculostatic; dermatological; antibacterial; virucide; gynaecological;
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulating a gammadelta T-cell mediated immune response in a mammal, useful for treating inflammation in intestine, skin, lungs or reproductive tract, comprises administering to the mammal a soluble
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                Length 112,
                                                   2; Indels
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                  DB (
                                                     0; Mismatches
                  Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                      Murine T cell receptor Vgamma5 chain.
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                                                                                                                                                                                                              ABR82487 standard; protein; 120 AA.
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                  61.5%;
77.8%;
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gammadelta T cell receptor.
                                                                                                                                                                                                                                                                                   (first entry)
Query Match
Best Local Similarity 77.0
Lag 7; Conservative
                                                                                                                         104 WDSSGFHKV 112
                                                                                      3 WDSSGTHPV 11
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                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human, cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
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88.9%; Pred. No. 1.6e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan T, Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1047-1048; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2001; 2001WO-US019110.
                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                              WO200202641-A1
                                                                                                                                                                                                                                                         Homo sapiens.
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В
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Gaps

; 0

Score 40; DB 6; Length 120; Pred. No. 72; 0; Mismatches 2; Indels

Query Match 61.5%; Best Local Similarity 77.8%; Matches 7; Conservative

3 WDSSGTHPV 11

Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:114.

(first entry)

19-NOV-2002

ABP65370;

ABP65370 standard; protein; 469 AA.

ABP65370

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This invention describes novel antibodies that immunospecifically bind to Elymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthitis, immune, and autoimmune disorders and immune disorders and elemented of the systemic lupus erythematosus, rheumatoid arthitis, immune, and autoimmune disorders and elemented the statement by the such as concer, immune, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and activity such as concer, immune, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, rheumatoid arthitis, and autoimmune disorders and elemented the systemic lupus erythematosus, and autoimmune disorders and elemented the systemic lupus erythematoid and elemented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                Human BLyS binding scFv SEQ ID 353.
                                                                                                ABP44342 standard; protein; 249 AA
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16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
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RESULT 15
ABP44342
ID ABP44342
XX
AXC ABP441
XX ABP442
XX BLY8;
KW BLY8;
KW BLY8;
KW ANTIA
XX HOWO
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rine present into the control of the properties of the present into present in the present in ABQB1842 and ABQB1843, or a sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at least 90% identity or which hybridises with the sequence given in ABQB1842 and ABQB1843. Also described is a polymucleotide (II) encoding a fusion protein, comprising a sequence selected from 1097 sequences given in ABQB2828 to ABPG6354 ligated in frame to a polymucleotide encoding a ctivities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of activities, and can be used as an inhibitor of Salmonella. (I) (which is a lift dobacterium longum in a biological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented creal based products, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the sufidobacterium related nucleotide sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Bifidobacterium sequences given in the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given in the Sequence of the Bifidobacterium sequences given the Sequence of the Bifidobacte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                            Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a polynucleotide (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 40; DB 5; I
87.5%; Pred. No. 3.2e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 114; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001EP-00102050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a biological sample.
                                                                                                                                                                                                                                                                                                                  Bifidobacterium longum.
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                                                                                                                                                                                                                                                                                                                                                                      EP1227152-A1
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61.5%; Score 40; DB 5; Length 249; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels

Best Local Similarity 88.5 Matches 8; Conservative

Query Match

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed cativity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in printed specification, but was obtained in processing the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%; Score 39; DB 4; Length 61; 50.0%; Pred. No. 50; 4; Indels ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 31808; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                 Novel human diagnostic protein #1440
                                        ABG01449 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631
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23-AUG-2000; 2000US-00649167
                                                                                                                          (first entry)
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N-PSDB; AAS65636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                                          13-FEB-2002
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                  ABG01449;
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RESULT 17
ABG01449
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The invention relates to novel isolated human secreted polypeptides (I)

and polymucleotides (II). (I) and (II) are useful for treating

conditions such as arthritis, nephritis, Crohn's disease,

ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

involved in increasing haematopoiesis, stem cell survival, bone growth

and remodeling. (I), (II) and modulators of (II) are useful for

prophylaxis or treatment of one or more cancers. (II) is also useful for

creating transgenic animals useful for studying the in vivo activities of

the polypeptide as well as for studying modulators of the polypeptides.

(I) induces the proliferation of neural cells and regeneration of nerve

and brain tissue and is useful for the treatment of central and

parkinson's disease, Huntington's disease, and amyotrophic lateral

calerosis. In addition, (I) is involved in chemotactic or chemokinetic

activity, regulation of haematopoiesis and is useful for treating myeloid

cor lymphoid cell disorders, platelet disorders such as thrombocytopenia

and for regeneration of bone, cartilage, tendon, ligament and/or nerve

tissue growth, and in tissue repair, healing of burns, incisions, ulcers,

for treating osteoporosis, osteoarthritis, bone degenerative disorders and

protection or regeneration and treatment of lung or liver fibrosis,

creperfusion injury in various tissues, various immune deficiencies and

disorders including severe combined immunodeficiency (SCID), bacterial or

thougal infections, autoimmune disorders en multiple sclerosis,

theumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

cheumatoid arthritis, diabetes mellitus, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou P;
                                                                                                                                                                                                                  ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodonical disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                 secreted protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Agundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou
Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tiannes for direction
                                                                                                                                                       Novel human secretory protein, Seq ID No 626.
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                  AAU28269 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-2000; 2000US-00574454.
17-JUN-2000; 2000US-00596193.
14-JUL-2000; 2000US-00616847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-2001; 2001WO-US004942.
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20-OCT-2000; 2000US-00693267.
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200166689-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                          18-DEC-2001
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Zhao QA,
                                                               AAU28269;
AAU28269
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Local Similarity 50.0 1 NSWDSSGTHP 10 10 HQWDEQGAHP 19

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reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide (I) related to dendritic cells of the immune system and the polynucleotide (II) encoding (I). (I) is useful for screening for candidate therapeutic agents. (II) is useful for studying the presence, amount, distribution and normalcy of certain gene products produced by or expressed on dendritic cells. (II) is also useful to facilitate the discovery of compositions and methods useful for diagnosing and treating certain disease states. (I) and (II) are useful for diagnostic and therapeutic purposes. (I) is useful in binding studies, for construction and expression of modified molecules, for structure/function studies and for the preparation of polyclonal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides related to dendritic cells of the immune system, useful in the treatment of conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; dendritic cell; immune system; haematopoietic cell; immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 4; Length 162;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dendritic cell-derived protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= unknown
/note= "Encoded by awt"
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abnormal physiology or development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 21-22; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU75568 standard; protein; 305 AA
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                                                                                                                                                                                                                                                                                                                                                                  60.08;
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.00,
7, Conservative
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                                                                                                                                                                                                                                                                                                  Sequence 162 AA;
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AAU75568
ID AAU75568
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AXC AAU755
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DT 08-MA;
DX Human
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monoclonal antibodies. (I) is also useful as immunogenic components (e.g. antigens) for preparing antibodies or as targets for binding agent studies. (I) is useful in the treatment of conditions associated with abnormal physiclogy or development, e.g. disease or disorder associated with abnormal expression or abnormal signaling by a dendritic cell. (I) is also useful in the regulation and development of hemaropoinetic cells. The binding agent is useful to isolate and purify the immunogenic components by immunoaffinity chromatography, and as probes to distinguish expression libraries for particular expression products. (II) is useful as templates for the recombinant production of peptides and polypeptides, as probes and primers for the detection of the human genes, for chromosome mapping and as probes or to design PCR primers to identify chomologous genes in other mammalian species. The present sequence represents the amino acid sequence of human dendritic cell-derived
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Molecules for Disease Detection and Treatment; MDDT; MDDT-angonist; Gene therapy; cardiant; cytostatic; europyretetive; cardiovascular disorder; neurological disorder; cell proliferative disorder; autoimmune disorder; inflammatory disorder; developmental disorder; cancer; steroid metabolic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule for disease detection and treatment (MDDT)-54 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thornton M, Au-Young JK, Azimzai Y, Bandman O, Barroso I; Baughn MR, Becha SD, Borowsky ML, Ding L, Duggan BM, Elliott VS; Emerling BM, Forsythe IJ, Gandhi AR, Gietzen KJ, Gorvad AE; Griffin JA, Gururajan R, Hafalia AJA, Ring HZ, Ison CH, Jones KA, Lal PG, Lee EA, Lee S, Li JX, Lu DAM, Marquis JP, Lehr-Mason PM; Chawlan NK, Arvizu CS, Sanjanwala B, Sornasse T, Swarnakar A; Tang YT, Thangavelu K, Tran B, Tran UK, Warren BA, Xu Y, Yao MG; Yue H, Zebarjadian Y, Chang H;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.9e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ39144 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0304298P.

2001US-0305324P.

2001US-0307003P.

2001US-0308185P.

2001US-0310096P.
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50.0%;
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08-MAR-2002; 2002US-0363649P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50...
5; Conservative
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254 HQWDEQGAHP 263
                                                                                                                                                                                                                                                                                                                                                                                                                              1 NSWDSSGTHP 10
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                                                                                                                                                                                                                                                                                                                   Sequence 305 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2001;
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                                                                                                                                                                                                                                                                                   protein #2
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This invention relates to novel polypeptides associated with Molecules for Disease Detection and Treatment (MDDT) and the cDNA sequences which encode them. MDDT-antagonists, MDDT-agonists or gene therapy may produce cardiant, cytostatic and neuroprotective activities. The polypeptides and Composition for the invention may be useful for the preparation of a associated with decreased expression or over-expression of functional MDDT proteins, for example cardiovascular, neurological, cell proliferative, autoimmune/inflammatory or developmental disorders. They may also be useful in the treatment and diagnosis of cancer, diseases treated with steroids and disorders caused by the metabolic response to treatment with steroids. The present sequence is the amino acid sequence of a human Molecule for Disease Detection and Treatment (MDDT) of the
                             New Molecules for Disease Detection and Treatment polypeptides, useful for preparing a composition for diagnosing or treating e.g. cardiovascular or neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 39; DB 6; Length 305; 50.0%; Pred. No. 2.9e+02;
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Matches 5; Conservative
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Gaps

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4; Indels

1; Mismatches

AAB71910 standard; protein; 311 AA. (first entry)

Human, ISOM, isomerase; antiasthmatic; antiallergic; dermatological; antidiabetic; immunosuppressive; cytostatic; antiinflammatory; osteopathic; antipsoriatic; antirheumatic; antiarthritic; anti-HIV; antiarteriosclerotic; antithyroid; nephrotropic; neuroprotective; hepatotropic; gene therapy; immune disorder; autoimmune disease; diabetes mellitus; cancer; cell proliferative disorder.

99US-0149388P 17-AUG-1999;

(INCY-) INCYTE GENOMICS INC

WPI; 2001-202861/20 N-PSDB; AAF60311 Tang YT;

Tran B, Hillman JL, Baughn MR, Lal P;

Yue H,

Lu DAM,

Bandman O,

Novel human isomerases useful for diagnosing, preventing and treating immune disorders, inflammatory disorders and cell proliferative disorders

Claim 1; Page 88-89; 102pp; English.

including cancer.

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The present sequence is an isolated human isomerase (ISOM) polypeptide. It is useful for treating a disease or condition associated with decreased or increased expression of functional human isomerase. It is useful for treating immune disorders such as inflammation, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome (AIDS), allergies, namenia, asthma, atherosclerosis, Crohn's disease, atopic dermatitis, glomerulonephitis, Grave's disease, Hashimoto's thyroiditis, multiple sclerosis, osteoporosis, rheumatoid authinitis, psoriasis, myccardial or pericardial inflammation, and autoimmune diseases, diabetes mellitus, cancers and cell proliferative disorders such as actinic keratosis, prostatitis, cirrhosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, secreted protein, arthritis, Crohn's disease; sepsis, shock, ischaemia-reperfusion injury, haematopoiesis, cancer, neuropathy, transgenic animal, Alzheimer's disease; Parkinson's disease, burn, amyotrophic lateral sclerosis, platelet disorder; thrombocytopenia, ulcer; osteoporosis, bone degenerative disorder; periodontal disease; gut protection; lung, liver fibrosis; immune deficiency; infection; severe combined immunodeficiency, SCID; autoimmune disorder; allergy, multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J;
                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                      Score 39; DB 4; Length 311;
Pred. No. 3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secretory protein, Seq ID No 250.
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14-JUL-2000; 2000US-00616847.
19-SER-2000; 2000US-00665353.
20-OCT-2000; 2000US-00693267.
                                                                                                                                                                                                                                                                                      60.08;
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19-MAY-2000; 2000US-00574454.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                       Sequence 311 AA;
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                                                                                                                                                                                                                     myelofibrosis
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Zhao QA,
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intramarcty contactous were as arturita, neparation; crown as arturita, neparation; crown as arturita, neparation; crown as arturita, neparation; crown and increasing haematopoiesis, stem cell survival, bone growth and emodulators of (II) are useful for and remodulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptides as well as for studying modulators of the polypeptides.

(I) induces the proliferation of meural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and perkinson's disease, Huntington's disease, and amouropathies, such as Alzheimer's, parkinson's disease, Huntington's disease, and amouropathies, concenting myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, or periodoncal disease. Furthermore, (I) is also useful for get correction or regeneration and treatment of lung or liver fibrosis. reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of thythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides activity and can act as an antigen in a vaccine composition to raise an immune response. AdU28020-AAU28395 represent novel human secreted protein The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, amino acid sequences of the invention 

Sequence 324 AA;

Gaps ö Length 324; Score 39; DB 4; Length 527, Pred. No. 3.1e+02; 60.0%; Local Similarity 77.8 es 7; Conservative Query Match Matches

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RESULT 23

ABU03132 standard; protein; 683 AA.

(first entry) 21-JAN-2003 ABU03132;

Alpha amylase polypeptide #93.

Alpha amylase, enzyme, starch linkage hydrolysis, starch liquefaction, starch breakdown catalysis, textile desizing; lignocellulosic fibre, enzymatic de-inking; recycled paper; high-maltose syrup; dough; high glucose syrup; corn-wet milling process; detergent; baking process; beverage; oil field; fuel ethanol; brewing process; staling; starch modification ABU03132
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AAC ABU
DT 21--XXX
XXX
DT 21--XXX
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Unidentified

WO200268589-A2.

06-SEP-2002.

21-FEB-2002; 2002WO-US005068

21-FEB-2001; 2001US-0270495P. 21-FEB-2001; 2001US-0270496P.

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The invention relates to a purified polypeptide with alpha-amylase activity and the polymucleotide encoding it. The polypeptide is useful for hydrolysing starch linkages, for catalysing the breakdown of a starch, for modifying small molecules, for liquefying starch, for washing an object, for textile desizing, for treating lignocellulosic fibers, for improving fibre properties, for enzymatic de-inking of recycled paper pulp, for producing a high-maltose or high-glucose syrup or a mixed syrup, and for increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging think formed during production operations and found within the cuber completed well bore. The polypeptide is also useful for preparing a dough or a baked product proparated from the dough and in corn-wet milling processes, detergents, baking processes, beverages, oil fields (fuel ethanol), brewing processes and starch modification in the paper and pulp industry, for removing starch containing stains from a material and for reducing staining of
                                                                                                                                                                                                    Novel purified polypeptide with alpha-amylase activity, useful e.g. fo
liquefying starch, for textile desizing, for treating lignocellulosic
fibers, and for producing high-maltose or high-glucose syrup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             starch containing stains from a material and for reducing staling of bakery products. Sequences ABU03040-ABU03144 represent alpha amylase polypeptides of the invention
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66.7%; Pred. No. 7e+02;
iive 1; Mismatches 2; Indels
                                                                                          Frey G;
                                                                                                                                                                                                                                                                                                 Claim 30; Fig 16; 301pp; English
14-MAY-2001; 2001US-0291122P.
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Matches 6; Conservative
                                                                                        Richardson T,
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364 NNWDYLGTH 372
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AAU92973 standard; protein; 1336 AA. (first entry) 02-JUL-2002 AAU92973; AAU92973 

Arabidopsis transcription factor #11.

Agriculture, metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence. plant; transcription factor; transgenic

Arabidopsis thaliana.

WO200215675-A1.

28-FEB-2002.

22-AUG-2001; 2001WO-US026189.

22-AUG-2000; 2000US-0227439P. 16-NOV-2000; 2000US-00713994. 16-NOV-2000; 2000US-00713994. 18-APR-2001; 2001US-00837944.

(MEND-) MENDEL BIOTECHNOLOGY INC.

21-OCT-2002; 2002US-00278173. 23-MAR-1999; 99US-0125814P. 22-MAR-2000; 2000US-00533393.

RIECHMANN J

RIEC/) ZHAN/)

PINE/

JIANG C. BROUN P.

(JIAN/)

PINEDA O.

ZHANG J.

EG G

PILG/)

KEDD/)

Arabidopsis thaliana.

US2003061637-A1

27-MAR-2003

plant stability

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The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered behance to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a chance given in the specification. The isolated or sequences comprising sequence information selected from one of 464 fully defined sequence given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polymeptide or antisense nucleic acid, thereby producing a modified trait, and selecting or antisense nucleic acid, into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polymental stress response (e.g. drought), microbial disease response response (e.g. drought), microbial disease response response response traits listed in the specification). The present sequence and many other traits listed in the specification). The present sequence and many other traits listed in the specification).
                                                                                                                                                                                                                                                                                                                                                 isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                       Keddie J;
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                                                                                                                                                                                                                                    Jiang C,
                                                                                                                                                                                                                                  Dubell AJ, Heard J, J
lber JL, Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 40; Page 118-123; 941pp; English.
                                                                                                                                                                                                                                                       Reuber JL,
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798 NSWDASGS 805
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                                                                                                                                         REUBER J L.
RIECHMANN J
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               CREELMAN R. DUBELL A J.
                                                                                                       ADAM L.
RATCLIFF O.
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Matches 6; Conserv
                                                 HEARD J.
JIANG C.
KEDDIE J.
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New transgenic plant comprising a recombinant polynucleotide, useful for altering a plant's trait for increasing plant stability.

Claim 1; SEQ ID NO 128; 159pp; English

Adam L;

Yu G;

Riechmann JL, Pineda O, Zhang U, ...

Keddie J, Heard J,

Broun P,

Jiang C, Bro

Samaha R;

SAMAHA R.

SAMA/)

ADAM L

WPI; 2003-555503/52.

N-PSDB; ADA15572

REUBER L. RATCLIFFE O.

(HEAR/) (REUB/) (RATC/) (ADAM/)

PILGRIM M. KEDDIE J. HEARD J.

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                                         Gaps
                                               ADA15573 standard; protein; 1336 AA.
                                                 ADA15573;
                                              RESULT 25
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Transgenic plant; plant; transcription factor; trait; root;

A. thaliana protein, SEQ ID NO:128.

(first entry)

06-NOV-2003

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The invention discloses a transgente plant naving an a transpent of the combinant polynucleotide with at least 6 consecutive amino acids of one of the amino acids sequences given in the specification. The recombinant polynucleotide with at least 6 consecutive amino acids of one of the amino acids sequences given in the specification. The recombinant polynucleotide. Also claimed are methods for altering the expression levels of at least one gene of a plant, altering the expression levels of at least one gene of a plant, altering a trait associated with a plant's roots and altering a plant's trait. The ecombinant polynucleotide the promoter is constitutive or inducible or root-active. The method for altering a trait associated with roots comprises transforming a plant with the recombinant polynucleotide.

Toot-active. The method for altering a trait associated with roots comprises transformed plants and identifying a transformed plant with the recombinant polynucleotide and selecting the transformed plants and identifying a transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting the transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting the transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting a plant of the transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting a plant of the transformed plant. The method for altering a plant in the plant is plant comprises providing a database sequence comparing the database sequence criteria and transforming the selected database sequence in the plant. The methods also comprises providing a test polynucleotide, hybridising the test polynucleotide at a polynucleotide and selecting the test polynucleotide and selecting the test polynucleotide and selecting the test polynucleotide and selected sequence criteria and transforming a plant with the recombinant polynucleotide at low stringents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the plant. The transgenic plant is useful for altering a plant's for increasing plant stability. The sequence presented is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ransforming the hybridising test polynucleotide in a plant to alter
The invention discloses a transgenic plant having an A. thaliana
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Pred. No. 1.5e+03;
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US-08-384-106A-21
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42, Appl
50, Appl
67, Appl
7103, Ap
35, Appl
35, Appl
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1060, Ap
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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                                                                                                                                                                                                                                                                        389414 segs, 51625971 residues
            GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 150 summaries
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65
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
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Maximum DB seq length: 200000000
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Perfect score:
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670, App 20, Appli 2, Appli 2, Appli 4781, Ap 16, Appli 4, Appli 4, Appli

5021, Ap 185, App 8, Appli

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RAGISTRATION NUMBER: 18 872

REFERENCE/DOCKET NUMBER: 7683-
TELECOMUNICATION INPORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUIENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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Matches 6; Conserv
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Sequence 24066, Application US/09252991A

Sequence 24066, Application US/09252991A

Fabricant No. 65517-095

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 448
                                                                     Sequence 2, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1286, Appli
Sequence 1286, Appli
Sequence 1856, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 8008, Appli
Sequence 8224, Appli
Sequence 8224, Appli
Sequence 6637, Appli
Sequence 6637, Appli
Sequence 6637, Appli
Sequence 6637, Appli
Sequence 6637, Appli
Sequence 6637, Appli
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US-09-252-91A-21695

US-09-053-197A-8

US-09-08-761A-8

US-09-08-761A-8

US-09-08-03A-8008

US-09-489-033A-8024

US-09-513-6637

US-09-134-000C-6086

US-09-134-000C-6086

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US-09-134-000C-6086

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US-09-252-991A-2519

US-09-252-991A-2519

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US-08-725-459B-2

US-08-725-459B-2

US-08-725-459B-2

US-08-725-459B-2

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US-08-725-459B-2

US-08-725-459B-2

US-08-725-459B-2

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US-08-384-106A-22
US-09-240-906-2
US-09-240-906-4
US-09-483-597-2
US-09-483-597-2
PCT-US96-01643-9
PCT-US96-05252-2
PCT-US96-05252-4
US-09-489-039A-7286
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Sequence 6, Application US/08716679; Patent No. 5846800; GENERAL INFORMATION:

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STAIL:

COUNTRY: USA

ZIP: 22440-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PLEATION PC-DOS/MS-DOS

SOFTWARE: PALEATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,571A

FILING DATE: 28 JUNE 1996

FILING DATE: 28 JUNE 1996

FILING ATTE: AATTON:
           SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,571A
FILING DATE: 28 UINE 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC 8.
REGISTRATION NUMBER: 32,181
REPRENCE/DOCKET NUMBER: 1422-0264P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1070-8000
TELECOMMUNICATION 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IZU, Hiroyuki
APPLICANT: KUROME, Yoko
APPLICANT: IZUMI, Yoshiya
APPLICANT: SANO, Mutsumi
APPLICANT: SANO, Mutsumi
APPLICANT: TATO, Ikunoshin
APPLICANT: TTO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Fallo Church
CONTRADENCE AUGGINA
CITY: Fallo Church
CONTRADENCE AUGGINA
CITY: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1;
Pred. No. 1.4e+02;
3; Mismatches 2
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08672571A
Patent No. 5795765
                                                                                                                                                                                                                                               TELERAX: (703) 205-8050
TELEX: 248345
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRRACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity
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APPLICANT: IZU, Hiroyuki
APPLICANT: KUROME, Yoko
APPLICANT: IZUMI, Yoshiya
APPLICANT: IZUMI, Yoshiya
APPLICANT: SATO, Ikunoshin
APPLICANT: ITO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 2; Length 92;
Pred. No. 26;
1; Mismatches 3; Indels
                      APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435

RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Migrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECHONE: 212-790-9090
TELECHONE: 212-869-8864/9741
TELERAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
                                                                               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08672571A Patent No. 5795765 GENERAL INFORMATION:
  APPLICANT: Schlessinger, Joseph
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IBM PC compatible
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LENGTH: 92 amino acids
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Best Local Similarity 60...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-716-679-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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19 TWDSGNTEPV 28
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STRANDEDNESS: un
                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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Sequence 1. Sequence 5. Sequence 5. Sequence 5. Sequence 5. Sequence 7. Sequence 7. Sequence 7. Sequence 7. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. Seque
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Pred. No. 4.8e+02;
2; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                    Query Match
58.5%; Score 38; DB 1; I
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 2.
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ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.;
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEFAX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
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Patent No. 5856162
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
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Best Local Similarity 55.6
Matches 5; Conservative
; STRANDEDNESS: single
; TOPOLGY: linear
; MOLECULE TYPE: peptide
US-08-672-571A-1
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MOLECULE TYPE: protein
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APPLICANT: Vogel, Wolfgang
APPLICANT: Vogel, Wolfgang
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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APPLICANT: Sap, Jan M.
APPLICANT: Sap, Jan M.
APPLICANT: Ullrich, Azel
APPLICANT: Fuchs, Miriam
APPLICANT: Fuchs, Miriam
APPLICANT: Puchs, Miriam
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,644
FILING DATE: 24-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,244
FILING DATE: 01-U1-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 55.6
Matches 5; Conservative
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MOLECULE TYPE: protein
US-08-449-644-8
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ADDRESSEE: PENNIE &
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STATE: New York
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STATE: New York
COUNTRY: U.S.A.
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58.5%; Score 38; DB 2; 155.6%; Pred. No. 4.8e+02; tive 2; Mismatches 2
                                                                                                                    Score 38; DB 2;
Pred. No. 4.8e+02;
                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08769399
Patent No. 5976852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P103:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 252-3216
TELEFAX: (415) 952-9816
TELEFX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                         58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1452 amino acids
                                                                                                                    Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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            STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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MOLECULE TYPE: protein
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Matches 5; Conserv
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                                                                               US-08-991-258A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-991-953A-4
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Sequence 4, Application US/08991258A

Patent No. 5928897

GENERAL INFORMATION:
APPLICANT: Cheng, Jill

APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA

TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

CITY: San Francisco

COUNTRY: United Stafes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2; Length 1452;
Pred. No. 4.8e+02;
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ches 2; Indels
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               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/087,244A
PILING DATE: 01-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTONEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION UNDRER: 30,742
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.5%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1452 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 SWDTENSHP 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                           amino acid
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GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Labsky, Laurence A.
APPLICANT: Labsky, Laurence A.
TITLE OF INVENTION: PHOSPHATASE, PTP. LAMBDA
TITLE OF INVENTION: PHOSPHATASE, PTP. LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
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Length 1452;
                                                      2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
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7; Conservative
                                                                                              141 WTDSAGTHP 149
                                                   3 W-DSSGTHP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                     US-08-350-260A-349
       Matches
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US-09-562-737-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.5; DB 4; Length 749; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1452;
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| Sequence 97, Application US/09562737
| Parent No. 6428967;
| GENERAL INFORMATION:
| APPLICANT: Herz, Joachim
| APPLICANT: Gotthardt, Michael
| TITLE OF INVENTION: LDL Receptor Signaling Pathways
| TITLE OF INVENTION: LDL Receptor Signaling Pathways
| CURRENT APPLICATION NUMBER: US/09/562,737
| CURRENT FILING DATE: 2000-05-01
| NUMBER OF SEQ ID NOS: 132
| SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT IRPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.78;
77.88;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
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LENGTH: 749
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Gaps
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APPLICANT: Nissim, Ahuva
APPLICANT: Onbason, Kevin Stuart
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

RPELICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION DATA:
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Indels
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STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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1; Mismatches
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FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/150,002 FILING DATE: 31-MAR-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/307,619 FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                 Sequence 349, Application US/08350260A Patent No. 5962255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Clough, David W
REGISTRATION NUMBER: 36,107
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INFORMATION FOR SEQ ID NO: 349:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-350-260A-349
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                        Score 37; DB 2; Length 11;
Pred. No. 4.1;
0; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bartnicki, Audrey L.
REGISTATION WUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/GB92/00883 FILING DATE: 15-MX-1992 APPLICATION NUMBER: PCT/GB93/00605 FILING DATE: 24-MAR-1993 APPLICATION NUMBER: US 08/150,002 FILING DATE: 31-MAR-1994 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION UNMERR: US/09/104,337A

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMERR: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMERR: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                    Sequence 349, Application US/09104337A Sequence No. 6492160 GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                56.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nissim, Ahuva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                       Query Match
Best Local Similarity 72.7.

"...na 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEOUENCES:
                                                                                                                                                                                        1 NSWDSSGTHPV 11
                                                                                                                                                                                                                                       1 NSRDSSGNHRV 11
                             linear
STRANDEDNESS:
                           ; TOPOLOGY: 1
US-08-350-260A-430
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                                                                         Gaps
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APPLICANT: Winter, Gradew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Wisin, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Dinding pairs
NUMBER OF SEQUENCES: 602
                                                                       ;
0
                           Score 37; DB 2; Length 11;
Pred. No. 4.1;
                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 66606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATE: US/08/350,260A
FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAK-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAK-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28111/32372
                                                                                                                                                                                                                                                                               Sequence 430, Application US/08350260A Patent No. 5962255 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REBERENCE/DOCKET NUMBER: 2811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INPORMATION FOR SEQ ID NO: 430:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                      Query Match 56.9%;
Best Local Similarity 72.7%;
Matches 8; Conservative (
                                                                                                                      1 NSWDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                  1 NSRDSSGNHRV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                US-08-350-260A-430
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Indels
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
Mismatches
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,375
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PPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,876
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ICATION NUMBER: 60/048,893
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Patent No. 6525174
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APPLICATION NUMBER: 60/
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8; Conservative
                                        1 NSWDSSGTHPV 11
                                                                               1 NSRDSSGNHRV 11
Matches
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                                                              Gaps
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
INVENTION: Methods for producing members of specific
binding pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 4; Length 11; Pred. No. 4.1;
                   Length 11;
                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bartnicki, Audrey L.
REGISTATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                          RESULT 16
US-09-104-337A-430
Sequence 430, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
CENT: Winter, Gregory Paul
Griffiths, Andrew David
Hilliams, Samuel Cameron
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO: 430: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
               Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                  1 NSWDSSGTHPV 11
                                                                                                                                           1 NSRDSSGNHRV 11
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Best Local Similarity
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Gaps
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APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diann M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT APPLICATION NUMBER: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 3; Length 32;
Pred. No. 13;
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                                                         APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: OCTERNESS C.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Isolation and Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/09167681A Patent No. 6265561
  Sequence 42, Application US/09167681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/08273146
Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenten, John H.
Martin, Mark T.
Titmas, Richard C.
Williams, Richard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darsley, Michael J
Fitzgerald, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Rodger
McCafferty, John
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                        56.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                             TYPE: PRT
, ORGANISM: Homo sapiens
US-09-167-681-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 WDSSGTHPV 11
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WDSSGTHPV 11
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14 WELSRTHPV 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Smith.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-167-681-50
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 32
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Pred. No. 8.9;
3; Mismatches 2; Indels
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Pred. No. 13;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09167681A
Fatent NO. 6265561
GENERAL INFORMATION:
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Roftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Greeness, Diana M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REPERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 32
                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
                                                                                                   EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-08-06
                                              EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1007
APPLICATION NUMBER: 60/048,949
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 66.7.,
6; Conservative
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; ORGANISM: Homo sapiens
US-09-205-258-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-167-681-34
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US-09-167-681-42
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TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION: Catalytic Antibodies using Phage Technology NUMBER OF SEQUENCES: 71
CORRESPONDENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                 COUNTRY: USA
ZIP: 20852
COMPUTER LEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFTCATION: HOFORMATION:
NAME: RYAN, JOHN W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION HOPERMATION:
TELEFAX: 301-984-8000
TELECOMMUNICATION HOPERMATION:
TELEFAX: 301-984-8000
TELECOMMUNICATION HOPERMATION:
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NESOLIA 2.2. P6-7103

Sequence 7103, Application US/09621976

Sequence 7103, Application US/09621976

Sequence 7103, Application US/09621976

Seath No. 6639063

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Johert, S.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFWMARE: Patent.pm

SEQ ID NO 7103

LENGTH: 95
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NSWDSSGTHPV 11
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RESULT 23 US-08-665-202-35

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SERVENT INFORMATION:

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APPLICANT: SCHIEK TOOKE

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ADDRESSER: TOOKE TOOKE

CONTRY: USA A

COUNTRY: USA A

APPLICANTON NUMBER: US 60/000,236

FILING DATE: 13-UNA-195

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FILING DATE: USA A

APPLICANTON NUMBER: US 60/000,236

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Search completed: September 27, 2004, 12:17:14 Job time : 34 secs

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Sequence 348, Application US/09673395A
Facent No. 6620923
GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
TITLE OF INVENTION NUMBER: US/09/673,395A
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT PILING DATE: 2000-10-17
SEQ ID NO348
ENGRENT PILING DATE: 2000-10-17
SEQ ID NO348

LENGTH: 103
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 14-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UN-1996
FILING DATE: 13-UN-1996
ATORNEY AGENT INFORMATION:
NAME: HULLEATION NUMBER: US 03307E-061411
TELECOMMUNICATION NUMBER: 02307E-061411
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
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Pred. No. 41;
0; Mismatches
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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353, App 540, App 28149, A 273242,

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Sequence 188, App
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US-10-029-386-28149

US-10-029-386-28149

US-10-221-279-626

US-10-291-172-626

US-10-291-172-626

US-10-291-172-820

US-10-291-173-820

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US-10-385-305-188

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US-10-38-305-188

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US-10-293-418-1115
US-09-880-748-1116
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Sequence 225421,

Result No.

Sequence 125,

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Sequence Sequence

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Score 51; DB 9; Length 11; Pred. No. 0.24; 0; Mismatches 2; Indels

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US-10-231-USBS-1/3

Sequence 173, Application US/10251085B

Publication No. US20040072164A1

GENERAL INFORMATION:
APPLICANT: Bondish, Katherine S.
APPLICANT: Brederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: INTURENCE TOSHIAK!
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR PLING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
LENGTH: 110
TYPE: PRT

CORANISM: human
APPLICANT: Holet, Thor
TITLE OF INVENTION: Improvements to ribosome display
FILE REFERENCE: 84633
CURRENT APPLICATION NUMBER: US/09/817,661
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/193,802
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                Query Match 78.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative (
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                  NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 21
LENGTH: 11
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                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-661-21
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US-10-029-926B-27

US-10-032-037B-27

US-10-032-423A-27

US-09-880-748-1941

US-09-880-748-1941

US-09-880-748-1941

US-10-293-418-1942

US-10-293-418-1942

US-10-293-418-1967

US-09-880-748-1931

US-09-880-748-1931

US-09-880-748-1931

US-10-293-418-1937

US-10-293-418-1937

US-09-880-748-2038

US-09-880-748-2038

US-09-880-748-2038

US-09-880-748-2038

US-09-880-748-2038

US-09-880-748-2038

US-10-293-418-2038

US-09-880-748-1932

US-10-293-418-1932

US-10-293-418-1933

US-10-293-418-1933
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US-09-880-748-2031
US-10-293-418-1303
US-10-293-418-1911
US-10-293-418-2031
US-10-293-418-2060
US-10-293-418-2060
US-09-880-748-1424
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US-09-880-748-2046
US-09-880-748-2106
US-10-293-418-1424
US-10-293-418-1444
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US-09-880-748-1678
US-09-880-748-1742
US-09-880-748-1762
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%309-817-661-21 %Sequence 21, Application US/09817661 % Patent No. US20020076692A1 %GENERAL INFORMATION: APPLICANT: Osbourn, Jane

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Sequence 173, Application US/10737252

Sequence 173, Application US/10737252

Publication No. US20040175736A1

Sequence 173, Application US/10737252

Publication No. US20040175736A1

GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Enablaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
FILE REFERENCE: 1087-21 CIP
CURRENT APPLICATION NUMBER: US/10/737,252

CURRENT FILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 10/251,085

PRIOR FILING DATE: 2002-09-19
92 WDSSGDHPV 100
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Gaps

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Score 49; DB 12; Length 110; Pred. No. 4.2; 0; Mismatches 1; Indels

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APPLICANT: Ruben et al.

TITLE OF INVENTANION:

FILE REFERENCE: PF5.23P2

CURRENT APPLICATION NUMBER: US/10/293,418

FILE REFERENCE: PF5.23P2

CURRENT APPLICATION NUMBER: US/10/293,418

FRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-67

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR PILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

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PRIOR FILING DATE: 2000-10-17
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Sequence 1116, Application US/09880748

Sequence 1116, Application US/09880748

Publication No. US_20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

ITILE OF INTENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.3

CURRENT FILIAG DATE: 2001-06-15

FRIOR APPLICATION NUMBER: 06/212,210

FRIOR APPLICATION NUMBER: 66/210,816

PRIOR APPLICATION NUMBER: 66/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16
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Pred. No. 26;
1; Mismatches 2; Indels
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Pred. No. 26;
1; Mismatches 2; Indels
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; Sequence 1115, Application US/10293418
; Publication No. US20030223996A1
                                                                                                                                                                   70.8%;
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Best Local Similarity 72.,
                                                                                                                                                                                                                      8; Conservative
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228 HSWDSSGNHVV 238
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228 HSWDSSGNHVV 238
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                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1115
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CORGANISM: Homo sapiens
US-10-293-418-1115
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Best Local Similarity
Matches 8; Conserv
        SEQ ID NO 1115
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US-10-424-599-177279

US-10-424-599-177279

US-10-424-599-177279

Sequence 177279, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 177279
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Sequence 1115, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880, 748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

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PRIOR FILING DATE: 2001-03-21
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Pred. No. 4.2;
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US-10-424-599-177279
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 110
                                                                                                                                                                                                                                                                        75.4%;
88.9%;
                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                   TYPE: PRT
ORGANISM: human
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Query Match 63.1
Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                        3 WDSSGTHPV 11
                                                                                                                                                       ORGANISM: artificial
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Sequence 10, Application US/10779461
PUBLICATION No. US20040166544A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS
FILLE REPRESENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
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Sequence 1116, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF533P2
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Pred. No. 54;
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                                                                                                                                                                                                                                                                                                             1; Mismatches
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CURRENT PEDELICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-6-15
PRIOR FILING DATE: 2001-6-15
PRIOR FILING DATE: 2001-6-15
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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Pred. No.
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1116
                                                                                                                                                                                                                                                                67.7%;
77.8%;
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77.88;
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Best Local Similarity 77.8
T. Conservative
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226 HSWDSSGNH 234
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226 HSWDSSGNH 234
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CORGANISM: Homo sapiens
US-10-293-418-1116
                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-880-748-1116
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                                                                                                                                                          LENGTH: 247
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US-10-47-963-194069
US-10-47-963-194069
Sequence 194069, Application US/10437963
Sequence 194069, Application US/10437963
Sequence 194069, Application US/20040123343A1
SEQUENCE 194069, Application US/20040123343A1
GENERAL INFORMATION: Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Baukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Branch II, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE IS-22-15-22-18
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-6-15

PRIOR PLING DATE: 2000-6-15

PRIOR PLING DATE: 2000-17

PRIOR PLING DATE: 2000-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16
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Pred. No. 1.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT4530_90147C.1.pep
                                                                                                                                                                                                                                                                                                    16;
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Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 183
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 245
TYPE: PRT
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70.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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2 AWDSSSDHP 10
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ORGANISM: Mus musculus
                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapien
US-09-563-222-25
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ORGANISM: Glycine max
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Best Local Similarity
Matches 6; Conserv
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
    APPLICANT: Ruben et al.
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
    TILE REFERENCE: PF523P2
    CURRENT PELING DATE: 2001-11-27
    PRIOR PILING DATE: 2001-11-16
    PRIOR PILING DATE: 2001-11-19
    PRIOR PILING DATE: 2001-06-15
    PRIOR PILING DATE: 2001-06-15
    PRIOR PILING DATE: 2001-06-15
    PRIOR PILING DATE: 2001-06-15
    PRIOR PILING DATE: 2001-03-21
    PRIOR PILING DATE: 2001-03-21
    PRIOR PILING DATE: 2001-03-21
    PRIOR PILING DATE: 2000-03-16
    PRIOR PILING DATE: 2000-10-17
    PRIOR PILING DATE: 2000-10-17
    PRIOR PILING DATE: 2000-10-17
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    PRIOR PILING DATE: 2000-06-16
    PRIOR PILING DATE: 2000-06-16
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Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: ENFARROTIC CELLS
FILE REPERENCE: 310098.406
                                                                                                                                                                                                                                                                                                         Score 41; DB 10; Length 246;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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Pred. No. 1.6e+02;
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1980
LENGTH: 246
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81.8%;
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81.8%;
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Best Local Similarity 81.0
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Best Local Similarity 81.8
Matches 9; Conservative
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US-09-880-748-1980
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US-10-293-418-1980
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                                                                                                                                                                                                         TYPE: PRT
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US-10-424-599-243244

US-10-424-599-243244, Application US/10424599

| Sedience 243244, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua |
| APPLICANT: Zhou Yihua |
| APPLICANT: Cao Yongwei |
| TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| CURRENT APPLICATION NUMBER: US/10/424,599 |
| CURRENT FILING DATE: 2003-04-28 |
| SEQ ID NOS: 285684 |
| LENGTH: 90 |
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Sequence 18, Application US/10340536

Sequence 18, Application US/10340536

Sequence 18, Application No. US20030175212A1

GENERAL INFORMATION:

APPLICANT: Born, Willi

APPLICANT: Born, Willi

APPLICANT: Additug, M. Kemal

ITLE OF INVENTION: Use of Soluble Gamma Delta T Cell Receptors for Regulating T Cell

ITLE OF INVENTION: Byline Coll

TILE OF INVENTION: Use of Soluble Gamma Delta T Cell Receptors for Regulating T Cell

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Pred. No. 89;
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US-10-424-599-243244
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 10;
Pred. No. 15;
1; Mismatches 2
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CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 25
LENGTH: 13
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Best Local Similarity 66.7
Matches 6; Conservative
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Publication No. US20030059937A1
GENERAL INPORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                            Indels
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  Pred. No. 2.3e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
0; Mismatches 1;
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CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PLICATION NUMBER: 60/240,816

PRIOR PLICATION NUMBER: 60/240,816

PRIOR PLICATION NUMBER: 60/276,248

PRIOR PLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEC ID NOS: 3239
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88.9%;
Best Local Similarity 88.5
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 353
                                                                                                                                  228 NSRDSSGTH 236
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CRGANISM: Homo sapiens
US-09-880-748-540
                                                                                  1 NSWDSSGTH 9
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US-09-880-748-540
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Publication No. US20030175212A1

GENERAL INFORMATION.

### APPLICANT:

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Fublication No. US20030059937A1

GENERAL INFORMATION:

APPLICAT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                  61.5%; Score 40; DB 14; Length 112; 77.8%; Pred. No. 1.1e+02;
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                                                                                                              0; Mismatches
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                                                                                                                                                                                                                    104 WDSSGFHKV 112
                                                                                                                                                                 3 WDSSGTHPV 11
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US-10-340-536-16
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                                                Query Match
Best Local Similarity
Matches 7; Conserv
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US-10-340-536-18
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thous A
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 117
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; Sequence 626, Application US/10221278
; Publication No. US20040034208A1
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR APPLICATION NUMBER: 09/65,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-07-14
; PRIOR PILING DATE: 2000-07-14
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                           PERTURE:

OTHER INFORMATION: MAP TO AL137798.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89

OTHER INFORMATION: WISSPROT HIT: P04072, EVALUE 8.60e-01
US-10-029-386-28149
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                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 39; DB 14; Length 86
60.0%; Pred. No. 1.2e+02;
tive 2; Mismatches 2; Indels
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US-10-424-599-273242
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Pred. No. 1.6e+02;
2; Mismatches 1
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LOCATION: (1)..(117)
OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040031072A1
; GENERAL INFORWATION:
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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51 SSWESGGTSP 60
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64 WDSSNTNPL 72
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ORGANISM: Glycine max
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Carlon C.
APPLICANT: Penn, Carlon C.
APPLICANT: Parzel, David R.
APPLICANT: Penn, Carlon C.
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GENERAL INVENTALING:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPREBNCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/311,469

PRIOR APPLICATION NUMBER: 60/310,817

PRIOR APPLICATION NUMBER: 60/30,499

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-65-15

PRIOR PILING DATE: 2001-65-15

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/270,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-6-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 249
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Pred. No. 2.38+02;
0; Mismatches 1; Indels
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
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Publication No. US20030223996A1
GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 85..
                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                     228 NSRDSSGTH 236
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                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-353
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US-10-293-418-540
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 249
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Search completed: September 27, 2004, 12:27:47 Job time : 133 secs
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ORGANISM: Oryza sativa
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPLICANT: Hygeq, inc.
TITLE OF INVENTION: No. US20030228584Alel Nucleic Acids and Polypeptides
FILE REPERENCE: 2127-2045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-06-17
PRIOR PLING DATE: 2000-06-17
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Pred. No. 2.2e+02;
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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Publication No. US20040123343A1
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR PILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-291-172-626
Sequence 626, Application US/10291172
Publication No. US20030228584A1
GENERAL INFORMATION:
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Barbazuk, Brad
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Best Local Similarity 77.0
                                                                                                                                                                                                                                                      Query Match 60.0
Best Local Similarity 77.6
Matches 7; Conservative
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CORGANISM: Homo sapiens
US-10-291-172-626
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US-10-221-278-626
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LENGTH: 162
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 164780
LENGTH: 301
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US-10-437-963-164780
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anslated from GB/EMBL/IAF074612; NID:93822037; rain KIM5	Query March  Query March  Bast Local Similarity 70.0%; Pred. No. 42; DB 2; Length 130;  Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 2 SWDSSGTHPV 11  Db 79 SWDEVGGHPV 88  RESULT 2  F97245  probable HD superfamily hydrolase [imported] - Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: F97245	Nivoling, u.; Breton, u.; Ometronko, N.; Markarova, N.S.; Zeng, W.; Gibbon, N.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 J. Bacteriol. 183, 4823-4838, 2001 J. Bacteriol. 183, 4823-4838, 2001 J. Bacteriol. 183, 4823-4838, 2001 J. Bacteriol. 183, 4823-4838, 2001 J. Reference and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Accession: F97245 A; Accession: F97245 A; Residues: L-98 «KUR» A; Residues: 1-98 «KUR» A; Cross-references: GB:AE001437; PIDN:AAK80753.1; PID:GI5025850; GSPDB:GN00168 A; Experimental source: Clostridium acetobutylicum ATCC824 C; Genetics: A; Genetics:	Query Match Best Local Similarity 77.8%; Pred. No. 4.6; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 2 SWDSGTHP 10  Db 40 SWDQSGTPP 48  RESULT 3 TABSULT 3 TABSULT 3 TABSULT 3 TABSULT 3 TABSULT 3	Appointed to the EMBL Data Library, February 1996 C; Accession: T27931 R; McMurray, A. submitted to the EMBL Data Library, February 1996 A; Reference number: Z20441 A; Reference number: Z20441 A; Reference number: Z20441 A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL> A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-339 cMIL- A; Residues: J-399 cMIL-
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C;Accession: S09713
R;Hughes-Jonose, N.C.1 Bye, J.M.; Beale, D.; Coadwell, J.
R;Hughes-Jonose, N.C.1 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of A;Reference number: S09710; MUID:90262535; PMID:2111699
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                                     A;Note: this sequence was determined from the differentiated gene hybrote: the authors translated the codon ACG for residue 2 as Ser and ACA for residue 59 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: T-cell receptor
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C; Species: Mus musculus (house mouse)
C; Accession: B24775
R; Garman, R.D.; Doherty, P.J.; Raulet, D.H.
C; Accession: B24775
R; Garman, R.D.; Doherty, P.J.; Raulet, D.H.
R; Garman, R.D.; Doherty, P.J.; Raulet, D.H.
A; Reference number: A90880; MUD:86218086; PMID:3486721
A; Accession: B24775
A; Molecule type: DNA
A; Residues: 1-120 < GAR>
A; Residues: 1-120 < GAR>
A; Cross-references: GB:W31337; NID:g201668; PIDN:AAA40316.1; PID:g201669
A; Note: this sequence was determined from the differentiated gene
A; Note: the authors' translation contained an addition Cys after 14-Val
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 40; DB 2; Length 120; 77.8%; Pred. No. 8.5; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                    Score 40; DB 2; Length 110;
Pred. No. 7.7;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                   61.5%;
77.8%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 77.6
Then 7. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 WDSSGFHKV 120
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Matches 7; Conserv
A, Residues: 1-110 <GAR>
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                                                                                                                                                                                                                                                                                                                C; Date: 24-May-2001 Meguence_revision 24-May-2001 #text_change 03-Aug-2001
C; Date: 24-May-2001 #90543
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M. Bur. J. Immunol. 22, 491-498, 1992
Bur. J. Immunol. 22, 491-498, 1992
A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A;Reference number: A49037; MUID:92164730; PMID:1311262
                                                                                                                                                                                                                                                     hypothetical protein MYPU_2500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
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C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 24-Sep-1999
C;Accession: C24775
R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
Cill 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Reference number: A90880; MUID:86218086; PMID:3486721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL445566; PID:g14089663; PIDN:CAC13423.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCR C gamma 1 chain V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: C49254
                                                                                                                                                                                                                                                                                          Species: Mycoplasma pulmonis
Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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A;Residues: 1-18 <EZQ>
A;Cross-references: GB:S90689; NID:g246310; PIDN:AAB21558.1; PID:g246311
A;Experimental source: FF3 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:90689, NCBIP:90691)
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Best Local Similarity 77.0
7; Conservative
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SWNSNGTHYV 57
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   SWDSSGTHPV 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
Molecule type: DNA
Residues: 1-456 <KUR>
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C;Genetics:
A;Gene: MYPU 2500
A;Genetic code: SGC3
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A; Status: prelimina
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C49254
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Gaps

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Cyaccessum, nessons sequencing Consortium.

Science 282, 2012-2018, 1998

A; File: Genome sequence of the nematode C. elegans: a platform for investigating biology A; File: Genome sequence of the nematode C. elegans: a platform for investigating biology A; Reference number: A75000; MUID: 9905613; PMID: 9881916

A; Note: see websites genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; A; Accession: A88363

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-201 < STO

A; Cross-references: GB: Chr_II; PIDN: CAB04194.1; PID: 93876448; GSPDB: GN00020; CESP: F26411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: January Russian (garden pea)
C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Aug-1999
C;Accession: T06528
R;Kardailsky, I.V.; Sherrier, D.J.; Brewin, N.J.
Plant Physiol. 111, 49-60, 1995
A;Title: Identification of a new pea gene PsNlec1 that encodes a lectin-like glycoproteir A;Reference number: Z15736
A;Accession: T06528
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Andlecule type: mRNA
A;Residues: 1-270 < kAx>
A;Residues: 1-270 < kAx>
A;Cross-references: EMBL:U31981; NID:g974303; PIDN:AAC49367.1; PID:g974304
A;Experimental source: cv. Wisconsin Perfection
C;Genetics:
A;Gene: Nlec1
C;Superfamily: plant lectin
                                                                                                                                                                                                                                                                                                               protein F26H11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88363
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C;Species: Synechocystis sp.
Score 40; DB 2; Length 988; Pred. No. 83; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 39; DB 2; Length 201; 66.7%; Pred. No. 22;
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Pred. No. 30;
0; Mismatches 3; Indels
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     61.5%;
66.7%;
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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A; Map position: 2
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R;Geshi, N.; Brandt, A.
Barta 204, 295-304, 199
A;Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L. seed A;Reference number: 216340; MUID:98192006; PMID:9530873
A;Accession: T08081
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myrosinase-binding protein (clone indmbp2) - rape

C;Species: Brassica napus (rape)

C;Species: Brassica napus (rape)

C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-Jul-2000

C;Accession: T08102

Br;Taipalensuu, J.; Erikeson, S.J.; Rask, L.

Bur J. Biochem. 250, 680-688, 1997

A;Riipale The myrosinase binding protein from Brassica napus seeds possesses lectin activ

A;Reference number: 216355; MUID:98121188; PMID:9461290

A;Reference number: Zi6355; MUID:98121188; PMID:9461290

A;Resique; preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Mesidues: 1-988 c/All.

A;Residues: 1-988 c/All.

A;Residues: 1-988 c/All.

A;Experimental source: cv. Hanna; leaves
                                                                                                                                                  Σ̈́
                          hypothetical protein SPAC22H10.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T38214
R;Grishchuk, K; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, February 1996
A;Reference number: 221778
                                                                                                                                                                                                                        A;Accession: T38214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DDA
A;Rolecule type: DBV
A;Rosidues: 1-629 <DBV
A;Ross-references: EMBL:Z69730; PIDN:CAA93611.1; GSPDB:GN00066; SPDB:SPAC22H10.11c
A;Experimental source: strain 972h-; cosmid c22H10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22H10.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Brassica napus (rape)
Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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60.0%;
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66.7%;
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Best Local Similarity 60.0.
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Best Local Similarity 66.7
Lac 6; Conservative
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probable SCARECROW gene regulator [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02736; A84692
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ronr submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
A;Reference number: Z14710
A;Reference number: Z14710
A;Reference number: Lanslated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: Lranslated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AC005315; NID:g3461834; PID:g3461846
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
B;Lin, X.; Raul, S.; Rounaley, S.D.; Shen, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, W.; Vanbken, S.E.; Umayam, L.; Tallon, L., Sub, 1999
A;Title: Sequence and annalysis of chromosome Z of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: Drealing and annalysis of chroman Asheromental Arabidopsis thaliana.
A;Status: Drealing and Arabidopsis thaliana.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B4862
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. K. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.S.; Nature, 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; WUID:20083487; PMID:10617197
A;Reference prediminary
A;Reference base DNA
A;Residues: 1-295 <STO>
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A;Molecule type: DNA
A;Residues: 1-1336 <STO>
A;Cross-references: GB:AE002093; NID:g3461846; PIDN:AAC33232.1; GSPDB:GN00139
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Pred. No. 1.7e+02;
2; Mismatches 0; Indels
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                                 Length 995;
                                                                                        2; Indels
                              Score 39; DB 2; I
Pred. No. 1.2e+02;
1; Mismatches 2;
                                 60.0%;
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                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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A;Map position: 2
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Matches 6; Conserv
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A,Map position: 2
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A;Residues: 1-402 <KAN>
A;Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16677.1; PID:g165174
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s1r0731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable CHP-rich zinc finger protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 1.6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: G85024
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                  R;Kaneko, T.; Saro, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Cross-references: EMBL:Z81094; PIDN:CAB03153.1; GSPDB:GN00023; CESP:F58G11.2
A;Experimental source: clone F58G11
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                  C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S74525
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Pred. No. 47;
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Pred. No. 79;
2; Mismatches
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A;Reference number: Z19640
A;Accession: T22942
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A;Map position: 5
A;Introns: 79/1; 195/1; 642/1; 678/2; 796/1
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54.5%;
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Best Local Similarity 54.5
6; Conservative
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DSWESSSTH 205
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Best Local Similarity
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Molecule type: DNA
Residues: 1-652 <STO>
A; Variety: PCC 6803
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Gene: AT4g01930
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Best Local Similarity Matches 5; Conserv

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Pred. No.

55.6%;

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endoglycosylceramidase (EC 3.2.1.123) - Rhodococcus sp.
NyAlternate names: Cer glycanase; endoglycoceramidase
C;Species: Rhodococcus sp.
C;Species: Rhodococcus sp.
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 08-Sep-2000
C;Accession: JC7332
R;Sakaguchi, K.; Okino, N.; Sueyoshi, N.; Izu, H.; Ito, M.
J. Blochem. 128, 145-152, 2000
A;Title: Cloning and expression of gene encoding a novel endoglycoceramidase of Rhodococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-482 <SAK>
A;Experimental source: strain C9
C;Comment: This enzyme, a member of type II enzyme, cleaves the glycosidic linkage betwee
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligopetide ABC transporter, periplasmic binding component CAC3179 [imported] - Clostric Cispecies: Clostridium acetobutylicum (cispecies: Clostridium) (cispecies: Clostridium) (cispecies: Clostridium) (cispecies: A) 2011 (cispecies: Cispecies:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C;Species: Zea mays (maize)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C;Accession: A53311
R;Liu, L.; Pesacreta, T.C.
submitted to GenBank, May 1999
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%;
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Best Local Similarity 45.5
Matches 5, Conservative
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184 NFWNTTGKHP 193
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||||: ||
NSWDNRGT 80
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Matches 5; Conserv
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A;Gene: CAC3179
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195318
Nife oxidoreductase nifE [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid proceductase nifE [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95318
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows proc. Natl. Acad Sci. US.A. 98, 9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-451 <TOV>
A;Cross-references: EMBL:Z49321; NID:g1008176; PIDN:CAA89337.1; PID:g1008177; GSPDB:GN00
C;Genetics:
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A; Residues: 1-476 < KUR>
A; Residues: 1-476 < KUR>
A; Residues: 1-476 < KUR>
A; Cross-references: GB x 2006469; PIDN: AAK65110.1; PID: g14523548; GSPDB: GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Bela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Science 293, 668-670, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; WUID: 21368234; PMID: 11474104
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A;Genome: plasmid
C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain
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C,Species: Saccharomyces cerevisiae
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002
C,Accession: S56818
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Pred. No. 79;
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Pred. No. 84;
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                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Accession: $56818

**Pohl, T.M.; Allinovic, G.

submitted to the Protein Sequence Database, September 1995

A;Reference number: $56793
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1; Mismatches

58.5%;

Query Match Best Local Similarity 66.,

WESSGVHSV 341 3 WDSSGTHPV 11

333

ò g A;Status: preliminary

A, Accession: D95318

C; Superfamily: lipoate-protein ligase

A;Cross-references: SGD:S0003582 A;Map position: 10L

A; Gene: MIPS: YJL046w

A; Accession: S56818

1; Mismatches

Conservative

Query Match Best Local Similarity

58.5%;

Gaps

ö

Length 1369;

predicted

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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

Atuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005172; NID:g2494131; PIDN:AAB80640.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology C;Keywords: 2Fe-2S; metalloprotein F;43,48,51,73/Binding site: 2Fe-2S cluster (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 2; Length 136
Pred. No. 2.6e+02;
0; Mismatches 2; Indels
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75.0%;
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A;Molecule type: DNA
A;Residues: 1-1369 <STO>
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NyContains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 21-Jan-2000
C,Accession: A56493; I55393
R,Zhang, J.S.; Longo, P.M.
J. Cell Biol. 128, 415-431, 1995
A,Fitle: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the A,Reference number: A56493; MUID:95146548; PMID:7844155
A,Accession: A56493
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Residues: 1-1290 -RES>
A,Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919
R,Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J. J. Biol. Chem. 268, 26503-26511, 1993
A,Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cikeywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas F;80-166/Domain: fibronactin type III repeat homology <3FR>
F;80-166/Domain: bibronactin type III repeat homology <3FR>
F;67-1290/Domain: protein-tyrosine-phosphatase homology <4PP2>
F;931/Active site: Cys (phosphocysteine intermediate) #status predicted
F;931/Active site: substrate phosphate (Arg) #status predicted
F;1222/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1228/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: I55393
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 831-1290 <RE2>
A;Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                               A; Molecule Lype: mRNÅ
A; Residues: 1-1099 <-LIU>
A; Residues: 1-1099 <-LIU>
A; Cross-references: GB: AF147738; NID: g4885025; PIDN: AAD31926.1; PID: g4885026
A; Experimental source: cultivar B73 inbred line
C; Generics:
A; Gene: zem3
A; Gene: zem3
C; Superfemily: myosin heavy chain 95F; myosin motor domain homology
F; 101-757/ Domain: myosin motor domain homology <-MMO>
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Pred. No. 2.5e+02;
1; Mismatches 3; Indels
   A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leucocyte common antigen-related protein (LAR) - rat (fragment)
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Fibronect Human pro

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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                                                                                                                                     An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Complementarity determining region (CDR)
heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Complementarity determining region
neavy chain"
                                                                                                                                                                                                                                                                                                                                                               region
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note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                             note= "Complementarity determining
                                                                                                                                                                   ALIGNMENTS
                            ADM04464
AAB71910
AAU2908081
ADM232664
ABW23915
ADW23915
ADW23915
ADW23915573
ADW230544
ADW231525
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                                                                                                                            ABP01278
AAR72861
ADM05567
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                        AAB68087 standard; protein; 249 AA
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note= "linker"
                                                                                                                                                                                                                                                                                                                                                                                         light chain"
110. .127
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88. .98
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                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain<sup>*</sup>
177. .193
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Synthetic.
Macaca fascicularis.
WO200130854-A2
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AAB68087;
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Human ca-M
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Alloiococ
Anti-TGF
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Murine T
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Human BLy
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Bifidobac
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Aao15005 GPI-linke
                                                 April 28, 2005, 17:57:45; Search time 82.8438 Seconds (without alignments) 51.354 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                           Abp45104 B
Adg95931 S
Abp45105 B
Adg95932 S
                                                                                                                                                                                                                                                                                                                                                                                                                                               Adg96796 8
Aau70345 B
Adb09502 B
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Abp44342 I
Adg95169 S
Adg95356
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Aar12264
Abr82488
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Abg01449
Abo54515
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                                                                                                                                                    21,05692
      5.1.6
Compugen Ltd
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                    2105692 segs, 386760381 residues
      GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          US-10-088-639A-2_COPY_88_98
65
                                   protein search, using sw model
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ADG95931
ABP45105
ADG95932
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ABB06006
ABP45969
ADG96796
AAUT0345
AAW15538
AAW12534
AAW15538
AAR12264
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ABP44342
ADG95169
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ABO75320
ABP65370
ABG01449
ABG01449
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AA015005
                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                             geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp201s:*
geneseqp201s:*
geneseqp2003s:*
geneseqp2003bs:*
                                                                                                                                                                                                                       A_Geneseq_16Dec04:
                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                               1 NSWDSSGTHPV 11
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2445
2446
2446
2446
1110
11110
11111
1112
1120
2449
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2449
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Post-processing:

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Minimum DB Maximum DB

Title: Perfect score:

Sequence:

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The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial tumour cells and in target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to tumour deposits in humans
                                                                                                                                                                Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                      Tordsson MJ, Kearney PP;
                      Ohlsson LG,
                                                                                                                                                                                                                                                              Claim 1; Page 55-56; 75pp; English
                      Karlstroem PJ,
                                                                                           WPI; 2001-308619/32.
                                                                                                                   N-PSDB; AAF84797
                      Brodin TN,
Nilson BHK;
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                                                               Gaps
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                             100.0%; Score 65; DB 4; Length 249; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                              Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
Sequence 249 AA;
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AAO15005 standard; peptide; 11 AA. (first entry) 98 1 NSWDSSGTHPV 11 88 NSWDSSGTHPV 16-AUG-2002 AA015005; RESULT 2 ð 셤

Ribosome display system; specific binding pair; sbp; anti-FITC; VL CDR3; scFv antibody generation; GFI-linked cell surface receptor. GPI-linked cell surface receptor-specific VL CDR3 peptide sequence.

Unidentified

WO200175097-A2

11-OCT-2001

31-MAR-2000; 2000US-0193802P

26-MAR-2001; 2001WO-GB001319

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Osbourn J, Holet T;

WPI; 2002-010788/01.

specific binding pair member (I) that binds a complementary specific binding pair member of encapsidating specific binding pair member/ribosome complexes in a viral coat, comprises the use of a ribosome display system Obtaining

Example 7; Page 42; 61pp; English.

The invention comprises a method (ribosome display system) for obtaining a specific binding pair (sbp) member that binds a complementary sbp member of interest. The method involves incubating mRNA molecules encoding an sbp and lacking an in-frame stop codon, allowing ribosome translation of the mRNA to produce the encoded sbp member, forming complexes comprising ribosome, mRNA, and encoded sbp member displayed on the ribosome. The ribosome display system is useful for the selection of an sbp member able to bind a complementary sbp member. The present amino acid sequence represents a GPI-linked cell surface receptor-specific VL CDR3 peptide X00000000000X8

Sequence 11 AA;

Gaps ; 0 Length 11; 2; Indels 5; ed. No. 0.1; Mismatches 8 Score 51; Pred. No. .,0 78.5%; 81.8%; Query Match 78.5 Best Local Similarity 81.6 Matches 9; Conservative

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1 NSWDSSGTHPV 11 셤 ð

11 1 NSWDSSGNHVV

RESULT 3 ABR54947

ABR54947 standard; protein; 110 AA.

ABR54947;

(first entry) 30-JUN-2003 IgG light chain clone HBL4a 3D6 SEQ ID NO:173.

Engineered template, single primer amplification, antibody library, nucleic acid amplification. 

sapiens Ношо

Synthetic.

WO2003025202-A2

19-SEP-2002; 2002WO-US029889 27-MAR-2003

19-SEP-2001; 2001US-0323455P.

(ALEX-) ALEXION PHARM INC

Renshaw M; Lin Y, Maruyama T, Frederickson S, Bowdish KS,

WPI; 2003-313359/30.

Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined sequence

Example 3; Fig 8e; 68pp; English.

The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers and nucleotides under conditions suitable for polymerisation of the nucleotides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at the other end. M1 is useful for to the predetermined sequence at the other end. M1 is useful for amplifying a nucleic acid. M1 can be used for products that can be ligated into a suitable expression vector, where the vector can be used to transform an appropriate host organism to produce the polypeptide or

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             of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of one target nucleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence located on the same or different nucleic acid molecules. ACC62635 to ACC62753 and ABRS4991 to ABRS4999 represent sequence used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytosteatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
 M1 is useful to amplify a family
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                                                                                                                                                                                                   6; Length 110;
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                                                                                                                                                                                                 Score 49; DB 6
Pred. No. 2.7;
0; Mismatches
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protein encoded by the target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BLyS binding scFv SEQ ID 1115.
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                                                                                                                                                                                               75.4%;
88.9%;
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16-MAR-2001; 2001US-0276248P.
14-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2001; 2001WO-US019110
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                                                                                                                                                                            Query Match
Best Local Similarity 88.5
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                                                                                                                                                                                                                                                                                                          92 WDSSGDHPV 100
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                                                                                                                                                                                                                                                                        3 WDSSGTHPV 11
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                                                                                                                                                           Sequence 110 AA;
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                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45104;
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888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                             ŏ
                                                              acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method the invention
administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lugus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (cvID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to novel antibodies that immunospecifically bind
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain antibody that immunospecifically binds BLyS SeqID 1115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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                                                                                                                                                                                     Length 249;
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                                                                                                                                                                                     Score 46; DB 5
Pred. No. 21;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 ADG95931 standard; protein; 249 AA.
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                                                                                                                                                                                       70.8%;
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                    Sequence 249 AA;
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disorders and

and activity such as cancer, immune, and autoimmune

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BHyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirhemmatic and antiAHDS activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in bloggical samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
               activities such as antirheumatic, antiarthritic, neuroprofective, antinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                       Gaps
Accordingly, they can be described as exhibiting various
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                                                                                                                                                                                   7; Length 249
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                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                   Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-027379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                   70.8%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BLyS binding scFv SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                              228 HSWDSSGNHVV 238
                                                                                                                                                                                                                                                           1 NSWDSSGTHPV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-114799/15.
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                Sequence 249 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45105;
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                     RESULT 6
ABP45105
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13g34 and encodes a protein that is a member of the tumour chromosome 13g34 and encodes a protein that is a member of the tumour corrects superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy (DR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods of the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ADS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
            diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. oommon variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (BIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single chain antibody that immunospecifically binds BLyS SeqID 1116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody, B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis, asthma; rheumatoid arthritis; AlDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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                                                                                                                                                                            Length 247;
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                                                                                                                                                                          Score 44; DB 5
Pred. No. 44;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     ADG95932 standard; protein; 247 AA.
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                                                                                                                                                                        67.78;
77.88;
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                            1 NSWDSSGTH 9
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                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                      Sequence 247 AA;
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                                                                                                  the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG95932;
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for the manufacture of medicament for the treatment of cancer or

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The invention relates to a novel c-Met protein tyrosine kinase antibody or its antigen binding portion that specifically binds to c-Met. The c-Met antibody comprises any one of 1-60 fully defined sequence of 238, 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino acids as given in the specification, or its fragment. The invention comprises a pharmaceutical composition comprising the c-Met protein tyrosine kinase antibody and a carrier; an isolated call that produces the c-Met protein tyrosine kinase antibody; and an isolated nucleic acid molecule that comprises a nucleic acid sequence that encodes a heavy chain or its antigen-binding portion of the c-Met protein tyrosine kinase antibody and an aciden-binding portion of the c-Met protein tyrosine kinase antibody. The c-Met protein tyrosine kinase antibody are cybthalmological, antiinflammatory, analgesic, vasotropic, antibody is and osteopathic activities. The c-Met protein tyrosine kinase antibody is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-Met, tyrosine kinase antibody; antigen binding; cytostatic; ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic; osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis; retinopathy; uveitis; ocular photophobia; macular degeneration; pain; acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
                   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel c-Met protein tyrosine kinase antibody or its antigen-binding portion specifically binding to c-Met, useful for manufacture of medicament for treating cancer or tumor and for treatment of ophthalmic
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shieh JJ;
activities such as antirheumatic, antiarthritic, neuroprotective,
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                                                                                                                                                                                    DB 7; Length 247;
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                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                    Score 44; DB 7
Pred. No. 44;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis, HGF; osteoporosis; cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                ADS09248 standard; protein; 245 AA.
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                                                                                                                                                                                 Query Match 67.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases such as glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morton PA, Arbuckle JA,
                                                                                                                                                                                                                                                                                                            226 HSWDSSGNH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PHAA ) PHARMACIA CORP
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N-PSDB; ADS09308.
                                                                                                                                             Sequence 247 AA;
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                       tumour. The c-Met protein tyrosine kinase antibody is useful for diagnosing the presence or ligation of c-Met expressing tissue. The c-Met protein tyrosine kinase antibody is useful for detecting c-Met in a biological sample in vitro or in vivo. The c-Met protein tyrosine kinase antibody is also useful in the treatment or prevention of ophthalmic diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic retinopathy), uveitis, ocular photophobia, macular degeneration and pain associated with acute injury to the eye. The pharmaceutical composition is useful for the treatment of hyperproliferative disorders such as restenosis after angloplasty, and psoriasis, and for the treatment of animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
                                                                                                                                                                                                                                                                                                                                                              sequence represents the protein of a phage display generated human c-Met antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human proteins with cancer suppressing activity. Also described are the polynucleotides encoding the proteins and a process for preparing the proteins by DNA recombination. The proteins and polynucleotides can be used in the treatment of diseases such as cancer. The present sequence represents a human cancer suppressing protein from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer suppressing protein PP844 SEQ ID NO:26
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70.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 8
Pred. No. 65;
0; Mismatches
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Matches 7; Conservative
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Best Local Similarity
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1 NSWDSSGTHP 10
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160 NSWSSSRHP 169 셤

ABP45969 standard; protein; 246 AA ABP45969

ABP45969;

(first entry) 19-AUG-2002

Human BLyS binding scFv SEQ ID 1980.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimme disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

WO200202641-A1

10-JAN-2002

15-JUN-2001; 2001WO-US019110

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P.

25-MAY-2001; 2001US-0293499P

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan T, Hilbert D; Choi GH, Barash SC, Ruben SM,

WPI; 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2763-2764; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention 

Sequence 246 AA;

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                               Gaps
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0
63.1%; Score 41; DB 5; Length 246; 81.8%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels
                                Conservative
          Best Local Similarity
Matches 9; Conserv
    Query Match
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225 NSRDSSGTHLV 235
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RESULT 11

ADG96796 standard; protein; 246 AA.

ADG96796;

11-MAR-2004 (first entry)

Single chain antibody that immunospecifically binds BLyS SeqID 1980.

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumation arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

WO2003055979-A2.

10-JUL-2003

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Ä Vaughan TJ, Hilbert Choi GH, Barash SC, Ruben SM,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1980; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13d3 and encodes a protein that is a member of the tumour chromosome 13d3 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single consists and methody molecules (scYvs) derived, preferably, from the variable crossent invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, inflammatory constructions are useful for identifying immune disorders as AIDS and proliferative disorders including leukamia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprofective, antiritammatory, antiasthmatic, antiarthritic, neuroprofective, antiritammatory, antiasthmatic, antiallergic and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences 

Sequence 246 AA;

Gaps .; 0 Score 41; DB 7; Length 246; Pred. No. 1.4e+02; 0; Mismatches 2; Indels 63.1%; 81.8%; Query Match
Best Local Similarity 81.8
Matches 9; Conservative

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1 NSWDSSGTHPV 11

Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.

Alloiococcus otitis.

WO2003048304-A2.

12-JUN-2003

Alloiococcus otitis antigenic protein SEQ ID NO:3442.

(first entry)

20-NOV-2003

ADB09502;

Mcmichael JC, Russell DP, Zagursky RJ;

(AMHP ) WYETH HOLDINGS CORP.

WPI; 2003-505284/47.

Fletcher LD,

N-PSDB; ADB09501,

25-NOV-2002; 2002WO-US036123 29-NOV-2001; 2001US-0333777P. 18-NOV-2002; 2002US-0426742P.

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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polymucleotides cells), comprising using a library of two different polymucleotides concoding different immunoglobulin binding protein (1gBP) polypeptides that peptides in transferded cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP carray in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (RR) of a native IgM, IgG, IgM, IgD, IgB, IgY, kappa or lambda immunoglobulin molecule. The method is cueful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin cerived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                    complementarity determining region; framework region; IgBP;
transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
                                                                                                                                                                                                                                                                Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40, DB 5, Length 13;
Pred. No. 8.3;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                           IgD; IgE; IgY; IgM; kappa; lambda; CHBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14; 129pp; English.
                                                                                                                                                                                                                            Human lambda III light chain CDR3.
                                                                                                              AAU70345 standard; peptide; 13 AA
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66.7%;
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                                                                                                                                                                                         (first entry)
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225 NSRDSSGTHLV 235
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                              AAU70345
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The present invention describes an isolated polymucleotide (1) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a dram-positive bacterium. Also described: (1)
an isolated polypeptide that is encoded by the polymucleotide (1), its
complement, despensate variant or fragment; (3) a genetically engineered
complement, despensate variant or fragment; (3) a genetically engineered
composition comprising the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (5) an immunogenic
composition comprising the polymucleotide that is comprised in the
expression vector; (6) a pharmaceutical composition comprising the
copyeptide of (1) and a carrier; (7) a protein chip comprising the
copyeptide of (1) and a carrier; (7) a protein chip comprising an array
of the polypeptides of (1), their biological equivalent or fragment; (8)
immunogenic composition; (9) detecting and/or identifying Alloiococcus
cutridis in the biological sample; (10) a kit comprising a nontainer
containing the novel polymucleotide, its degenerate variant or fragment,
containing the novel polymucleotide, its degenerate variant or fragment
containing the novel polymucleotide, its degenerate variant or produce the
polympetide from the culture. (1) can be used in gene therapy. The
polymucleotides, polypeptides, antibodies and compositions of the present
corrections and monitoring of effects during drug clinical trials.
The polymucleotides are useful for expressing and detecting Alloiococcus
cutridis. The present sequence represents an Alloiococcus otitidis
contraining resumer inventer on a place of the present sequence represents an Alloiococcus
cotitidis. The pareams requesting and detecting Alloiococcus
cotitidis. The pareams the present sequence represents an Alloiococcus otitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
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Pred. No. 83;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       otitidis. The present sequence represents a
antigen protein from the present invention.
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70.0%;
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Matches 7; Conservative
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%XCCCCCCCCCCCCCCCCCCCCCCCCCX8X474X83X4X44X4X4X4X4X8XX8XX8XX8XX8XX8XX
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1 NSWDSSGTHP 10 74 SSWSSSGTWP 65 ઠે

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Gaps ;

2; Indels

6; Conservative 2 SWDSSGTHP 10 AWDSSSDHP 10 RESULT 14

ADB09502 standard; protein; 107 AA.

RESULT 13 ADB09502 ID ADB09

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Monoclonal antibody; rhesus D; blood-typing; CDR;
                                                                                                                                                                                                                                            haemolytic disease of the newborn; HDN
                                                                                                                                                                                 Anti-human RhD PAG-1 MAb (VL chain).
                                     AAR12264 standard; protein; 111 AA.
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                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-1991.
                                                                                                                      25-MAR-2003
15-AUG-1991
                                                                              AAR12264;
                                                                                                                                                                                                                                                                                                                                                         Region
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                   AAR12264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide sequence comprises the VL domain of human scFv antibody 1046, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood Immediate binding domains of human antibodies (see AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic cides encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for
                                                                                                                                                                                     Transforming growth factor beta-1; TGF-beta-1; human; antibody engineering; scFV; phage display; Jung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post engoladial infarction; post-angioplasty restencesis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                     macrophage deficiency disease; macrophage pathogen infection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson JE, Vaughan TJ, Williams AJ, Green JA, Jackson RH;
Bacon L, Johnson KS, Wilton AJ, Tempest PR, Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2; Length 110;
Pred. No. 85;
0; Mismatches 1; Indels
                                                                                                                                                Anti-TGF beta-1 scFv antibody 10A6 VL domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Fig 1b(ii); 184pp; English.
                   AAW15538 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%;
88.9%;
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                                                                                                      (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-215360/20.
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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19-JAN-1996;
                                                                                                      27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        GB2305921-A.
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                                                               AAW15538;
AAW15538
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(BLOO-) CENT BLOOD LAB AUTHORITY.

89GB-00025590.

89GB-00025590

13-NOV-1989;

location/Qualifiers

(revised)
(first entry)

49..55 /label= CDR2

88. .100 /label= CDR3

23. .33 /label= CDR1

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                                                                                                                                                              The DNA sequence of eleven monoclonal antibodies are represented in Q119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing blood- typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA
DNA encoding complementary determining regions - of human anti-rhesus antibodies, useful in prodn. of monoclonal antibodies and for passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 28, 2005, 18:17:24 Job time : 85.8438 secs
                                                                                                                    Disclosure; Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%;
75.0%;
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Best Local Similarity
Matches 6; Conserv
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immunisation.
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Gaps

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Query Match
Best Local Similarity 66.
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US-09-563-222C-25
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4, Appli
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97, Appli
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Sequence 6, Appli
Sequence 6, Appli
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                                                                                         April 28, 2005, 18:06:50 ; Search time 22.3438 Seconds (without alignments) 36.750 Million cell updates/sec
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(cgn2_6/ptodata/1/laa/5A_COMB.pep:*

(cgn2_6/ptodata/1/laa/5B_COMB.pep:*

(cgn2_6/ptodata/1/laa/6A_COMB.pep:*

(cgn2_6/ptodata/1/laa/6B_COMB.pep:*

(cgn2_6/ptodata/1/laa/ReCOMB.pep:*

(cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-252-991A-24066

US-08-716-679-6

US-08-716-679-6

US-09-248-796A-20780

US-09-672-571A-1

US-09-672-571A-1

US-08-672-571A-1

US-08-672-571A-1

US-08-672-971-4

US-08-652-971-4

US-08-652-971-4

US-08-991-285A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-991-953A-4

US-08-9104-337A-330

US-09-104-337A-430

US-09-167-681-42

US-09-167-681-42

US-09-167-681-42
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US-09-104-337A-349
US-09-104-337A-430
US-09-104-337A-430
US-09-167-681-34
US-09-167-681-42
US-09-167-681-67
US-09-167-681-67
US-08-273-146-67
US-08-655-202-35
US-08-655-202-35
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               US-10-088-639A-2_COPY_88_98
                                                             protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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Match Length
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1075
11452
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             Copyright
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                                                                                                                                                             Title:
Perfect score:
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Maximum DB
                                                             OM protein
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                                                                                                                                                                                              Sequence:
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                                                                                            Run on:
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GENERAL INFORMATION:
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                                                                                              DB 4; Length 448;
90;
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                                                                                                                                                                                                                                                                                                                                                                                                  NOVEL RECEPTOR-TYPE PROTEIN PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: I2
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONTRY: U.S.A.
ZIP: 1005-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Plan PC-Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/447,464
FILING DATE: 24 MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2
Pred. No. 36;
1; Mismatches
                                                                                            61.5%; Score 40; DB 100.0%; Pred. No. 90; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08447464
Patent No. 5840842
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
APPLICANT: Yan, Hai
TITLE OF INVENTION: PHOSPHOTYROSIN
TITLE OF INVENTION: PHOSPHOTYROSIN
                     ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.5%;
60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-447-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||| | ||
19 TWDSGNTEPV 28
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252 DSSGTHP 258
                                                                                                                                                                        4 DSSGTHP 10
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STRANDEDNESS: un
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US-08-447-464-6
   LENGTH: 448
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RESULT 4 US-08-116-679-6 ; Sequence 6, Application US/08716679 ; Patent No. 5846800

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196-1132

CURRENT PAPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING JATE: 1998-08-13

SEQ ID NO 20780

LENGTH: 345
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APPLICANT: Yan, Hai
APPLICANT: Yan, Hai
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2731.
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PACOMPUTER: PC-DOS/MS-DOS
SOFTWARE: PACHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
FILING DATE:
FILING DATE:
FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 7683-043
TELECHONIONICATION NUMBER: 7683-043
TELECHONIONICATION INFORMATION:
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; Sequence 20780, Application US/09248796A
; Patent No. 6747137
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; ORGANISM: Candida albicans
US-09-248-796A-20780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60...
6; Conservative
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STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-8308
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TELEX: 24
    APPLICANT:
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                       Gaps
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                                                                                                                                  58.5%; Score 38; DB 4; Length 345; 62.5%; Pred. No. 1.5e+02;
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2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1
Pred. No. 2e+02
3; Mismatches
                     1; Mismatches
                                                                                                        Sequence 3, Application US/08672571A Patent No. 5795765 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08672571A
Patent No. 5795765
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IZU, Hiroyuki
APPLICANT: KUROME, Yoko
APPLICANT: IZUMI, Yoshiya
APPLICANT: SANO, Mutsumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |:::| ||
164 NFWNTTGKHP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSWDSSGTHP 10
                                       3 WDSSGTHP 10
                                                    66 WDGTGXHP 73
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                  US-08-672-571A-3
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NESOLIA (1980)

1. Sequence 8308, Application US/09949016

2. Sequence 8308, Application US/09949016

3. Patent No. 6812339

4. GENERAL INFORMATION:

5. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

7. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7. FILE REPERENCE: CL001307

7. CURRENT APPLICATION NUMBER: 60/241, 755

8 PRIOR PILING DATE: 2000-10-20

7. PRIOR APPLICATION NUMBER: 60/231, 498

8 PRIOR APPLICATION NUMBER: 60/231, 498

8 PRIOR PILING DATE: 2000-09-08

8 NUMBER OF SEQ ID NOS: 207012

8 SEQ ID NOS: 207012

8 SEQ ID NO SI 207012

8 SEQ ID NO SI 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
APPLICANT: ITC, MARCE

TITLE OF INVENTION: Gene Encoding Endoglycoceramidase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747

CITY: Falls Church
STREET: P.O. Box 747

CITY: Teals Church
STREET: P.O. Box 747

CONTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OMERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/08/672,571A

FILING DATE: 28 JUNE 1996

CLASSIFICATION NUMBER: US/08/672,571A

FILING DATE: 28 JUNE 1996

CLASSIFICATION NUMBER: 1422-0264P

FILING DATE: 28 JUNE 1996

CLASSIFICATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0264P

TELEFRANCE/DOCKET NUMBER: 1422-0264P

TELEFRANCE/DOCKET NUMBER: 125-8000

TELEFRANCE (703) 205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.5%; Score 38; DB 1; 1 50.0%; Pred. No. 2.1e+02;
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3; Mismatches
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 490 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-672-571A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |:::| ||
193 NFWNTTGKHP 202
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Best Local Similarity
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ADDRESSEE: PENNIE & EDMONDS
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US-08-087-244A-8
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-449-644-8
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Gaps
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APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.5%; Score 38; DB 2; Length 1452; 55.6%; Pred. No. 6.6e+02; Live 2; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fuchs, Miriam
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIOLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION UNDRER: 33,055
REFERENCE/DOCKET NUMBER: 9103;
TELEPHONE: (415) 225-3216
TELEPHONE: (415) 952-9881
TELEPHONE: (415) 952-9881
TELERX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08449644
Patent No. 5856162
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                                                                                                                                            Sequence 4, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
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Ullrich, Axel
Vogel, Wolfgang
Fuchs, Miriam
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Best Local Similarity 55.6
Matches 5; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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434 SWDTDNSHP 442
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                                      2 SWDSSGTHP 10
                                                                             57 SWDTENSHP 65
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-652-971-4
                                                                                                                                                         US-08-652-971-4
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  Matches
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5.7 2; Indels
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Patent No. 5863755
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Ulrich, Axel
APPLICANT: Vogel, Wolfgang
APPLICANT: Wolfs Mixiam
TITLE OF INVENTION: PHOSPHATASE-KAPPA
                                                                                                                                    COMPUTER: TIDEN PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,644
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/087,244
FILING DATE: 01-U1-1993
ATTORNEY/AGENT INFORMATION:
NAME: COPUZZI, LAURA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
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Pred. No. 6.6e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 76! TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.5
Best Local Similarity 55.6
Matches 5; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 SWDTENSHP 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
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U.S.A.
                                       New York
Y: U.S.A.
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2, Indels

55.6%; Pred. No. 6.6e+02; tive 2; Mismatches 2

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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                       RESULT 13
US-08-769-399-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1452;
                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,258A
FILING DATE: 17-DEC-1997
CLASSIFICATION 3435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
FILING DATE: 24-MAY-1996
ATTONEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 34,190
RETERRENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELEFRANIS: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                Score 38; DB 2; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                          7683-042
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMDPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08991258A
Patent No. 5928887
                  NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
RELECOMMUNICATION INFORMATION:
FELEPHONE: 212-790-9090
TELEPHONE: 212-86-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              58.5%;
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.6.
....hes 5; Conservative
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SEQUENCE CHARACTERISTICS
LENGTH: 1452 amino ac
                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOI
STREET: 4 Embarcader
                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 SWDTENSHP 442
                                                                                                                                                                                                                                                                                                                                                                                                            2 SWDSSGTHP 10
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                                                                                                                                                                                                                                                                                          US-08-087-244A-8
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US-08-991-258A-4
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58.5%; Score 38; DB 2; Length 1452;

Query Match

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Patent No. 6083748

GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                        Sequence 4, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
TUTLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genenteeh, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1452;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P. TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 225-3216
(415) 952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
COUNTRY: United States
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910 371-7168 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                         434 SWDTDNSHP 442
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2 SWDSSGTHP 10
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Sequence
US-09-562-737-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.5%; Score 38; DB 3; Length 1452; Best Local Similarity 55.6%; Pred. No. 6.6e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09562737
; Sequence 97, Application US/09562737
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Herz, Joachim
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; TITLE REFERENCE: UTSW0708
; CURRENT APPLICATION UWBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
                                                                             COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
                                                                                                                                                                                                                                                                                                                                                                             NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/WTK
TELECOMMUNICATION: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acids
STRANDEDNESS:
                     California
: United States
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-08-991-953A-4
San Francisco
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US-09-562-737-97
                     STATE: CE
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| ||:|||| 141 WTDSAGTHP 149

3 W-DSSGTHP 10

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Search completed: April 28, 2005, 18:28:06 Job time: 23.3438 secs
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250, App 250, App 274871, 50343, A 166593,

Sequence Sequence

Sequence Sequence Sequence

US-10-783-950-25 US-10-424-599-243244 US-10-629-243244 US-10-340-536-18 US-10-340-536-16 US-09-880-748-353 US-09-880-748-353 US-09-880-748-353 US-10-293-418-353 US-10-293-418-353 US-10-293-418-353 US-10-293-418-353 US-10-291-12-626 US-10-291-13-626 US-10-291-17-626 US-10-291-17-626 US-10-291-17-626 US-10-291-17-250 US-10-291-17-250 US-10-291-17-250 US-10-291-17-626 US-10-291-17-626 US-10-291-17-626 US-10-425-114-53692 US-10-425-114-53692 US-10-425-114-69140 US-10-425-114-69140 US-10-425-114-69140 US-10-425-114-69140 US-10-385-305-188 US-10-425-114-69140 US-10-385-305-188 US-10-385-305-188 US-10-385-305-188 US-10-385-305-188 US-10-385-305-188

120488,

Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

3149, Ap 2, Appli

Sequence

Sequence Sequence

Sequence

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Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence 69140, A 8523, Ap 6568, Ap

Sequence

Sequence Sequence

Sequence

ALIGNMENTS

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US-09-817-661-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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April 28, 2005, 18:24:46 ; Search time 68.2344 Seconds (without alignments) 53.700 Million cell updates/sec
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                                                                                                                                                                                                                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                   1426032 segs, 333106140 residues
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                                                                                                                                                                                                                     Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                            US-10-088-639A-2_COPY_88_98
65
                                  - protein search, using sw model
                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                             1 NSWDSSGTHPV 11
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Query
Match Length D
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                                                  Run on:
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Sequence 21, Application US/09817661
Patent No. US20020076692A1
GENERAL INFORMATION:
APPLICANT: OBDOURN, Jane
TITLE OF INVENTION:
ITLE REFERENCE: 94633
CURRENT APPLICATION NUMBER: US/09/817,661
CURRENT FILING DATE: 2001-03-26
FRIOR APPLICATION NUMBER: US 60/193,802
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 173, Application US/10251085B; Publication No. US20040072164A1; Publication No. WARDION: APPLICANT: Bowdish, Katherine S.
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Matches 9; Conserv
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US-10-251-085B-173
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Sequence 173, App Sequence 173, App Sequence 177279, Sequence 1115, Ap Sequence 1116, Ap Sequence 1116, Ap Sequence 1116, Ap Sequence 194069, Sequence 1980, Ap Sequence 1980, Ap Sequence 1980, Ap

US-10-251-085B-173 US-10-737-255-173 US-10-424-599-177279 US-09-880-748-1115 US-10-293-418-1115 US-10-293-418-1116 US-10-293-418-1116 US-10-779-461-10 US-10-779-461-10 US-10-779-481-1980 US-10-293-418-1980 US-10-293-418-1980 US-09-880-748-1980 US-09-563-222-25

78.5 75.4 75.4 70.8 70.8 67.7 667.7 667.7 663.1 63.1 61.5

94444444444 9999944644

Sequence 21,

US-09-817-661-2

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Gaps
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TITLE OF INVENTION: Autibodies that Immunospecifically Bind BLyS
TITLE OF INVENTION: Autibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver: 2.0
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF5.239
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
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                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13109C.1.pep
US-10-424-599-177279
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1; Mismatches
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177279
LENGTH: 168
                                                                                                                                                                                                                                                                                     Score 49;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-748-1115
; Sequence 1115, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  75.4%;
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72.7%;
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Best Local Similarity 70.0°
Land 7; Conservative
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Best Local Similarity 72...
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-880-748-1115
                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-293-418-1115
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            APPLICANT: Renehaw, Mark
APPLICANT: End Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maryama, Mark
APPLICANT: Maryama, Mark
APPLICANT: Maryama, Toshiaki
TITLE OP INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/251,085B
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR APPLICATION NUMBER: US 60/323,455
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Hin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
TITLE REFERENCE: 1087-21 CIP
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR FILING DATE: 2002-09-19
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Publication No. US20040031072A1
GENERAL INPORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: Cavalic David K
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 173, Application US/10737252
Publication No. US20040175736A1
    Frederickson, Shana
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88.9%;
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SEQ ID NO 173
LENGTH: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 WDSSGDHPV 100
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Matches 8; Conserv
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                       ORGANISM: human
US-10-251-085B-173
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PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PRILOR PRIOR NUMBER: 60/277,379
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-116
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 WDSSSDHPV 234
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ORGANISM: Homo sapiens
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Sequence 1116, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-010-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239

SEQ ID NO 1116
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
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Pred. No. 46;
1; Mismatches 1; Indels
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 22;
1; Mismatches
              PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-16-17
SEQ ID NO 115
LENGTH: 249
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Best Local Similarity 72.7%;
Matches 8; Conservative
FILING DATE: 2001-06-15
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Best Local Similarity 77.6
Person 7; Conservative
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228 HSWDSSGNHVV 238
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226 HSWDSSGNH 234
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US-10-293-418-1115
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US-09-880-748-1116
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US-10-779-461-10

| Sequence 10, Application US/10779461
| Sequence 10, September 10, Application US/10779461
| Publication No. US20040166544A1
| Publication No. US20040166544A1
| GENERAL INFORMATION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS | FILE REFERENCE: 00980/1 | CURRENT APPLICATION NUMBER: US/10/779,461
| CURRENT APPLICATION NUMBER: 60/447,073 | PRIOR FILING DATE: 2003-02-13 | NUMBER OF SEQ ID NOS: 161 | SOFTWARE: Patentin version 3.2 | SEQ ID NO 10 | LENGTH: 245
                                                                   Gaps
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Score 44; DB 15; Length 247;
Pred. No. 46;
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                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-10
                                                                1; Mismatches
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTIONAL INGUINGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REPERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/10/783,950
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Sequence 25, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: BUKARYOTIC CELLS
FILE REPERENCE: 310.098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 15; Length 246;
Pred. No. 1.4e+02;
); Mismatches 2; Indels
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Pred. No. 11;
1; Mismatches 2; Indels
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                                                 PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 09/880,748
PRIOR PILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PRING DATE: 2001-03-16
PRIOR PRING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247

FUNDRER OF SEQ ID NOS: 3247
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81.8%;
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US-10-293-418-1980
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Best Local Similarity
Matches 9; Conserv
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Matches 6; Conserv
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US-10-783-950-25
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| Publication No. US20030059937A1
| GENERAL INCPRARTION:
| APPLICANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| FILE REFERENCE: PF523 |
| CURRENT APPLICATION WUMBER: US/09/880,748 |
| CURRENT FILING DATE: 2001-06-15 |
| PRIOR APPLICATION WUMBER: 60/212,210 |
| PRIOR PILING DATE: 2000-06-15 |
| PRIOR PLILING DATE: 2000-10-17 |
| PRIOR PLILING DATE: 2000-10-17 |
| PRIOR PLILING DATE: 2001-03-16 |
| PRIOR PLILING DATE: 2001-03-16 |
| PRIOR PLILING DATE: 2001-03-16 |
| PRIOR PLILING DATE: 2001-03-21 |
| PRIOR PLILING DATE: 2001-03-25 |
| PRIOR PLILING DATE: 2001-05-25 |
| NUMBER OF SEQ ID NOS: 3239 |
| SOFTWARE: Patentin Ver. 2.0 |
| LENGTH: 246
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; Sequence 1980, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVERINCON:
; FILE REFERENCE: PF523P2
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US-10-437-963-194069
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Pred. No. 1.4e+02;
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Matches 7; Conservative
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Best Local Similarity
Matches 9; Conserv
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Pred. No. 11;
1; Mismatches 2; Indels
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US-10-424-599-243244
## CURRENT FILING DATE: 2004-02-19
| PRIOR APPLICATION WUMBER: US/09/563,222
| PRIOR FILING DATE: 2000-05-02
| PRIOR FILING DATE: 2000-05-02
| PRIOR FILING DATE: 2001-05-02
| PRIOR FILING DATE: 2001-05-02
| PRIOR PLIOR TOWNER: 09/563,222
| PRIOR PLING DATE: 2000-05-02
| NUMBER OF SEQ ID NOS: 182
| SEQ ID NO 25
| LENGTH: 13
| TYPE: PRI
| TYPE: PRI
| ORGANIGM: Homo sapiens
| US-10-783-950-25
                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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2 AWDSSSDHP 10
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ORGANISM: Glycine max
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US-10-424-599-243244
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Search completed: April 28, 2005, 19:02:14 Job time : 69.2344 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

April 28, 2005, 18:05:55 ; Search time 15.125 Seconds (without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_88_98 65 1 NSWDSSGTHPV 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
п	42	64.6	130	~	T43606	yopE chaperone syc
7	41	63.1	98	~	F97245	probable HD superf
m	41	63.1	339	~	T27931	hypothetical prote
4	41	63.1	456	R	B90543	
S	40	61.5	18	7	C49254	_
9	40	61.5	110	~	C24775	T-cell receptor qa
7	40	61.5	120	7	B24775	
80	40	61.5	132	~	809713	bda chain
6	40	61.5	629	~	T38214	hypothetical prote
10	40	61.5	914	~	T08081	probable myrosinas
11	40	61.5	986	~	T08102	myrosinase-bindino
12	39	0.09	201	~	A88363	protein F26H11.1
13	39	60.09	270	~	T06528	lectin - garden pe
14	39	60.09	402	~	S74525	hypothetical prote
15	39	60.09	652	N	G85024	probable CHP-rich
16	39	60.0	995	~	T22942	hypothetical prote
17	39		1336	~	T02736	probable SCARECROM
18	38		295	~	E84862	hypothetical prote
19	38	58.5	451		S56818	
20	38		476	~	D95318	NifE oxidoreductae
21	38		482	~	JC7332	endoglycosylcerami
22	38	58.5	567	~	A97291	oligopeptide ABC t
23	38		1099	7	A59311	myosin VIII, ZMM3
24	38	58.5	1290	~	A56493	leucocyte common a
25	38	58.5	1369	7	D86178	hypothetical prote
26	38	58.5	1452	-	S17669	protein-tyrosine-r
27	38		1452	-	S17670	protein-tyrosine-p
28	38	58.5	1797	7	F69195	cell surface glyco
29	38	58.5	1898	7	S46216	leukocyte antigen-

Ig lambda chain -	Ig lambda chain V	hypothetical prote	hypothetical prote	aryl sulfotransfer	aryl sulfotransfer	phenol sulfotransf	aryl sulfotransfer	aryl sulfotransfer	aryl sulfotransfer	aryl sulfotransfer	phenol-sulfating p	aryl sulfotransfer	aryl sulfotransfer	exostose-related p	brefeldin A estera
S47184	S19663	C83704	B86918	JC5000	852791	G02924	A55451	JC2523	JC5249	S52794	I57945	JC5248	G01843	JC5935	A53050 ·
N	~	~	N	7	7	~	~	~	~	0	~	~	7	~	7
108	109	125	271	294	295	295	295	295	295	295	295	295	295	330	372
56.9	56.9	56.9	56.9	56.9	6.95	56.9	56.9	56.9	56.9	56.9	56.9	56.9	56.9	56.9	56.9
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37

## ALIGNMENTS

yopE chaperone sycE - Yersinia pestis plasmid pCD1

C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43606; T42911
C;Accession: T43606; T42911
J: Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: 222578; MUID:98422474; PMID:9748454
A;Accession: T43506
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA* XResidues: 1-130 «HUP» A;Cross-references: UNIRROT: P31491; EMBL:AF053946; NID:g2996222; PIDN:AAC62588.1; PID:g2 A;Experimental source: strain KIM

Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. fifect. Immun. 66, 4611-4623, 1998
Title: DNA sequencing and analysis of the low-ca2+-response plasmid pCD1 of Yersinia F. Reference number: Z22273; MUID:98427122; PMID:9746557

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A;Residues: 1-130 <PER> A;Cross-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69819.1; PID:g3822099 A;Experimental source: strain KIMS

A;Genome: plasmid pCD1 C;Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein sycE

Gaps ; 0 Score 42; DB 2; Length 130; Pred. No. 4.4; 0; Mismatches 3; Indels 64.6%; 70.0%; Conservative Query Match Best Local Similarity 7; Conserva

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2 SWDSSGTHPV 11

79 SWDEVGGHPV 88

g 8

F97245
probable HD superfamily hydrolase [imported] - Clostridium acetobutylicum
C;Species 14-Sep-2010 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97245
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: P97245

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TCR C gamma 1 chain V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
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Matches 7; Conservative
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7; Conserva
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A;Molecule type: DNA
A;Residues: 1-18 <EZQ>
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C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90543
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUD:21267165; PMID:11353084
A;Accession: B90543
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-456 AKUR>
A;Cross-references: UNIPROT:Q98QW0; GB:AL445566; PID:g14089663; PIDN:CAC13423.1; GSPDB:G
C;Genetics:
A;Genetics:
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ZK596.3 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: T2791
RimcMurray, A.
Submirray, A.
Submirted to the EMBL Data Library, February 1996
A;Reference number: Z20441
A;Reference number: Z20441
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-339 <WILL>
A;Residues: 1-339 <WILL>
A;Residues: 1-339 <WILL>
A;Residues: 1-339 <WILL>
A;Gross-references: UNIPROT.Q23547; EMBL:Z69386; PIDN:CAA93432.1; GSPDB:GN00022; CESP:ZR
A;Experimental source: clone ZK596
C;Genetics: A;Gene: CESP:ZK596.3
A;Map position: 4
A;Introns: 62/3; 110/3; 134/3; 200/1; 283/1
A;Status: preliminary
A;Molocule type: DNA
A;Molocule type: DNA
A;Cross-references: UNIPROT:Q97FD1; GB:AE001437; PIDN:AAK80753.1; PID:g15025850; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
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Pred. No. 25;
1; Mismatches 2; Indels
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Pred. No. 18;
2; Mismatches 1; Indels
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Pred. No. 4.8;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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19 NSWDISKTYP 28
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R.Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M. Eur. J. Immunol. 22, 491-498, 1992
A,Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T.A;Reference number: A49037; WUID:92164730; PMID:1311262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-110 cGAR>
A;Note: this sequence was determined from the differentiated gene
A;Note: the authors translated the codon ACG for residue 2 as Ser and ACA for residue 59
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
Cell 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Reference number: A90880; MUID:86218086; PMID:3486721
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R;Garman, R.D.; Doherty, P.J.; Raulet, D.H. Cell 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genu A,Reference number: A90880; MUID:86218086; PMID:3486721
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C,Species: Mus musculus (house mouse)
C,Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
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A,Residues: 1-120 cGAR>
A,Cross-references: GB.M13337; NID:g201668; PIDN:AAA40316.1; PID:g201669
A,Note: this sequence was determined from the differentiated gene
A,Note: the authors' translation contained an addition Cys after 14-Val
C,Genetics:
                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S90689; NID:g246310; PIDN:AAB21558.1; PID:g246311
A;Experimental source: FF3 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:90689; NCBIP:90691)
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Pred. No. 8.1;
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Pred. No. 1.2;
0; Mismatches
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myrosinase-binding protein (clone indmbp2) - rape
C;Species: Brassica napus (rape)
C;Date: 2:ImMay-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08102
R;Taipalensuu, J.; Eriksson, S.J.; Rask, L.
R;Taipalensuu, J.; Eriksson, S.J.; Rask, L.
R;Taipalensuu, J.; Eriksson, S.J.; Rask, L.
A;Title: The myrosinase binding protein from Brassica napus seeds possesses lectin acti
A;Reference number: Z16355; MUID:98121188; PMID:9461290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-988 <TAI>.
A;Cross-references: UNIPROT:P93065; EMBL:Y09437; NID:g1711295; PIDN:CAA70587.1; PID:g171
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R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C elcA;Note: published errata appeared in Science 283, 15, 1999; Science 283, 2103, 1999; and
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A;Cross-references: GB:chr_II; PIDN:CAB04194.1; PID:g3876448; GSPDB:GN00020; CESP:F26H11
                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P93659; EMBL:Y11482; NID:e1023100; PIDN:CAA72270.1; PID:e30
A;Experimental source: cv. Global; isolate a4; seedlings
A;Note: jasmonate inducible
                                 CiSpecies: Brassica napus (rape)
CiDate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
CiDate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
CiAccession: T080al
RiGeshi, N.; Brandt, A.
Planta 204, 295-304, 1998
A;Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L. A;Reference number: 216340; MUID:98192006; PMID:9530873
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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Pred. No. 78;
0; Mismatches
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A;Molecule type: mRNA
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Pred. No. 85;
0; Mismatches
      jasmonate inducible protein
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Similarity 66.7%;
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6; Conserv?
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            N;Alternate names:
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A;Map position: 2
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hypothetical protein SPAC22H10.11c - fission yeast (Schizosaccharomyces pombe
C;Species Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38214
A;Refishuk, K.; McIntoh, M.; McIntoh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, February 1996
A;Reference number: Z21778
A;Accession: T38214
A;Accession: T38214
A;Accession: T38214
A;Accession: T38214
A;Accession: T38214
A;Accession: T38214
A;Residues: 1-629 <DEV>
A;Cross-references: UNPROT:Q10304; EMBL:Z69730; PIDN:CAA93611.1; GSPDB:GN00066; SPDB:SF
A;Cross-references: Strain 972h-; cosmid c22H10
                                                                                                                                                                                                                                                                                                                                                                                                                        Substance chain V region - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C; Accession: S09713 #sequences and three-dimensional modelling of the VH and VL domains c shochen. J. 268, 135-140, 1990 A; Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains c A; Reference number: S09710; MUID: 90262535; PMID: 2111699 A; Accession: S09713 A; Accession: S09713 A; Accession: S09713 A; Residues: 1-132 < HUGA A; Accession: S09713 A; Residues: 1-132 < HUGA A; Accession: Immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology < IMM>
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A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22H10.11c
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A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                                                  Score 40; DB 2; Length 120;
Pred. No. 8.9;
0; Mismatches 2; Indels
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75.0%; Pred: No. 9.8;
tive 0; Mismatches 2; Indels
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probable myrosinase-binding protein - rape
                                                                                                            Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Length 652; 3; Indels

DB 2;

60.0%; 54.5%;

2; Mismatches Score 39; DB Pred. No. 81;

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C;Accession: G85024
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
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A;Status: preliminary
A;Moleotle type: DMA
A;Residues: 1-652 <STO>
A;Cross-references: UNIPROT:Q9SYJO; GB:NC_001268; NID:g7268577; PIDN:CAB80686.1; GSPDB:G
                                                    R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, the Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
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Best Local Similarity
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A;Map position: 4
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Plant Physiol. 111, 49-60, 1995
Ajritle: Identification of a new pea gene PsNlec1 that encodes a lectin-like glycoprotei
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Ajritle: Identification of a new pea gene PsNlec1 that encodes a lectin-like glycoprotei
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CjGenetics:
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CjGenetics:
Ajritle: Identification
CjGenetics:
Ajritle: Identification
CjSuperfamily: plant lectin
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A;Recession: S74525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <KAN>
A;Cross-references: UNIPROT:P72675, EMBL:D90899, GB:AB001339; NID:g1651650, PIDN:BAA1667
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0731
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hypothetical protein slr0731 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.
A;Variety: PCC 6803

C;Species: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S74525

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06528
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STRAIN=8081 / Serotype O:8;
STRAIN=8081 / Serotype O:8;
MEDDLINE=9017087; PubMed=2307658;
Forsberg A., Wolf-Watz H.;
"Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, Yer4, regulating yopE expression.";
of a novel conserved locus, Yer4, regulating yopE expression.";
-:- FUNCTION: POSITIVE REGULATOR OF YOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
NCBI_TaxID=630;
                          058791
083490
027993
059833
09kzj5
082mt8
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Q169329
Q169337
Q53395
Q16602
Q6711W5
Q6711W
P08293
P15272
Q6307
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P22409
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P26804
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P47563
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P50127
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P15651
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002791
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                                                                                                                 YNI6_YEAST
NIFX_RHISN
PGL1_ASPNG
GATR_PIG
                                                                                                                                                                            HSFY_HUMAN
ACDS MOUSE
ACDS MOUSE
ACDS MOUSE
ASP ACCA
ASP ANCCA
YF24 MYCLL
ASP ANCCA
YF26 MYCH
ENV MLVFR
CGRR_HAFR
CGRR_RAT
SERA_SCHPO
NIFE_AZOVI
ANN ECOLI
NIFE_RHILO
PSBB_CHLUO
ANN ECOLI
NIFE_RHILO
YL49 BRAJA
NIFE_BRAJA
NIFE_BRAJA
NIFE_BRAJA
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Y321_MYCGE
TRA1_COMTE
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STRAW
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'opE regulator.
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STRAIN-KIMS, / Biovar Mediaevalis; PLASMID=pCD1;
STRAIN-KIMS, / Biovar Mediaevalis; PLASMID=pCD1;
MEDLINE=98422474; PubMed=9748454;
Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
Kobayashi A., Brubaker R.R., Garcia E.;
"Structural organization of virulence-associated plasmids of Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=EV76; PLASMID=pYV019;
MEDLINE=90170873; PubMed=2307658;
Porsbarg A., Wolf-Watz H.;
"Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression.";
J. Bacteriol. 172:1547-1555 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis KIMS.";
Infect. Immun. 66:4611-4623(1998).
                                                                                                                                                                                                                                                                                                                   Gaps
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STRAIN=CO-92 / Blovar Orientalis; PLASMID=pCD1;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid pCD1, and Plasmid pYV019.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-KIMS / Biovar Mediaevalis; PLASMID-pCD1;
MEDLINE-98427122; PubMed-9746557;
Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                           Length 130;
                                                                                                                                                       EMBL; M34278; AAA27673.1; -.
InterPro; IPR005416; SycE chap.
PRINTS; PR01596; SYCECHAFRONE.
Virulence; Plasmid; Transcription regulation; Activator.
SEQUENCE 130 Aa; 14676 MW; 491B67B4C293CA5A CRC64;
                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YERA_YERPE STANDARD; PRT; 130 AA. P31491; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                             Score 42; DB 1
Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YopE regulator.
YERA OR YPCD1.05C OR Y5069 OR Y0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol, 180:5192-5202(1998)
                                                                                                                                                                                                                                                                             64.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                     7; Conservative
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Best Local Similarity
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01-FEB-1996 (
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                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDLINE 27184401; PubMed=11859360;

WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squoros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Rochies S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,

Nooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saudares R., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Ryalor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodffeau A., Cadleu B., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Raber D., Jimenez J., Sanchez M., del Rey F., Benito J.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                 64.6%; Score 42; DB 1; Length 130; 70.0%; Pred. No. 1.9; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                    PDB; 1JTA; 13-MAR-02.
InterPro; IPR05416; SycE chap.
BRINTS; PR01596; SYCECHAPRONE.
Virulence; Plasmid; Plasmid; Activator;
Complete proteome; 3D-structure.
SEQUENCE 130 AA; 14650 MW; 41A12BB29831CA5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C22H10.11c in chromosome
SPAC22H10.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 AA
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                                               -! - FUNCTION: POSITIVE REGULATOR OF YOPE.
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Best Local Similarity 70.0%;
7; Conservative
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Q10304;
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YD4B_SCHPO
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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   Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO BACTERIAL LIPOATE-PROTEIN LIGASE A (LPLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                   PotaBhkin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.1 kDa protein in MTR4-GYP6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 1; Length 451;
Pred. No. 37;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 40; DB 1; Length 629; 60.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 208 POLY-GLU.
629 AA; 71266 MW; A32FA33FEE27605D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 AA; 52085 MW; 637673A018B865AE CRC64;
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Cernuti L., Lowe T., McCombie W.R., Paulsen I., Potas Shpakovski G.V. Useery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 38; 66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49321; CAA89337.1; -.
PIR; S56818; S56818.
GermOnline; 141660; -.
SGD; S0003582; YJL046W.
InterPro; IPR004143; BPL LipA LipB.
InterPro; IPR004562; LipOyltrans.
Pfam; PF03099; BPL LipA LipB.
TIGREAMS; TIGR00545; lipOyltrans, 1.
Hypothetical protein.
SEQUENCE 451 A4; 52085 MW; 637673A0
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z69730; CAA93611.1; -.
PIR; T38214; T38214.
GeneDB SPombe; SPAC22H10.11c; -.
Hypothetical protein.
DOMAIN 201 208 POLY
                                                                                                                           Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 NSWKKSSSHP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                  Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hwan R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
-! FUNCTION: This protein may play a role in the biosynthesis of the
prosthetic group of nitrogenase (Few cofactor).
-!- PATHWAY: Fe-Mo cofactor biosynthesis.
-!- SIMIARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenaee iron-molybdenum cofactor biosynthesis protein nifE.
NIFE OR RAO452 OR SAMO030.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenase iron-molybdenum cofactor biosynthesis protein nifE.
NIFE OR Y4VN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                         Plasmid pSymA (megaplasmid 1).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 476; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TICK01283; nife; 1.
PROSTIE; PS00699; NITROGENASE 1 1; 1.
PROSTIE; PS00090; NITROGENASE 1 2; 1.
Nitrogen fixation; Plasmid; Complete proteome.
SEQUENCE 476 AA; 52358 MW; 83ECE94B4B14C713 CRC64;
                                                                                        476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005973; NifE.
InterPro; IPR000318; Nitrognse compl.
InterPro; IPR000510; Oxred nitrognsel.
Pfam; PF00148; oxidored nitro; 1.
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                       MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE007236; AAK65110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                        STANDARD;
333 WESSGVHSV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSWDNRGT 80
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Best Local Similarity
                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIFE RHISN
AC P55673;
DT 01-NOV-1997
DT 01-NOV-1997
DT 28-FEB-2003
DD NITCOGENBER ON NIFE ON Y4VN
                                                                                                                                                                                                                                                                                                          STRAIN=1021
                                                                                        RHIME
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                          NIFE RH
Q92ZLZ;
                                                                          NIFE RHIME
                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:394-401(1997).

-!- FUNCTION: This protein may play a role in the biosynthesis of the prosthetic group of nitrogenase (FeMo cofactor).

-!- PATHWAY: Re-Mo cofactor biosynthesis.

-!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                           MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilu K.W., Alice L.A., Liang H.;
"Phylogeny of Poaceae inferred from matK sequences.";
"no. Mo. Bot. Gard. 86:835-851(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       introns (By similarity). SIMILARITY: Belongs to the intron maturase family 2. Matk
                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBL_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 496; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; PREMODELO; Oxred nitrognsel.
Pfam; PF00148; oxidored nitro; 1.
TIGRFAMS; TIGR01283; nifE; 1.
PROSITE; PS000699; NITROGENASE_1 1; 1.
PROSITE; PSXALION; Plasmid.
Nitrogen fixation; Plasmid.
SEQUENCE 496 AA; 54793 MW; D78472D8F5410A3A CRC64;
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000318; Nitrognse_compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bromus inermis (Smooth brome grass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000102; AAB91902.1; -.
(strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.5%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                 Plasmid sym pNGR234a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 NSWDNRGT 80
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Matches 6; Conserv
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
    Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast
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Q9MUZ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ADTK BL

ADT 10-0CT-1

DT 10-0CT-1

DT 10-0CT-1

DE MATURE

GS MATK.

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            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-- SUNICARITY: Contains 1 MAM domain.
-- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-- SIMILARITY: Contains 4 fibronectin type III domains.
-- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
(R-PTP-mu).
                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92008644; PubMed=1655529; MEDLINE=92008644; PubMed=1655529; Gebbink M.B.G., van Etten I., Hateboer G., Suijkerbuijk R., Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.; "Cloning, expression and chromosomal localization of a new putative receptor-like protein tyrosine phosphatase."; FEBS Lett. 290:123-130(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatase mu.";
J. Biol. Chem. 272:27505-27508(1997).
-!- FUNCTION: May play a key role in signal transduction and growth
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98010572; PubMed=9346878;
Hoffmann K.M., Tonks N.K., Barford D.;
"The crystal structure of domain 1 of receptor protein-tyrosine
                                                                                                                                                                    58.5%; Score 38; DB 1; Length 511; 60.0%; Pred. No. 42;
                                                                                                                                                                                           3; Indels
                                                                                      InterPro; IPR000442; Intron maturse2.
InterPro; IPR02866; MatK.N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK.N; 1.
PRNM processing; Chloroplast.
SEQUENCE 511 AA; 61572 MW; 088497F25BE52C88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.
                                                                                                                                                                                                                                                                                               PRT; 1452 AA
                                                                                                                                                                                           1; Mismatches
                                                                           EMBL; AF164398; AAF66185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X58288; CAA41226.1; -. PIR; S17669; S17669. PDB; 1RPM; 01-APR-98.
                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
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A MIM, 176889.

R MIM, 176889.

R GO, GO:0005807; C:integral to plasma membrane; TAS.

R GO; GO:0005801; C:integral to plasma membrane; TAS.

R GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. O: GO:0006470; P:protein amino acid dephosphorylation; TAS.

R InterPro; IPR008985; COJA 11Ke lec_gl.

R InterPro; IPR003961; PN III-11Ke.

R InterPro; IPR003961; PN III-11Ke.

R InterPro; IPR003961; PN III-11Ke.

R InterPro; IPR003961; PN III-11Ke.

R InterPro; IPR003961; TYR_phosphatase.

R InterPro; IPR003961; TYR_phosphatase.

R InterPro; IPR0041; IG; 1.

R Fam; PF00047; IG; 1.

R Fam; PF00047; IG; 1.

R Fam; PF00102; Y phosphatase; 2.

R Fam; PF00102; Y phosphatase; 2.

R RINTS; RR00020; MAMDOMAIN.

R RINTS; RR00020; MAMDOMAIN.

R RNART; SM0019; IG; 1.

R SMART; SM0019; PTPC; 2.

R SMART; SM0019; PTPC; 2.

R ROSITE; PS00606; MAM_2; 1.

R ROSITE; PS006070; MAM_2; 1.

R ROSITE; PS006070; MAM_2; 1.

R ROSITE; PS00606; MAM_2; 1.
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PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE 1. PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR-TYPE PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50060; MAM 2; 1.

PROSITE; PS00383; TYR PHOSPHATASE 1; 2.

PROSITE; PS50056; TYR PHOSPHATASE 2; 2.

PROSITE; PS50055; TYR PHOSPHATASE 2; 2.

Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Immunoglobulin domain; Repeat; 3D-structure.

SIGNAL 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
(R-PTP-mu).
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUB-Lung;

MEDLINE=2008644; PubMed=1655529;

MEDLINE=2008644; PubMed=1655529;

MEDLINE=2008644; PubMed=1655529;

Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;

Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;

"Cloning, expression and chromosomal localization of a new putative receptor-like protein tyrosine phosphatase.";

FEBS Lett. 290:123-130 (1991).

-!-FINCTION: May play a key role in signal transduction and growth
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: Contains 1 MAM domain.
-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-1- SIMILARITY: Contains 4 fibronectin type III domains.
-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                   Length 1452;
                                                                                                                                                                                                                 Score 38; DB 1; Length 145
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                   AA; 163633 MW; 08175D3595A6C7E0 CRC64;
                                                                                                                                                                                                                   58.5%;
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
434 SWDTENSHP 442
                                                                                                                                                                                                                                                 SWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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Best Local Similarity
Local 5; Conserve
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ID PTPM MOUSE
AC P28828;
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PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
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PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
POTENTIAL.
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SMART; SM001409; IG; 1.

SMART; SM00147; MAM; 1.

SMART; SM00194; PTPC; 2.

PROSITE; PS00740; MAM; 1:

PROSITE; PS50060; MAM; 2; 1.

PROSITE; PS50050; TYR PHOSPHATASE 1; 2.

PROSITE; PS50050; TYR PHOSPHATASE 2; 2.

PROSITE; PS50050; TYR PHOSPHATASE PFP; 2.

PROSITE; PS50050; TYR PHOSPHATASE PFP; 2.

PROSITE; PS50050; TYR PHOSPHATASE PFP; 2.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
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MAM.
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Pred. No. 1.3e+02;
2; Mismatches 2;
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the Buropean Bioinformatics Institute. Ther use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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PIR; S17670; S15670.
HSSP; PS2827; IRPM.
MGD; MGI:102694; Ptprm.
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR008985; W III-like.
InterPro; IPR001361; FW III.
InterPro; IPR001361; FW III.
InterPro; IPR001361; IG-like.
InterPro; IPR001389; MAM_domain.
InterPro; IPR000389; MAM_domain.
InterPro; IPR000381; TYR_phosphatase.
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Pfam; PF00102; MAM; 1.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR00020; MAMOMAIN.
PRINTS; PR00020; PRTYPHPHTASE.
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Tardoya R., Abouheif E., Mayer A.;

"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"If proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).
"If proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).
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"If proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).
"If surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
"If condition activity to the C-terminal of the newly generated Natl. Insignate (N-product). This covalent actachment of a cholesterol moiety to the C-terminal of the newly generated Natl. Insigned (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the activity special series in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
"If active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01085; HH signal; 1. PRINTS; PR00632; SONICHHOG.
Probom; PD003042; HH signal; 1.
Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
NON TER
CONFLICT 17 17 Q -> M (IN REF. 2).
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                                                                                                                                                                                                                                                                                               P79729; Q9YGU3;
15-JUL-1999 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                   88 AA
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InterPro, IPR000320; HH_signal.
InterPro, IPR001657; Peptidase_C46.
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MEDLINE=97075114; PubMed=8917540;
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O62226; 1VHH.
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434 SWDTDNSHP 442
SWDSSGTHP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of bovine tracheobronchial phenol sulphotransferase CDNA and detection of mRNA regulation by cortisol."; Biochem. J. 311:209-217(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nonneman D.J., Shibuya H., Johnson G.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the sulfate conjugation of catecholamines and
of phenolic drugs.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96001918; PubMed=7575456;
Schauss S.J., Henry T., Palmatier R., Halvorson L., Dannenbring R.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. MCBI_TaxID=9913;
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phenol-sulfating phenol sulfotransferase (BC 2.8.2.1) (P-PST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol adenosine 3',5'-bisphosphate + an aryl sulfate.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Distal lung parenchyma.
-!- TISSUE SPECIFICITY: Distal lung parenchyma.
                                                                                                                                       Length 88;
                                                                                                                                                                      3; Indels
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R -> K (IN REF. 2).
A -> G (IN REF. 2).
HHPPG -> NHLED (IN REF. 2).
TK -> RN (IN REF. 2).
L -> M (IN REF. 2).
Q -> R (IN REF. 2).
                                                                                                         10069 MW; E3D34A0C36677FA6 CRC64;
                                                                                                                                    Score 37; DB 1;
Pred. No. 9.3;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                            294 AA
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TISSUE=Tracheobronchial;
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                                                                                                                                       56.9%;
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PIR; JC5000; JC5000.
HSSP; P50224; ICJM.
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P50225; Q02818; Q98UGG7;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2104 (Rel. 43, Last annotation update)
16-WAR-21014 (Rel. 43, Last sequence update)
17-WAR-21014 (Rel. 43, Last sequence update)
18-WAR-21014 (Rel. 4
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Heinrikson R.L., Falany C.N.;
"Sequence analysis and expression of the cDNA for the phenol-sulfating
form of human liver phenol sulforransferase.";
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"Human platelet phenolsulfotransferases: cDNA cloning, stable
expression in V79 cells and identification of a novel allelic variant
of the phenol-sulfating form.",
Biochem. Biophys. Res. Commun. 208:855-862(1995).
                                                                                                                                                                                                                                                                                    Gaps
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SEQUENCE FROM N.A.
TISSUE=Hippocampus;
MEDLINE=95169114; PubMed=7864863;
Hwarg S.-R., Kohn A.B., Hook V.Y.H.;
Hwarg S.-R., Kohn A.B., Hook V.Y.H.;
"Molecular cloning of an isoform of phenol sulfotransferase from "Molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase" in the phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of phenol sulfotransferase from "molecular cloning of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of an isoform of
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ozawa S., Nagata K., Shimada M., Ueda M., Tsuzuki T., Yamazoe Y.,
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                                Catecholamine metabolism; Steroid metabolism; Transferase. BINDING 259 265 PAPS BINDING SITE (POTENTIAL). SEQUENCE 294 AA; 34017 MM; 8ADEE67D47E69737 CRC64;
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                                                                                                                                                                                                 56.9%; Score 37; DB 66.7%; Pred. No. 34;
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ProDom; PD001218; Sulfotransferase; 1.
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MEDLINE=95209704; PubMed=7695643;
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NEDLINE=22388257; PubMed=12477932;

A Straubberg R.L. Peingold E.A. Grouse L.H., Derge J.G.,

A Altschul S.P., Zeeberg B.B., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Butcow K.H., Scheffer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Butcow K.H., Schefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Butcow K.H., Schefer C.F., Bhat N.K.,

B Altschul S.P., Joeden H., Moore T., Max S.I., Wang J., Heiseh F.,

A Stapleton M., Soares M.B., Boardo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

B Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Andriguez S., Sunchex M., Madan A., Rodrigues S., Sanchèz A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnicz J., Marra M.A.,

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"A single amino acid, Glu146, governs the substrate specificity of human dopamine sulfotransferase, SULTIA3.";
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CHARACTERIZATION.

BEDLINES-447998H.; PubMed=8093002;

Weronese M.E.; Burgess W., Zhu X., McManus M.E.;

"Functional characterization of two human sulphotransferase CDNAs that encode monnoamine- and phenol-sulphating forms of phenol sulphotransferase: substrate kinetics, thermal-stability and inhibitor-sensitivity studies.";
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Bernier F., Soucy P., Luu-The V.;
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promoters: Structure and expression of the gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dooley T.P., Huang Z.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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"Primary structures and properties o sulfotransferases in human liver."; Pharmacogenetics 5:8135-8140(1995).
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MEDLINE=94306556; PubMed=8033246;
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Raftogianis R.B., Her
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                                                                                                                                                                                                                                                                                                                                                                                         phenolic drugs and neurotransmitters. Is also responsible for the sulfation and activation of minoxidil. Mediates the metabolic activation of carcinogenic N-hydroxyarylamines to DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                       products and could so participate as modulating factor of cancer
                                                                                                                                                                                                                "Phenol sulfotransferase pharmacogenetics in humans: association of common SULTIA1 alleles with TS PST phenotype."; Biochem. Biophys. Res. Commun. 239:298-304(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                           Pharmacogenetics 10:163-169(2000).
-!- FUNCTION: Catalyzes the sulfate conjugation of catecholamines,
                                                                                                                                                                                                                                                                                             MEDLINE=20222641; PubMed=10762004;
Engelke C.E., Meinl W., Boeing H., Glatt H.;
"Association between functional genetic polymorphisms of human
                                                           Falany C.N., Zhuang W., Falany J.L.; "Characterization of expressed human phenol-sulfating phenol sulfotransferase: effect of mutating cys70 on activity and
                                                                                                                                                                    MEDLINE=98005125; PubMed=9345314;
Raftogianis R.B., Wood T.C., Otterness D.M., Van Loon J.A.,
Weinshilboum R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the sulfotransferase family.
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O; GO:0009308; P:amine metabolism; TAS.
nterPro; IPR000863; Sulfotransferase.
                                                                                                                                                       VARIANTS GLN-37; HIS-213 AND VAL-223.
                                                                                                                         Chem. Biol. Interact. 92:57-66(1994)
                           MUTAGENESIS OF CYS-70.
MEDLINE=94306582; PubMed=8033270;
Biochem. J. 302:497-502(1994).
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HSSP; P50224; ICJM.
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37; DB 1; Length 295; No. 34;

Score Pred. 1

56.9%;

Query Match Best Local Similarity

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Yamazoe Y., Ozawa S., Nagata K., Gong D.-W., Kato R.; "Characterization and expression of hepatic sulforransferase involved in the metabolism of N-substituted aryl compounds."; Environ. Health Perspect. 102:99-103(1994).
                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96065417; PubMed=7581483;
Ozawa S., Nagata K., Shimada M., Ueda M., Tsuzuki T., Yamazoe Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structures and properties of two related forms of aryl
                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 44), Last annotation update)
Phenol-sulfating phenol sulfotransferase 2 (EC 2.8.2.1) (P-PST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20222641; PubMed=10762004;
Engelke C.E., Meinl W., Boeing H., Glatt H.;
"Association between functional genetic polymorphisms of human
sulfotransferases 1A1 and 1A2.";
Pharmacogenetics 10:163-169(2000).
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Yamazoe Y., Nagata K., Ozawa S., Kato R.;
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"Gem. Biol. Interact. 92:107-117(1994).
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Her C., Raftogianis R., Weinshilboum R.M.;
"Human phenol sulfotransferase STP2 gene: molecular cloning, structural characterization, and chromosomal localization.";
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Dooley T.P., Huang Z.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  295 AA.
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Pharmacogenetics 5:S135-S140(1995).
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WDSSGTHPV
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                                                                                                                                                                                                                                    SULTIA2 OR STP2
                                                                                                                                P50226; P78393;
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
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Catecholamine-sulfating phenol sulfotransferase) (HAST3)
                                SULTIA3 OR STM
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Monoamine-sulfating phenol sulfortansferase (EC 2.8.2.1)
(Sulfotransferase, monoamine-preferring) (M-PST) (Thermolabile phenol sulfotransferase) (TL-PST) (Placental estrogen sulfotransferase)
FUNCTION: Catalyzes the sulfate conjugation of catecholamines, phenolic drugs and neurotransmitters. Is also responsible for the sulfation and activation of minoxidil. Mediates the metabolic activation of carcinogenic N-hydroxyarylamines to DNA binding products and could so participate as modulating factor of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol
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                                                                                                                                                                                        adenosine 3',5'-bisphosphate + an aryl sulfate. SUBUNIT: Homodimer (By similarity). SUBCELLULAR LOCATION: Cytoplasmic.
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Pfam; PF00685; Sulfotransfer; 1.
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MEDLINE=95100963; PubMed=7802665; Dooley T.P., Probst P., Murce P.B., Mole S.E., Liu Z., Doggett N.A.; Dooley T.P., Probst P., Murce P.B., Mole S.E., Liu Z., Doggett N.A.; "Genomic organization and DNA sequence of the human catecholamine-sulfating phenol sulfotranse fense (STM) "; Biochem. Biophys. Res. Commun. 205:1325-1332(1994).
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Jones A.L., Hagen M., Coughtrie M.W.H., Roberts R.C., Glatt H.,
"Human platelet phenolaulforransferases: cDNA cloning, stable
expression in V79 cells and identification of a novel allelic variant
of the phenol-sulfating form.",
Biochem. Biophys. Res. Commun. 208:855-862(1995).
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                                                                                                                                                                                                                                                                              MEDLINE=93371, PubMed=8363592; Zhu X., Veronese M.E., Bernard C.C., Sansom L.N., McManus M.E.; Zhu X., Veronese M.E., Bernard C.C., Sansom L.N., McManus M.E.; "Identification of two human brain aryl sulfotransferase cDNAs."; Biochem. Biophys. Res. Commun. 195:120-127(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bernier F., Lopez-Solache I., Labrie F., Luu-The V.; "Cloning and expression of cDNA encoding human placental estrogen
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"Human thermolabile phenol sulfotransferase gene (STM): molecular cloning and structural characterization.";
Biochem. Biophya. Res. Commun. 208:786-795(1995).
                                           Euteleostomi;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelé
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDLINE=95050600; PubMed=7961757;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulfotransferase."
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Pfam; PF00685; Sulfotransfer; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20013065; PubMed=10543947; Bidwell L.M., McManus M.E., Gaedigk A., Kakuta Y., Negishi M., Bidwell L.M., Martin J.L.; Pedersen L., Martin J.L.; Crystal structure of human catecholamine sulfotransferase."; J. Mol. Biol. 293:521-330 (1999).

-I- FUNCTION: Catalyzes the sulfate conjugation of phenolic monoamines (neurotransmitters such as dopamine, norepinephrine and serotonin)
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W. Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
TISSUB SPECIFICITY: Liver, colon, kidney, lung, brain, spleen, small intestine, placenta and Leukocyte.
PIM: The N-terminus is blocked.
SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94379981; PubMed=8093002; Veronese M.E., Burgess W., Zhu X., McManus M.E., Veronese M.E., Burgess W., Zhu X., McManus M.E., that oncomen characterization of two human sulphotransferase cDNAs that encode monomaine- and phenol-sulphating forms of phenol sulphotransferase: substrate kinetics, thermal-stability and inhibitor-sensitivity studies."; Biochem. J. 302:497-502(1994).
                                                                                                                                                                                                                                                                 Aksoy I.A., Callen D.F., Apostolou S., Her C., Weinshilboum R.M., "Therwolabile phenol sulfotransferase gene (STM): localization to human chromosome 16p11.2.", Genomics 23:275-277(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and phenolic and cathecol drugs.

ANALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.

SUBUNIT: Homodimer.
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004062; P:aryl sulfotransferase activity; TAS.
InterPro; IPR000863; Sulfotransferase.
                                                                                                                                                                    human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
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U37686; AAA86536.1; -.
                                                                                                                                                                                                                                     TISSUE=Lymphocytes;
MEDLINE=95130098; Pubmed=7829089;
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PDB; 1CJM; 10-NOV-99.
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Ogura K., Satsukawa M., Okuda H., Watabe T.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the sulfate conjugation of catecholamines and phenolic drugs and neurotransmitters (By similarity).
-!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Sukaryota: Metacag, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phenol-sulfating phenol sulfotransferase (EC 2.8.2.1) (P-PST).
                            PAPS BINDING SITE (POTENTIAL).
ProDom, PD001218; Sulfotransferase; 1.
Catecholamine metabolism; Steroid metabolism; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                          Length 295;
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Pred. No.
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Best Local Similarity
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                 3D-structure.
BINDING 2:
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15-MAR-2004
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MEDLINE=99253945; PubMed=10318803;
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EXTL2 OR EXTR2.
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exostosin-like 2 (EC 2.4.1.223) (Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Alpha-1,4-N-acetyllhexosaminyltransferase EXTL2) (Alpha-GalNAcT EXTL2) (EXT-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Boulle K., Van Roy N., Van Agtmael T., Bossuyt P., Willems P.J., "Identification and characterization of a novel member of the EXT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hori T.-A.;
"Structure, chromosomal location, and expression profile of EXTR1 and
"Structure, new members of the multiple exostoses gene family.";
Blochem. Biophys. Res. Commun. 243:61-66(1998).
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98111853; PubMed=9450183;
Wuyts W., Van Hul W., Hendrickx J., Speleman F., Wauters J.,
De Boulle K., Van Roy N., Van Agtmael T., Bossuyt P., Willem
                                                                                                                                                                  EMBL; D85514; DALAL-

PIR; G02924; G02924.

HSSP; P50224; LCJM.

InterPro; IPR000863; Sulfotransferase.

Pfam; PF00685; Sulfotransfer; 1.

ProDom; PD001218; Sulfotransferase.

Catecholamine metabolism; Steroid metabolism; Transferase.

Catecholamine metabolism; Steroid metabolism; Transferase.

259 265 PAPS BINDING SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    56.9%; Score 37; DB 1; Length 295; 66.7%; Pred. No. 34; ive 1; Mismatches 2; Indels
                            SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97:668-673(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 AA
SUBUNIT: Homodimer (By similarity)
             SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family, EXTL2.";
Eur. J. Hum. Genet. 5:382-389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98139867; PubMed=9473480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND SEQUENCE OF 54-83.
                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         180 WELSHTHPV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                               3 WDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of heparan sulfate.
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTL2 OR EXTR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein 2
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gguege;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exostosin-like 2 (EC 2.4.1.223) (Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Alpha-1.4-N-acetylglucosaminyltransferase EXTL2) (Alpha-GalNAcT EXTL2) (EXT-related
Kitagawa H., Shimakawa H., Sugahara K.;
"The tumor suppressor EXT-like gene EXTL2 encodes an alphal,
4-N-acetylhaxosaminyltransferase that transfers N-acetylgalactosamine
and N-acetylglucosamine to the common glycosaminoglycan-protein
linkage region. The key enzyme for the chain initiation of heparan
sulfate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Signal-anchor; Glycoprotein.

1 22 CYTOPLASMIC (POTENTIAL).

TDANAIN 23 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         -beta-D-galactosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 274:13933-13937(1999).
-!- FUNCTION: Glycosyltransferase required for the biosynthesis of heparan-sulfate and responsible for the alternating addition of beta-1-4-linked glucuronic acid (GLAA) and alpha-1-4-linked N-acetylglucosamine (GlcNAC) units to nascent heparan sulfate
                                                                                                                                                                                                                                                                                                                                                    glucuronosy1-(1->3) -beta-D-galactosy1-(1->3) -beta-D-galactosy1-
(1->4) -beta-D-xylosy1-proteoglycan = UDP + alpha-N-acety1-D-
glucosaminy1-(1->4) -beta-D-glucuronosy1-(1->3) -beta-D-galactosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolytic processing. SIMILARITY: Belongs to the glycosyltransferase family 47.
                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 330;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 602411; -.
Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 CLEAVAGE.
74 N-LINKED (GLCNAC. ..).
37465 MW; 6976BE7EC6F588C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUMENAL (POTENTIAL)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF000416; AAC02898.1; -. EMBL; AB009284; BAA24081.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:3516; EXTL2.
MIM; 602411; -.
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54
74
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111 WNSLGPHPI 119
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(1->3)-beta-D-galactosyl-(1->4)-beta-D-xylosyl-proteoglycan.

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                                                                                                                                                                                                                         Ackaraki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido II., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Suzuki H., Yamanaka I., Kiyosawa H., RA Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Badarelli R., Brada D., Brusic V., Chothia C., Corbani L.B., Cousins S., Blake J.A., Bradat D., Brusic V., Chothia C., Corbani L.B., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., RA Gasterland T., Gariboldi M., Gastic C., Godzik A., Gough J., RA Kanaji H., Kawaji H., Kawasi Y., Kedzierski R.M., King B.L., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ravasi T., Numata K., Oktdo T., Pavan W.J., Pertea G., Pesole G., RA Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M., Kang L., Wahnshaw Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Wakining L.G., Wynshaw Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Wakining L.G., Wanshaw Boris A., Yanagisawa T., Ronno H., Nakamuz M., Yang I., Yang I., Rawai J., Aizawa K., Arakawa T., Fukuda S., Raunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Rabalizume W., Imotani K., Ishikaka A., Harahalizaki Y., Banaki D., Shibata K., Sahani M., Waterston R., Lander E.S., Rogers J., Shington D., Shibata K., Sasaki D., Shibata K., Sasaki D., Shibata K., Sanadi O., Shinagawa A., Haraha H., Yoshino M., Waterston R., Lander E.S., Rogers J., Shination Of T., Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/G57 TISSUE=Mammary gland;

WEDLINE=22388257; PubMed=12477932;

RETAUSDECT R. L., Feingold E. A., Grouse L.H., Derge J.G.,

RETAUSDECT R. L., Feingold E. A., Grouse L.H., Derge J.G.,

RIAUSDER R. L., Feingold E. A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Batchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RABA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.A., McEwan P.J., McKernan K.J., Mamlek J.A., Gunaratne P.H.,

RICHAGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RIALSON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RAPAN J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RAPAN S.Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RAPAN S. R. L. L. L. Schein J.E., Jones S.J.M., Marra M.A.;

Reneration and initial analysis of more than 15,000 full-length
                                                             MEDLINE=20422478; PubMed=10965119; Muyrs W., yan Hul W.; Characterization and genomic localization of the mouse Extl2 gene."; Cytogenet. Cell Genet. 89:185-188(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Glycosyltransferase required for the biosynthesis of heparan-sulfate and responsible for the alternating addition of beta-1-4-linked glucuronic acid (GlcA) and alpha-1-4-linked N-acetylglucosamine (GlcNAc) units to nascent heparan sulfate
                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Embryonic head;
MEDLINE=22354683; PubMed=12466851;
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-GLAGALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-galactosyl-glucuronosyl-(1-31)-beta-D-galactosyl-(1->3)-beta-D-galactosyl-(1->4)-beta-D-xylosyl-proteoglycan = UDP + alpha-N-acetyl-D-glucosaminyl-(1->4)-beta-D-glucuronosyl-(1->3)-beta-D-galactosyl-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keen N.T., Tamaki S., "Structure of two percate lyase genes from Erwinia chrysanthemi EC16 and their high-level expression in Escherichia coli.";
J. Bacteriol. 168:595-606(1986).
-!- FUNCTION: Involved in maceration and soft-rotting of plant tissue.
-!- CATALYTIC ACTIVITY: Eliminative cleavage of (1->4)-alpha-D-galacturonan to give oligosaccharides with 4-deoxy-alpha-D-galact-
                                                                                                                                                                                                                                                                                                                                                                                       .-anchor, Glycoprotein.
21 CYTOPLASMIC (POTENTIAL).
22 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-enuronosyl groups at their non-reducing ends.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the polysaccharide lyase family 1. PLADES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X -> D (IN REF. 2). (POTENTIAL). SIFRAPERATOR
PATHWAY: Heparin/heparan sulfate synthesis.
SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                              SIMILARITY: Belongs to the glycosyltransferase family 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%; Score 37; DB 1; Length 330;
                                                                                                                                                                                                                                                                                                 EMBL, AKO19370; BAB31683.2; -.
EMBL, BC031438; AA431438.1; -.
MGD; MG1.1889574; EX.12.
Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37390 MW; 51F88BE5D3E5EADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUMENAL (POTENTIAL).
N-LINKED (GLCNAC. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
26-ccate lyase B precursor (EC 4.2.2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87056939; PubMed=3536853;
                                                                                                                                                                                                                                                                               EMBL; AF200973; AAG17542.1; -.
                                          similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
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                                                                                                                                                                                                                                                                                                                                                                                              Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA;
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                                        (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
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                                                                                                                                                                                                                                                                                                                                                                                              Fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=EC16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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PELB_ERWCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93276270; PubMed=8502994;
Yoder M.D., Keen N.T., Jurnak F.;
"New domain motif: the structure of pectate lyase C, a secreted plant
virulence factor.";
Science 260:1503-1507(1993).
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                  ;
0
                                                                                                                                56.9%; Score 37; DB 1; Length 375; 50.0%; Pred. No. 45; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88298652; PubMed=3042750; Tamaki S.J., Gold S., Robeson M., Manulis S., Keen N.T.; Structure and organization of the pel genes from Erwinia chrysanthemi EC156."; J. Bacteriol. 170:3468-3478(1988).
                                                                      1 22 PECTATE LYASE B.
23 375 PECTATE LYASE B.
93 176 BY SIMILARITY.
351 374 BY SIMILARITY.
240 240 POTENTIAL.
375 AA, 40234 MW, F3FE75D507B8F883 CRC64;
                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-YUR-1989 (Rel. 43, Last annotation update)
Pectate lyase C precursor (EC 4.2.2.2).
                                                                                                                                                                                                                               PRT; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
      EMBL; M14510; AAA24847.1; -.
PIR; B25158; WZWCPB.
HSSP; P1073; 1AIR.
InterPro; IPR002022; Amb_allergen.
Pfam; PP00544; pec_lyase; 1.
SWART; SW00656; Amb_all; 1.
Lyase; Multigene family; Signal.
                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                             329 DTWTSTGTYP 338
                                                                                                                                                                   1 NSWDSSGTHP 10
                                                                                                                                                                                                                                                                                            Erwinia chrysanthemi.
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subfamily.
                                                                                                                                                                                                                                                                                                                                               STRAIN=EC16;
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SEQUENCE
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P11073;
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Gaps

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Indels

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Pred. No. 83;

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55.6%;
                       5; Conservative
Best Local Similarity
Matches 5, Conserv
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                                                                                                                                                                                RESULT 21
GPRS_DROME
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01-WAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor [Contains: Knob protein GP76; Spike protein
PISE].
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M26527; -; NOT_ANNOTATED_CDS.
PIR; B32594; VCMVHL.
HSSP; P03385; 1MOF.
Interpro; IPR002050; Env_polyprotein.
Interpro; IPR00998; F MuLV bind.
Pfam; PF00429; ENV_polyprotein; 1.
Coat_protein; Glycoprotein; Polyprotein; Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                          DB 1; Length 375;
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                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMULV murine leukemia virus (Mus hortulanus virus).
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
VGII_TaxID=11799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDC77956E4B213D1 CRC64;
                                                                                                                                                                                                                                                  39943 MW; F76DD8195A35B886 CRC64;
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SPIKE PROTEIN PISE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 AA.
                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                             Score 37;
Pred. No.
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Voytek P., Kozak C.A.;
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                                                                                                                                                                                                                                                                                        56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecotropic virus, HOMULV.";
Virology 173:58-67(1989).
                                                                                                                                                                                                                                                                                          Query Match 56.9
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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329 DSWTSTGTFP 338
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42
197
290
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355
358
359
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371
375 AA;
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363
431
666 AA;
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ENV_MLVHO
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DEFENDENCE

RESULT 21

GPRS DROWE

TOTAL DOOR 1201 (Rel. 42, Least sequence update)

DIT OCTSO (Rel. 42, Least sequence update)

DIT OCTSO (Rel. 42, Least sequence update)

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Rel. 42, Rel. 43, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44, Rel. 44,
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AGL9 ARADE
Q386<u>9</u>4;
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Teksia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Genlles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., Mclenn J., Moule S., Murphy L., Oliver S., Osborne J., Quares S., Squares R., Selton S., Squares S., Squares R., Salston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 1302; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                  91 691 E -> D (IN REF. 3).

44 744 74 Q -> H (IN REF. 3).

88 788 D -> V (IN REF. 3).

98 808 Q -> L (IN REF. 3).

94 894 D -> V (IN REF. 3).

67 1167 R -> G (IN REF. 3).

60 1 1301 S -> N (IN REF. 3).

62 AA; 144768 MW; DA3603B725140215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                    Da Lage J.-L.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv3404C/MT3512/MD3438c precursor.
RV3404C OR MT3512 OR MTCYT9.24 OR MB3438C.
Mycobacterium tuberculosis, and
                      Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                           -!- SIMILARITY: Contains 1 BTB/POZ domain.
                                                                                                                                                                                                                                  EMBL; AE003806; AAF57972.2; -. EMBL; AF022713; AAD09150.2; -.
                                                            SEQUENCE OF 526-1302 FROM N.A.
                                                                                                                                                                                                                                                      FIYBASE; FBGN0024232; gprs.
InterPro; IPR000210; BTB_POZ.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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1121 DSYDSSGSYP 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                       STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                         1302
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Q50721;
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MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SPECIES—N.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
SPECIES—N.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEDCIES DOVIS, STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eighmeier K., Camus J.-C., Medina N., Mansoor H.,
Ratiner T., Eighmeier K., Camus J.-C., Monsempe C., Simon S.,
Pryor M., Duthoy S., Ggrodin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 10.7877-7882(2003).
-i- SIMILARITY: SOME, TO METHIONYL-TRNA FORMYLTRANSFERASE
(EC 2.1.2.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Apparagales, Orchidaceae, Epidendroideae, higher Epidendroideae, Vandeae, Arachnis x Vanda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 234 HYPOTHETICAL PROTEIN
RV3404C/MT3512/MB3438C.
234 AA; 26515 MW; 63FF857BB6FFAA8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Agamous-like MADS box protein AGL9 homolog (OM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT3512; -.
Tuberculist; RV3404c; -.
InterPro; IPR002376; formyl transf.
Pfam; PF00551; formyl_transf; 1.
Hypothetical protein; Signal; Complete proteome. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB
Pred. No. 40;
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SRQUENCE FROM N.A.
MEDLINE=94072738; PubMed=8251643;
                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z77165; CAB01019.1; -.
EMBL; AE007157; AAK47850.1; -.
EMBL; BX248346; CAD95625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%;
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hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                               laboratory strains."
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Boronenkov I.V.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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PIS3_HUMAN
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                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Phosphatidylinositol-4-phosphate 5-kinase type II alpha (EC 2.7.1.149)
(PIPSKII-alpha) (1-phosphatidylinositol-4-phosphate 5-kinase)
(PtdIns(4)P-5-kinase B isoform) (Diphosphoinositide kinase).
                                               Gaps
Lu Z.X., Wu M., Loh C.S., Yeong C.Y., Goh C.J.; "Nucleotide sequence of a flower-specific MADS box cDNA clone from orchid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boronenkov I.V., Anderson R.A.; "The sequence of phosphatidylinositol-4-phosphate 5-kinase defines novel family of lipid kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%; Score 36; DB 1; Length 250; 66.7%; Pred. No. 43; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS BOX 2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    250 AA; 28770 MW; 01EF94DADC499C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                               MADS-box.
K-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=95155363; PubMed=7852364;
                                         Plant Mol. Biol. 23:901-904(1993)
                                                                                                                                                                                                                                                                                 TRANSFAC, T03114; -.
InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 298-310 AND 381-382.
                                                                                                                                                                                                                                                                                                                 Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                  EMBL; X69107; CAA48859.1; -. PIR; S40405; S40405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          168
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P484<u>2</u>6;
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TISSUE-Hippocampus,

RELINE-2288257; PubMed=12477932;

RELINE-2288257; PubMed=12477932;

RELINE-2288257; PubMed=12477932;

RELINE-2288257; PubMed=12477932;

RELINE-2288257; PubMed=12477932;

RELINERATION R. Colling F.S., Magner L., Sheamen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roberton M., Mazon P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Roberton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBÜNIT: Homodimer (By similarity).
-!- TISSUB SPECIFICITY: EXPRESSED UBIQUITOUSLY, WITH HIGH LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Phosphatidylinositol-4-phosphate 5-kinase type III (EC 2.7.1.149) (phosphatidylinositol-4-phosphate kinase) (PIPSKIII) (PtdIns(4)P-5-kinase C isoform) (Diphospholnositide kinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 36; DB 1; Length 406; 75.0%; Pred. No. 72; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE BRAIN.
SIMILARITY: BELONGS TO THE PTDINS(4)P-5-KINASE FAMILY.
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Pfam; PF01504; PIP5K; 1.
Transferase; Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew, HGNC:8997; PIP5K2A.
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P53807;
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PIPSK3

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PIR; S57217; S57217.

GO; GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; NAS. GO; GO:0016310; P:phosphorylation; NAS.
InterPro; IPR002498; PIPSK.
InterPro; IPR002498; PIPSK.
SMART; SM00330; PIPSK; 1.
Transferase; Kinase.
SEQUENCE 406 AA; 46078 MW; E8DDPAF61A17534B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Divecta N., Truong O., Hsuan J.J., Hinchliffe K.A., Irvine R.F.;

"The cloning and sequence of the C isoform of Pedins4P 5-kinase.";

Biochem. J. 309:715-719 (1995).

-! FUNCTION: Catalyzes the phosphorylation of phosphatidylinositol-4-
phosphate on the fifth hydroxyl of the myo-inositol ring, to form
phosphate on the fifth hydroxyl of the myo-inositol ring, to form
phosphate a ADP + 1-phosphatidyl-1D-myo-inositol 5-
phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 5-
phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 5-
phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 5-
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                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOSI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE PTDINS(4)P-5-KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Leukocyte;
MEDLINE=95366942; PubMed=7639683;
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Search completed: September 27, 2004, 12:13:55 Job time : 28 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

666 64 63 63 63 63

Result Š. 

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SEQUENCE FROM N.A.
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Chayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogano S.;
"NEDO human CDNA sequencing project.";
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO24781; BAB15001.1; -
InterPro; IPR004443; YjeF_Nterm.
Pfam, PR0383; YjeF_N; 1.
Pfam, PR0383; YjeF_N; 1.
SEQUENCE 508 AA; 56105 MW; AAFABFD0222E23DB CRC64;
                   Homo sapiens [Human].
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR.2001 (TrEMBLrel. 16, Created)
1-MAR.2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
101-Orderical protein FLJ21128.
Hypothetical protein FLJ21128.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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7, Conservative
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Hypothetical protein.
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Q91mh7 arabidopsis
Q82jp7 streptomyce
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Q98q59 mycoplasma
Q9nw05 homo sapien
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Q86484
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Q8N355;
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Q96F86 ID Q96F86 AC Q96F86;

Last sequence update) Last annotation update)

Created)

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RESULT 1 Q8N355 ID Q8N3 AC Q8N3 DT 01-O DT 01-O

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YopE chaperone SycE.
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nes 7; Conserv
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                                                                                                                                           Plasmid pYVe227
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Matches
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                    SEQUENCE FROM N.A. Gu X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                        \tilde{Y}_0 J., Han L.H., I_1 "Novel human cDNA clones with function of inhibiting cancer cell
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Pred. No. 51;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031725; AAH31725.1; -.
EMBL; BC033484; AAH33484.1; -.
                                                                                                                                                                                                                                                          Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  al protein.
508 AA; 56077 MW; 95346F484FCFC3EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein.
508 AA; 55957 MW; DD1F449BEF1341C8 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to hypothetical protein FLJ21128.
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                                                                                                                                                                                                                                                                                                         InterPro; IPR004443; YjeF_Nterm. Pfam; PF03853; YjeF_N; 1. Hypothetical protein.
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Pfam, PP03853; YjeF_N; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                    EMBL; BC011534; AAH11534.1; -...
EMBL; BC021271; AAH21271.1; -..
EMBL; AF193058; AAG22486.1; -..
                                                                                                                                                                                                                                                                                                                                                                     66.2%;
70.0%;
                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Placenta, and Eye;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.0
7, Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         160 NSWSSSSRHP 169
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                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                      NCBI_TaxID=9606;
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MEDLINE=93268087; PubMed=8497188; Wattiau P., Cornelis G.R.; "SycE, a chaperone-like protein of Yersinia enterocolitica involved in Ohe secretion of YopB.";
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MEDLINE=21365706; PubWed=11472064;
Gasper J.S., Shina T., Inoko H., Edwards S.V.;
"Songbird genomics: analysis of 45 kb upstream of a polymorphic Mhc class II gene in red winged blackbirds (Agelaius phoeniceus).";
Genomics 75:26-34(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agelaius phoeniceus (Red-winged blackbird).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Passeriformes, Icteridae, Agelaius.
                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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EMBL, AF32873, 374, 2001.

HSSP, P24941; IBUH.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:000648; F:protein amino acid phosphorylation; IEA.

InterPro; IPR00219; Prot kinase.

InterPro; IPR001245; Tyr pkinase.

Pfam; PF00069; pkinase: 1
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 42; DB 2; 70.0%; Pred. No. 17; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 8:123-131(1993).

EMBL; AF102990; AAD16849.1; --
GO; QO:0004681; C:extrachromosomal DNA; IEA.
InterPro; IPR005416; SycE chap.
PRINTS; PR01596; SYCECHAPRONE.
   130 AA
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SMART; SM00220; S_TKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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PRELIMINARY;
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                                                                                                                                                                                                           Yersinia enterocolitica.
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Science 282:2012-2018(1998).
EMBL; Z69386; CAA93432.1; -.
PIR; T27931; T27931.
                                                                                                                           Query Match
Best Local Similarity 70...
7; Conservative
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Matches 7; Conservative
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investigating biology.";
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Q94H87;
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MEDLINE=21359325; PubMed=11466286;

Meelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL, AB0077778; AAK80753.1; -.
                                                                                                           Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                              64.6%; Score 42; DB 13; Length 66
66.7%; Pred. No. 1e+02;
ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McMurray A.A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
  ATP-binding; Kinase; Transferase.
SEQUENCE 669 AA; 73710 MW; 5987154DCB1C441A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016787; F:hydrolase activity; IEA.
Hydrolase; Complete proteome.
SEQUENCE 98 AA; 11692 MW; 929C71F938AC930A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                        98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               Predicted HD superfamily hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 18, (TrEMBLrel. 18, (TrEMBLrel. 24,
                                          Query Match
Best Local Similarity 66.7°,
Best Local Similarity 66.7°,
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Best Local Similarity 77.0
77.0
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ZK596.3.
Caenorhabditis elegans.
                                                                                                                                                                                              170 WDEDGAHPV 178
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                                                                                                                                                        11
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                                                                                                                                                        3 WDSSGTHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1488;
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01-OCT-2001 (
01-JUN-2003 (
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Q23547;
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AC 097FFD
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanhken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21267165; PubMed=11353084; Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.; Rome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                         Length 339;
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                                                                                                                                                 Indels
WORTHPEP; ZK596.3; CE06633.
SEQUENCE 339 AA; 39145 MW; 21CA0504F4CE1844 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          889D356B34946FB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative disease resistance protein.
                                                                                      63.1%; Score 41; DB 5; 70.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Pred. No. 99; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1461 AA
                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153 (2001).

Bubi; ALA45563; CAC13423.1; -.

PIR, B90543; B90543.

Mypulist; MYPU. 2500; -.

Hypothetical protein; Complete proteome.

SEQUENCE 456 AA; 53149 MW; 889D356B3
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein MYPU_2500
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70.0%;
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RESULT 12
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE TISSUE-Cerebellum;

MARAWA T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Arawa K., Izawa M., Nishik Y., Konno H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishik K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Camanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Robell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchioni L., Mashima J., Mazarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Halla M., Kalla M., Kalla M., Kalla M., Kalla M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M., Malana M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
             "Oryza sativa chromosome 3 BAC OSJNBa0090P23 genomic sequence.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084380; AAK52137.1;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 1461;
                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 10; Length 13. Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                   9A89A942B561D9F2 CRC64;
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SEQUENCE: 111 AA; 12221 MW; 1BC7884BF056C43B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.JUN-2001 (TrEMBLrel. 17, Created)
L.JUN-2001 (TrEMBLrel. 17, Last sequence update)
L.JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 111 AA
                                                                                                                                                                                                             INTEFFECT, ARMYCELLE, PERM, PFO0560; LRR; 14.
Pfam; PF01535; PPR; 5.
PRINTS; PR00019; LEURICHRPT.
TIGRFAMS; TIGR00756; PPR; 5.
GPOTENCE 1461 AA; 158782 MW;
                                                                                                                        InterPro; IPR001611; LRR.
InterPro; IPR007090; PRR. plant.
InterPro; IPR002885; PRR.
InterPro; IPR008941; TPR-like.
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Best Local Similarity 70.0
7; Conservative
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nes 8; Conservative
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White O., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 NSWPESGTSP
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Matches
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                                                                                                                                                                                                                        CG12414 protein.
NACR-ALPHA-80B OR NACRALPHA-80B OR CG12414 OR CG17552.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
261 AA.
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MEDLINE=20196006; PubMed=10731132;
PRELIMINARY;
                                                               TrEMBLrel.
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                                            Q9W5V6; Q9W5V5
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9VSW9Q
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7; Conservative
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HSSP; P11073; 1AIR
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Flybace; FB01031212; nAcR-alpha-80B.
GO; GO:0016020; C:membrane; IEA.
GO; GO:00163210; F:extracellular ligand-gated ion channel acti. ..; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. ..; IEA.
GO; GO:000511; F:neurotransmitter receptor activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
Pfam; PF02931; Neur chan memb.
Pfam; PF02931; Neur chan memb; 1.
Ffam; PF02932; Neur chan memb; 1.
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MEDLLINE=93003864; PubMed=1406275;
Hugouvieux-Cotte-Pattat N., Robert-Baudouy J.;
"Analysis of the regulation of the pelBC genes in Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. Microbiol. 6:2363-2376 (1992).
-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-GLUC-4-ENURONOSYL GROUPS AT
THEIR NOW-REDUCING ENDS.
EMBL; AJ132325; CAA10642.1; -.
EMBL; K67475; CAA47822.1; -.
PIR; S25263; S25263.
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                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hisadecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Clamp J.L., Bergman C., Berman B., Carlson J W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbarth W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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01-ATG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pectate lyase precursor (EC 4.2.2.2).
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Bust Local Similarity 60.0%,
Annual 6, Conservative
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STRAININCC 2705;

MEDLINE=2224977; PubMed=12381787;

MEDLINE=2224977; PubMed=12381787;

MEDLINE=2224977; PubMed=12381787;

MEDLINE=2224977; PubMed=12381787;

MARCHART M., Karmirantzou M., Sola B., Vilanova D., Berger B.,

Marchart M., Arigoni F.;

The genome sequence of Bifidobacterium longum reflects its adaptation

to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL., AE014635; AANA4022.1; -..

BRAGA M., ARO02241; -..

CO. GO:0005975; P:carbohydrate metabolism; IEA.

BRAGO GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR00111; Glyco hydro_GHD.

PRODM: PRO09740; GLHYDRLASE27.

PRODM: PRO095977; Glyco_hydro_GHD; 1.
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NCBI_TaxID=216816;
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                                                                                                                                                                                                                                                            Length 374;
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60.0%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                       SIGNAL 1 22 POTENTIAL.
CHAIN 23 374 PECTATE LYASE.
SEQUENCE 374 AA; 39891 MW; 0086E71012E13FD4 CRC64;
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01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-UND-2003 (TYEMBLrel. 24, Last annotation update)
SPRB.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible alpha-galactosidase.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0030570; F:pectate lyase activity; IEA.
GO; GO:0030570; F:pectate lyase activity; IEA.
Pfam; PF00544; pec lyase; 1.
SMART; SM00656; Amb_all; 1.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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045464
1D 04546.
AC 04546.
DT 01-NO
DT 01-NU
DT 01-10
DT 01-10
DE SPRB.
OS Baccil
OX NCBI.
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Taipalensuu J., Eriksson S.J., Rask L.;
"The myrosinase binding protein from Brassica napus seeds possesses
lectin activity and has a highly similar vegetatively expressed wound
inducible counterpart.";
Eur. J. Biochem. 250:680-688(1997).
EMBL; Y09417; CAA70587.1; -
PIR; T08102; T08102.
                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UNA-2093 (TrEMBLrel. 24, Last annotation update)
Myrosinase binding protein.
Brassica napus (Rape).
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 40; DB 10; Length 988; 66.7%; Pred. No. 3.4e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U41279; AAK31432.1; -.
wormbep; C17C3.1C; CE27072.
Hypothetical protein.
SEQUENCE 60 AA; 7054 MW; CA8069E3967A80F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P18674; 1JOT.
InterPro; IPR001229; Jacalin_lectin.
Pfam; PF01419; Jacalin; 6.
SEQUENCE 988 AA; 104331 MW; 6C1DB595F56F246C CRC64;
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Last annotation update)
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988 AA
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PRT;
                                                                                                                                                                                                                                               TISSUE=Leaf;
MEDLINE=98121188; PubMed=9461290;
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Best Local Similarity 66...
6. Conservative
PRELIMINARY;
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                 NCBI_TaxID=3708;
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                                                                                                      Alkalophilic Bacillus sp. strain LG12 has a series of serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geshi N., Brandt A.;

Two jasmonate inducible proteins from Brassica napus seedlings
Two jasmonate inducible proteins from Brassica napus seedlings
Two jasmonate inducible proteins and jacalin.";

blomologous to myrosinase binding proteins and jacalin.";

EMBL, Y11482; CAA72270.1;

PIR; T08081; T08081.

PIR; T08081; T08081.

InterPro; IPR01129; Jacalin_lectin.

Pfam; PF01419; Jacalin; 6.

SEQUENCE 914 AA; 96911 MW; 9126F5BB2482155F CRC64;
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                                                                         Schmidt B.F., Woodhouse L., Adams R.M., Ward T., Mainzer S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 40; DB 2; Length 824; 53.3%; Pred. No. 2.8e+02; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        OD655CB86AFB5CFF CRC64;
                                                                                                                                                                                                                                         GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006289; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Jasmonate inducible protein.
                                                                                                                            genes.";
Appl. Environ. Microbiol. 61:4490-4493(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB.
EMBL; U39230; AAC43578.1; -.
HSSP; Q45670; 1DBI.
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PROSITE; PRO0137; SUBTILIASE HIS; 1.
PROSITE; PRO0138; SUBTILASE SER; 1.
HYDYCOLASE; Protease; Securine protease,
SEQUENCE 824 AA; 88338 MW; ODESSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
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                                 STRAIN=LG12;
MEDLINE=96086035; PubMed=8534117;
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00082; Peptidase_S8; 1. Pfam; PF00395; SLH; 1.
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273 NSWGSSGDFDPNHPI 287
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Best Local Similarity 53.3%
Best Local 8; Conservative
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Best Local Similarity
               FROM N.A.
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RESULT 16 P93659

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Matches

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Gaps

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"Tropheryma wipple: illustrates the diversity of gene loss patterns in small genome bacterial pathogens.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AEDIGESO; AAO44226.1; -.
COMPLETE proteome.
SEQUENCE 254 AA; 28732 MW; 32C29A6FEBE00FDO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UCT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Raoult D., Audic S., Robert C., Ogata H., Suhre K., Drancourt M.,
Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Tropheryma.
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77.8%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029136; AAH29136.1; -
InterPro; IPR007803; Asp_Arg_Hydrox.
InterPro; IPR05118; Asp_Arg_Hydrox; 1.
Hypotehical protein.
NON_TER
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                        250 AA.
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TISSUE-Colon, and Kidney;
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Matches 7; Conservative
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                                                                       100 SWRSRGFHPV 109
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2 SWDSSGTHPV 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Q40987
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN cDNA 2900006N09 gene.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Tropheryma.
NCBI_TaxID=218496;
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                                            DB 5; Length 60;
                                                                                                                             4; Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034275; AAH34275.1; -.
InterPro; IPR07033; ASP_Arg_Hydrox.
Pfam; PF0511B; Asp_Arg_Hydrox; 1.
SEQUENCE 230 AA; 24622 MW; 30FC26C4B4FF991F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BX251410; CAD66818.1; -.
GO; GO:0005524; F:ATP binding; IEA.
Hypothetical protein; ATP-binding; Complete proteome.
SEQUENCE 231 AA; 26160 WW; FDCA4252708664A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein (Possible ATP-binding).
                                   Score 39; DB E Pred. No. 24;
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                                                 60.0%;
54.5%;
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Best Local Similarity 77.8'
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                                                                                                                                      6; Conservative
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                                            Query Match
Best Local Similarity
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TISSUE=Brain;
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01-OCT-2002
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Q820Z3
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AC 08N4H
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118 SWDFSGTTP 126
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                                                                                                                                                             Q8S860,
Q8S860;
                                                                                                          RESULT 25
085860
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                                                                                                                                                                   Pisum sativum (Garden pea).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
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                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wisconsin Perfection; TISSUB=Root nodules;
STRAIN=Wisconsin Perfection; TISSUB=Root nodules;
MEDLINE=96222420; PubMed=8685275;
Radailsky I.V., Sherrier D.J., Brewin N.J.;
"Identification of where gene, PsNlec1, encoding a lectin-like glycoprotein isolated from the symbiosomes of root nodules.";
Plant Physiol. 111:49-60(1996).
PHR: T06528; T06528.
HSSP: P05046; ISBD.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2e+02;
0; Mismatches 3; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040933, AAH40933.1; -..
InterPro; IRR07803; ASP_Arg_Hydrox.
Pfam; PP05118; ASP_Arg_Hydrox; 1.
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                                                                          Last sequence update)
Last annotation update)
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR001220; Lectin_legA.
InterPro; IPR001220; Lectin_legB.
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                                                                                                                                                                                                                         Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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SEQUENCE FROM N.A.
Spiegel L.A., Nascimento L.U., de la Bastide M., Vil D.M.,
Preston R.R., Huang E.N., See L.H., Shah R.S., O'Shaughnessy A.,
Rodriguez M.A., Shekher M., Kirchoff K.A., Baker J.P., Schutz K.,
Bedhia N.N., McCombie W.R.;
"Genomic Sequence Oryza sativa, Niponbare Strain, Clone
OSJNBA0061KZ1 From Chromosome 10, Complete Sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF04720; DUF506; 1.
TIGRFAMB; TIGRO1615; A_thal_3542; 1.
HYDChhetical protein: A_thay CR63AB612D5151B3 CRC64;
                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Ruchastein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marra M.A.,
Johns S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
L. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; S02013;
PIR; S09713;
PIR; S12441; S12441.
PIR; S12441; S12441.
PIR; S12527; S30527.
HSSP; PO1842; LILL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_W.
PF07654; CI-set; I.
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PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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TISSUBEROR and Placenta;

TISSUBEROR DELO. 1073/pnas.242603899;

TISSUBEROR B.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B.L., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Antachul S.F., Jordan H., Moore T., Max S.L., Wang J., Heiseh F.

A papteron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonchiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley W.C., Make J., M. Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia B.D., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia B.D., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Gu X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Li H.N., Yu Y., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                         ö
                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
5-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ21128 (Hypothetical protein PP844).
Name=FLJ21128; Synonyms=PP844;
                                          66.2%; Score 43; DB 2; Length 234; 77.8%; Pred. No. 32;
                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu J., Han L.H.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
Strauuberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011534; AAH11534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56077 MW; 95346F484FCFC3EA CRC64;
            234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                            508 AA
                                                                       0; Mismatches
                                                                                                                                                                                                          PRT;
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Pfam; PF03853; YjeF N; 1.
Hypothetical protein.
SEQUENCE 508 AA; 56077 NW; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                        Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                 109 WDSSSDHPV 117
                                                                                                      3 WDSSGTHPV 11
Hypothetical protein. SEQUENCE 234 AA; 2
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                           Query Match
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MEDLINE-ZEGH II, and FVB/N; TISSUE-Mammary tumor;

MEDLINE-ZEGH II, and FVB/N; TISSUE-Mammary tumor;

MEDLINE-ZEGH II, and FVB/N; TISSUE-Mammary tumor;

MEDLINE-ZEGH S. PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-ZEGH R. D. Felingold E. A., Grouse L. H., Derge J. G.,

MA Klausner R. D., Collins F. S., Wagner L., Schamfer C. F., Bhat N. K.,

A Altschul S. F., Zeeberg B. Buetow K. H., Schaefer C. F., Bhat N. K.,

A Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,

A Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,

A Brownstein M. J., Usdin T. B., Toshiyuki S., Carninci P., Prange C.,

A Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,

A Richards S. Worley K. C., Hale S., Garcia A. M., Gabbs R. A.,

Milalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,

Milting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,

Milting M., Madan A., Young A. C., Schwutz J., Myers R. M., Butterfield Y. S.,

Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S.,
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Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,

Buzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,

Nakamura Y., Isogai T., Sugano S.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO24781; BAB15001.1;

Interpro; IPR004443; YjeP_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                   Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Length 508;
                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ21128.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) AA517853 protein (CDNA clone MGC:36552).
Name=Clk3; Synonyms=AA517853;
      2.
Score 43; DB 2
Pred. No. 72;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               PRT;
66.2%;
      Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 70.0
nes 7; Conservative
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                                                                                                                               1 NSWDSSGTHP 10
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79 SWDEVGGHPV 88

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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

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01-JUL-1993 (
01-JUL-1993 (
25-OCT-2004 (
                                                                         YERA YERPE
P31491;
                                                           YERA_YERPE
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                                             RESULT 6
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              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression."; J. Bacteriol. 172:1547-1555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-structure; Activator; Plasmid; Transcription regulation; Virulence. SEQUENCE 130 AA; 14676 MW; 491B67B4C293CASA CRC64;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                        DB 2; Length 508; 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 130;
                                                                                                   STRAIN=CZECH II, and FVB/N; TISSUE=Mammary tumor;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                           InterPro; IPRO04443; YjeF_Nterm.
Pfam; PP03853; YjeF_N; 1.
SEQUENCE 508 AA; 55957 MW; DDIF449BEF1341C8 CRC64;
                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 1;
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                        0; Mismatches
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081 / Serotype O:8 / Biotype 1B;
                                                                                                                                                                                                                                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90170873; Pubmed=2307658; Forsberg A., Wolf-Watz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M34278; AAA27673.1; --
PDB; 1N5B; X-ray; A/B/C/D=1-130.
InterPro; IPR010261; Cest.
InterPro; IPR005416; SycE_chap.
                                                                                                                                               EMBL; BC031725; AAH31725.1; -. EMBL; BC033484; AAH33484.1; -. MGD; MGI:1098670; Clk3.
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                                                                                                                                                                                                                                                     66.2%;
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70.0%;
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Best Local Similarity 70.0
المرات
                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=yerA;
Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                  160 NSWSSSSRHP 169
                                                                                                                                                                                                                                                                                                                    1 NSWDSSGTHP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05932; CesT;
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YopE regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=8081 /
                                                                                                                                                                                                                                                                                                                                                                                                                          YERA YEREN
P314<u>9</u>0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pYV
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YERA YEREN
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Gaps

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3; Indels

SWDSSGTHPV 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=91001 / Biovar Mediaevalis; PLASMID=pCD1;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERTINECO-92 Blovar Orientalis; PLASMID=pCD1;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin M., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                        STRAIN=EV 76; PLASMID=pYV019;
MEDLINE=90170873; PubMed=2307658;
Forsberg A., Wolf-Watz H.;
"Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression.";
J. Bacteriol. 172:1547-1555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis KIM5.";
Infect. Immun. 66:4611-4623(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-KIMS / Biowar Mediaevalis; PLASMID-pCD1;
MEDLINE-98422474; PubMed-9748454;
Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
Kobayashi A., Brubaker R.R., Garcia E.;
"Structural organization of virulence-associated plasmids of Yersinia
                                                                                                                                                      Plasmid pCD1, and Plasmid pYV019.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis; PLASMID=pCD1;
MEDLINE=98427122; PubMed=9746557;
Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
Blattner F.R.;
                                                                                                                          Name=yerA; OrderedLocusNames=YPCD1.05c, y5069, y0078, pCD82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                     (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 45, Last annotation update)
130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Positive regulator of yopE.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 180:5192-5202(1998).
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STANDARD;
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                                                                                                      YopE regulator.
                                                                                                                                                Yersinia pestis
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InterPro; IPR005416; SycE_chap.
Pfam; PF05332; CesT; 1.
PRINTS; PR01596; SYCECHAPRONE.
Plasmid.
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llarity 70.0%; Pred. No. 25;
Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14650 MW; 41A12BB29831CA5A CRC64;
                                                                                                                                                                                               PIR; T43606; T43606.
PDB; JUXA; X-ray; A/B=1-130.
PDB; JKGZ; X-ray; A/B=1-130.
InterPro; IPR010361; CesT.
InterPro; IPR05416; SycE_chap.
Pfam; PF05922; CesT; 1.
PRINTS; PR01596; SYCECHAPRONE.
PSINUTS; PR01596; SYCECHAPRONE.
Transcription regulation; Virulence.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=93268087; PubMed=8497188;
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                                                                          AF074612; AAC69819.1; -. AF053946; AAC62588.1; -. AL117189; CAB54882.1; -. AE017043; AAS58593.1; -.
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                                          EMBL; M34279; AAA27671.1; -.
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Matches 7; Conserv
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EMBL, BX936599; CAF2367.1; -. InterPro; IPR001261; SycE. Chap.

Pfam; PP05912; CesT., L. L. Cest.
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Agelaius phoeniceus (Red-winged blackbird).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Icteridae; Agelaius.
NCBI_TaxID=39638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=273123;
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SEQUENCE FROM N.A.
MEDLINE=21365706; PubMed=11472064; DOI=10.1006/geno.2001.6596;
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Pred. No. 25;
                                                       Length 130;
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SEQUENCE 130 AA; 14649 MW; 490B89BA3293CA5A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                          64.6%; Score 42; DB 2; 70.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pseudotuberculosis IP 32953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SycE, yerA; putative yopE chaperone. ORFNames=pYV0024;
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                                                                                                                        Conservative
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
MOSZER I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Mucleic Acida Res. 29:2145-2153 (2001).
EMBL, AL445563; CAC13423.1; -.
PIR, B90543; B90543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                           the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McMurray A.A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z63386; CAA93432.2; -
FR; T27931; T27931.
WormBese; WBGene00014008; ZK596.3.
WormPep; ZK596.3; CE35705.
Hypothetical protein.
SEQUENCE 322 AA; 37172 MW; 224385DFB225AD80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.1%; Score 41; DB 2; Length 456
70.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 2; Indels
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SEQUENCE 456 AA; 53149 MW; 889D3356B34946FB5 CRC64;
                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-Ocr-2001 (TrEMBLrel. 18, Created)
01-Ocr-2001 (TrEMBLrel. 18, Last sequence update)
01-UJVN-2003 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein MYPU 2500.
OrderedLocusNames=MYPU_2500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.1%; Score 41; DB 2; 70.0%; Pred. No. 97;
        322 AA
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        PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                 Hypothetical protein ZK596.3.
ORFNames=ZK596.3;
                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nemi
investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0.
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Matches 7; Conservative
        PRELIMINARY;
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                                                                                                                                                                                       Caenorhabditis elegans
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Gasper J.S., Shiina T., Inoko H., Edwards S.V.;
"Songirid genomics: analysis of 45 kb upstream of a polymorphic Mhc
class II gene in red winged blackbirds (Agelaius phoeniceus).";
Genomics 75:26-34(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
STRAIN=21359325; PubMed=11466286.
DOI=10.1128/JD.193.6.4823-4838.2001;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; coursille P., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                         GOS 40.0005524; F.ATB binding; IEA.
GOS GO:0005524; F.ATB binding; IEA.
GO; GO:0004674; F.Protein serine/threonine kinase activity; IEA.
GO; GO:00046713; F.Protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P.Protein amino acid phosphorylation; IEA.
InterPro; IPR01009; Kinase like.
InterPro; IPR001299; Prot kinase.
InterPro; IPR0012290; Ser Ehr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.6%; Score 42; DB 2; Length 669; 66.7%; Pred. No. 1.4e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.1%; Score 41; DB 2; Length 98; 77.8%; Pred. No. 28; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 AA; 73710 MW; 5987154DCB1C441A CRC64;
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SEQUENCE 98 AA; 11692 MW; 929C71F938AC930A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 18, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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01-UTN-2003 (TrEMBLrel. 24, Last and
Predicted HD superfamily hydrolase.
OrderedLocusNames=CAC2809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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EMBL, AE007778; AAK80753.1; -.
PIR; P97245; P97245.
                                                                                                      EMBL; AF328738; AAK08500.1; -. HSSP; Q13153; 1F3M.
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Best Local Similarity 77.0
Best Accountage 77.0
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nes 6; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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                                                                                                                                                                                            STRAIN=ATCC 10895;
Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
Philippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 2; Length 458; Pred. No. 1.4e+02; 3; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084380; AAK52137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White O., Fraser C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         C4A99D20DCE2BE65 CRC64;
                                                                                                    Last annotation update)
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Last annotation update)
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    -!- SIMILARITY: Belongs to the cyclin family

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Interpro; IPR006670; Cyclin.
Interpro; IPR011028; Cyclin.like.
Interpro; IPR006671; Cyclin.li
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                                                                                                                                                                                                                                                                                                         Pfam; PF00134; Cyclin_N; 1.
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Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                 PRINTS; PR01415; ANKYRIN. SMART; SM00385; CYCLIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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19 NSWDISKTYP 28
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                                                                                                                                                                                                                                                                                                                                                           458 AA;
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                                                                                                                      ORFNames=ADR384W;
                                                                                                                                                                NCBI_TaxID=33169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                        Q758Z3;
05-JUL-2004
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05-JUL-2004
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatan N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=2053093; PubMed=11076861; DOI=10.1101/gr.152600;
Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
library, clone:1500010020 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-Kirrel3;
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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0
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                        1461 AA; 158781 MW; 9A89A942B561D9F2 CRC64;
                                                                                                                                                                                                                                                                              63.1%; Score 41; DB 2; Le 70.0%; Pred. No. 4.8e+02; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AA.
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
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                                                                           InterPro; IPR08940; Prenyl_trans.
Pfam; PF00560; LRR_1; 18.
Pfam; PF01535; PPR; 5.
                           LRR plant.
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TIGREAMS, TIGR00756; PPR; 5.
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                        IPR007090;
IPR002885;
IPR001611;
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Matches 7; Conserv
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   InterPro;
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                           InterPro;
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SEQUENCE FROM N.A.
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Arakawa T., Azaminca S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koaya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Fakahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Muramatsu M., Hayashizaki Y.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AK005197, BAB23877.1;
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yondda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Firkin Hiegrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA; 12221 MW; 1BC7884BF056C43B CRC64;
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GO:0005886; C:plasma membrane; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 111 AA; 12
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Search completed: April 28, 2005, 18:24:20 Job time : 73.1562 secs

Gaps

Query Match
62.3%; Score 40.5; DB 2; Length 111;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 1; Indels

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